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Sequence 18, Appl
Sequence 18, Appl
Sequence 9, Appli
Sequence 21, Appli
Sequence 27521, A
Sequence 32578, A
Sequence 1003, Ap
Sequence 1003, Ap
Sequence 299, App
Sequence 2926, App
Sequence 2926, App
Sequence 2143, A
                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/08672345C
Patent No. 594865B
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper and Dunham LLP
STREET: 1188 Avenue of the Americas
CITY: New York
STREET: New York
CITY: New York
COUNTRY: New York
CITY: Now York
COUNTRY: Now York
COUNTRY: Now York
COUNTRY: Now York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White: JOhn P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05.55/51400
TELERBONDINICATION INFORMATION:
TELEFAX: 212-378-0400
TELEFAX: 212-378-0400
TELEFAX: 212-391-0525
INFORMATION FOR EQUI INO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
US-09-029-348-14
US-08-563-825-18
US-09-500-821-18
US-09-508-188-18
US-09-586-881-8
US-09-248-608-18
US-09-289-578-9
US-09-252-991A-27521
US-09-252-991A-27521
US-09-252-991A-32578
US-09-252-991A-32578
US-09-252-991A-32578
US-09-252-991A-32578
US-09-252-991A-3143
US-09-252-991A-21143
US-09-252-991A-21143
US-09-252-991A-21143
US-09-252-991A-21143
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100.0%; Pred. No. 3e+05;
.ive 0; Mismatches 0;
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   MOLECULE TYPE: peptide
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Best Local Similarity
Matches 7; Conserv
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   US-08-672-345C-23
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     Sequence 97, Appl Sequence 97, Appl Sequence 6, Appli Sequence 7, Appli Sequence 104, App Sequence 112, App Sequence 20, Appl Sequence 20, Appli Sequence 5, Appli
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Sequence 26, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 97, Appli
Sequence 97, Appli
Sequence 98, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           September 30, 2004, 06:00:45; Search time 11.8644 Seconds (without alignments) 30.459 Million cell updates/sec
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Sequence
Sequence
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Section | Sect
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                                                                                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1 LMSTRAS 7
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Perfect score:
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                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                   Run on:
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Gaps

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APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                0575/51400
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; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERSONG/CKCT NUMBER: 0575/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Murinae gen. sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Murinae gen. sp
                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide US-08-672-345C-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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US-09-214-095D-23
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                Sequence 26, Application US/08672345C
Patent No. 5548658
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                CUDNIATE: 0000

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATCLASSIFICATION: 435
ATCLASSIFICATION: WINBER: 28,678
REFERENCY. UNMBER: 0575/51400
TELECHOMUNICATION INFORMATION:
TELECHOME: 212-278-0400
TELEFRAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
INFORMATING ACIDS
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/672,345C FILING PATE: 24-JUN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Cooper and Dunham Lip
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-672-345C-26
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100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 3e+05;
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                                                0; Indels
                                                                                                                                                                                                                                                                Sequence 23, Application US/09214095D
Patent No. 6280987
Fatent No. 6280987
Fatent No. 6280987
Fatent No. 6280987
Fatent No. 6280987
FILE SPERRICAT: Landry, Donald
FILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERRICATION TOWNER: US/09/214,095D
CURRENT RILING DATE: 1999-07-19
FOURTH FILING DATE: 1999-07-19
FOURTHARE: Patentin version 3.0
FOURTHARE: Patentin version 3.0
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Pred. No. 2;
0; Mismatches
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100.08;
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Best Local Similarity 100.
Matches 7; Conservative
   Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 LMSTRAS 61
                                                                                         55 LMSTRAS 61
                                                          1 LMSTRAS 7
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-672-345C-8
                                                                                                                                                    RESULT 8
US-08-672-345C-7
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                                                                                     RESULT 6
US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION:
; FILE REFERENCE: 51400-A-POT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT APPLICATION NUMBER: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 29
; TENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: COUNTRY: USA
ZIP: 10036
ZIP: 10036
ZIP: 10036
ZIP: 10037
ELOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARTEN: PC-DOS/MS-DOS
SOFTWARE: PARTEN: PC-DOS/MS-DOS
SOFTWARE: PARTEN: PC-DOS/MS-DOS
SOFTWARE: PARTEN: PC-DOS/MS-DOS
SOFTWARE: PARTENIN DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: Z4-UUN-1996
CLASSIFICATION: JOAN P.
NAME: White, John P.
REJESPHONE: JOAN P.
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08672345C
Petent No. 5548658
CENEAL INFORMATION:
CENEAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
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STATE: New York
COUNTRY: USA
                                 LMSTRAS
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US-08-672-345C-6
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                                                                                                                                                                                             Sequence 7, Application US/08672345C
| Sequence 7, Application US/08672345C
| Patent No. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. APPLICANT: Landry Donald, W. ITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF INVENTION: AND ADRESSES: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CIRET: New York STATE: New York COUNTRY: USA
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAD PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: 0575/51400
FREGISTATION NUMBER: 0575/51400
TELEPRIC OMMUNICATION INFORMATION:
TELEPRIC OMMUNICATION INFORMATION:
TELEPRIC 12-278-0400
TELEPRIC 212-278-0400
TELEPRIC 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
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Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPET and Dunham LLP
;
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Query Match
100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                           55 LMSTRAS 61
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CORRESPONDENCE: ADDRESS: ADDRESSEE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York; STATE: New York; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARES PATENTIN STILL SUBJECT SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 05.75/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10-278-0400
TELEPAX: 212-378-0400
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               NAME: White, John P.
RECISTRATION VUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0555/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein
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US-08-672-145C-98
is Sequence 98, Application US/08672345C
is Patent No. 594658
is GENERAL INFORMATION:
is APPLICANT: Landary Donald, W.
TITLE OP INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 1002
                                                                                                                                                                                                                                                 RESULT 11
US-08-672-345C-97

Sequence 97, Application US/08672345C

Patent No. 5946658

GENERAL INFORMATION:

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSE: Cooper and Dunham Lib

STREST: 1185 Avenue of the Americas

CITY: New York

STREST: 1185 Avenue of the Americas

COUNTRY: USA

ZIP: New York

COUNTRY: USA

ZIP: PODOS/MS-DOS

SOFTWARE: PRACATION DATE:

COMPUTER: IBM PC Compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENTE PATENTION NUMBER: US/08/672,345C

FILING DATE: 24-UUN-1996

CLASSIFICATION NUMBER: US/08/672,345C

FILING DATE: 24-UUN-1996

CLASSIFICATION NUMBER: US/08/672,345C

TELECOMMUNICATION INPORMATION:

REGISTRATION NUMBER: 28/678

REGISTRATION NUMBER: 0575/51400

TELEPRAN: 212-239-0525

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: AmbrENGES estimates

TYPE: amino acide

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TTELERAL IS ANINO ACIDE

TELENGTH: IS ANINO ACIDE

TELENGTH: IS ANINO ACIDE

TELERAL IS ACIDE

THE ACIDE
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LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
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Best Local Similarity 100.
Matches 7; Conservative
                                                           TYPE: PRT; ORGANISM: Murinae gen. sp
US-09-214-095D-7
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Matches 7; Conserv
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US-09-214-095D-8
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                     SEQ ID NO 7
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Patent No. 6280987

GENERAL INFORMATION:

TITLE CO INVENTION:

FILE REFERENCE:

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SEG ID NO 6

LENGTH: 113
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rc-Bos/Ms-DOS
SOFTWARE: Patentin Rc-Bos/Ms-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CRARACTERISTICS:
LENGTH: 113 amino acids
TOTAL STATEMENT IN ACIDS
THENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION:
APPLICANT: Landry, ANTI-COCAINE CATALYTIC ANTIBODY
TITLE BEPERRENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Murinae gen. sp.
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-214-095D-7
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US-09-214-095D-6
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100.0%; Score 31; DB 3; Length 113; 100.0%; Pred. No. 2; 0; Indels ive 0; Mismatches 0; Indels
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Sequence 8, Application US/09214095D

Patent No. 6280987

GENERAL INPORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REPEBRICE: 51400-A-ECT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: September 30, 2004, 06:38:16 Job time : 12.8644 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 30, 2004, 05:55:56; Search time 9.76271 Seconds (without alignments) 88.677 Million cell updates/sec Run on:

US-09-674-716B-7 48 1 QQLVEYPFT 9 Title: Perfect score: Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	ubiquinol-cytochro	kappa	g kappa chain V	kappa	g kappa	probable calmoduli	Ig lambda chain V	phosphatidyl synth	Ig kappa chain pre	hypothetical prote	mesJ protein VC224	hypothetical prote	ical	hypothetical prote	Ig kappa chain V r	Ig kappa chain V r	lysozyme (EC 3.2.1	hypothetical prote	glycerol-3-phospha	ubiquinol-cytochro	B. subtilis YxiO p		ic-nucl	ong-chain-fa	-chain-f	-chain-f	-chain-f	ine-tRNA	hypothetical prote
SUMMARIES		C42622	6	_	KVMS51	KVMS67	A85363	836277	T38148	B29775	A86371	D82100	D89903	S76367	T01906	126317	D26317	AD3322	D83163	D90527	S41834	AG1614	A11251	34	158	9094	F85791	2072	7048	2113
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RESULT 2
G30538
Ig kappa chain V region (253.15E2) - mouse (fragment)
Ig kappa chain V region (253.15E2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996
C;Accession: G30538
R;Clafiin, J.L.; Berry, J.

30	ataxin-1 - human hypothetical prote hemoglobin delta c 1g light chain V r 1g kappa chain pre lg kappa chain protention protent of probable 2-hydroxy probable 2-hydroxy probable dicarboxy biliverdin reducta biliverdin reducta biliverdin reducta hypothetical prote conserved hypothet probable bHLH DNA-		<pre>cytochrome b - honeybee mitochondrion /bee) -1994 #text_change 03-Jun-2002</pre>	of honeybee mitochondrial DNA. PMID:1533894	neybee Apis mellifera: complete sequence and ç PMID:8417993	PIDN:AAB96809.1; PID:9552449	logy; cytochrome b6 homology; plastoquinol- heme; iron; metalloprotein; mitochondrion; eductase 17K protein homology <17K> ligands) (low potential) #status predicted ligands) (high potential) #status predicted	DB 2; Length 383; .55; es 0; Indels 0; Gaps 0;	
33 68.8 816 33 68.8 816 33 68.8 817 33 33 68.8 817 33 33 66.7 112 34 32 66.7 112 35 66.7 112 313 66.7 112 3		AL	se (EC 1.10.2.2) cyt nellifera (honeybee) revision 09-Sep-1994	992 ATPase genes of D:92261310; PMI	ome of the honeybee (D:93114603; PMID:8	3; NID:9336279;	tochrome b homctron transfer; tomology <cb6> homology <cb6> plastocyanin re on (His) (axial on (His) (axial</cb6></cb6>	Score 43; Pred. No. 0 2; Mismatch	
33 68.8 31 33 68.8 32 32 66.7 34 32 66.7 35 32 66.7 36 32 66.7 39 32 66.7 41 32 66.7 42 32 66.7 43 32 66.7 44 32 66.7 43 32 66.7 44 32 66.7 44 32 66.7 45 32 66.7 48 32 66.7 48 32 66.7 48 32 66.7 48 32 66.7 49 32 66.7 40 41 41 41 41 41 41 41 41 41 41 41 41 41			reducta n Apis n quence	2971 r, Y.C. -482, 1 b and b	M87052 r, Y.C. 993 ial gen 960; MU	L:L0617	me b; c; in; elecrome b l rome b l rome b6 oquinol heme ir	89.6 77.8 vative	ο κ 4
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RESULT CASSOL AND AND ACCESS AND			lol-cytoc es: mito ty: ligu 09-Sep-	sion: C4 er, R.H. ol. Evol : The Cy ence num	us: prelliule type lues: 1-3 l-referen er, R.H. is 133, 9 i: The mi ence num	us: preli ule type lues: 1-3 i-referen	ic code: family: rds: chr: 0/Domain: 1/Domain: 4/Bindin:	Match Local Si	1 41
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	RESULT C42622	ubiquir C;Speci A;Varie C;Date:	C, Acces R, Crozi Mol. Bi A, Title A, Refer A, Acces	A, Statu A, Molec A, Resid A, Crosi R, Crozi Genetic A, Title A, Refer A, Acces	A;Statu A;Molec A;Resid A;Cross C;Genet	A, Genon A, Genet C, Super C, Keywc F, 14-34 F, 14-21 F, 23-3	Query Best Match	B &

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RESULT 3 KVMS16

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C,Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: A85363
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 17/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp main disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into last C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aritle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Reference number: A85363
A;Accession: A85363
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <STO>
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                                                                                                                                                                                                                                                                                                                       Tile Rappa chain precursor V region (VK167) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000 C;Accession: A01909 U.

R;Selsing, E.; Storb, U.
Cell 25, 47-58, 1981 A;Tile: Somatic mutation of immunoglobulin light-chain variable-region genes. A;Reference number: A01909; MUID:82002223; PMID:6791832
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Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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F21-120/Product: Ig kappa chain V region (VK167) #status predicted <WAT>
F;36-115/Domain: immunoglobulin homology <IMM>
F;43-113/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable calmodulin-binding protein [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2; Length 467;
Pred. No. 12;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A01909
A;Molecule type: DNA
A;Residues: 1-120 <SEL>
A;Note: the sequence was determined from the germline gene C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.18;
75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                     94 QQLVEYPLT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             α
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RyAppollay.

RyAppollay.

Mol. Immunol. 17, 711-718, 1980

Aprile: Amino acid sequence of the light chain variable region of M511, a phosphorylche Aprile: amino acid sequence of the light chain variable region of M511, a phosphorylche Apecession: A01910

Apocession: A01910

Apocession: A01910

Apocession: A01910

Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

Comment: An amunoglobulin hererotectramer submit consists of two identical light (kap hain disulfide bonds. In some cases, such as Igh and IgM, the submits associate into la constantine immunoglobulin V region; immunoglobulin homology
J. Immunol. 141, 4012-4019, 1988

A; Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A; Afeference number: A30534; MUID:89035545; PMID:3141511

A; Accession: G30538
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-74 < CLA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C;Accession: A01910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.5%; Score 42; DB 1; Length 112; Best Local Similarity 88.9%; Pred. No. 0.24; Aatches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 42; DB 2; Length 74;
88.9%; Pred. No. 0.15;
tive 0; Mismatches 1; Indels
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Best Local Similarity 88.9
Matches 8; Conservative
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F;36-115/Domain: immunoglobulin homology <IMM>

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Cipecies: Arabidopsis thaliana (mouse-ear cress)
Cipace: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
Cipaces on a 86371 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Ansure 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Feference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mesJ protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
C;Accession: D82100
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
C;Accession: Datableva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833; PMID: 109552301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA*
A;Residues: 1-440 cHEI.
A;Cross-references: GB:AE004296; GB:AE003852; NID:g9656799; PIDN:AAF95386.1; GSFDB:GN0012
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A;Accession: A6671
A;Catus: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <STO>
A;Coss-references: GB:AE005172; NID:g4056452; PIDN:AAC98025.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                      Query Match 72.9%; Score 35; DB 2; Length 120; Best Local Similarity 85.7%; Pred. No. 7.2; Matches 6; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 480
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                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F508.25 - Arabidopsis thaliana
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85.7%; Pred. No. 31;
iive 1; Mismatches (
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C,Superfamily: Cell cycle protein MesJ
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Matches 6; Conservative
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114 QQIVEYP 120
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269 QLLEYPF 275
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Rightifichs, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993

M.Title: Human anti-self antibodies with high specificity from phage display libraries. A; Reference number: S36256; MulD:93178448; PMID:7679990

A; Reference number: S36256; MulD:93178448; PMID:7679990

A; Recession: S36277

A; Retains preliminary; nucleic acid sequence not shown

A; Residues: 1-108 cGRI>
A; Residues: 1-108 cGRI>
C; Residues: 1-108 cGRI>
C; Reperfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology < INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dhosphatidyl synthase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Spacesoion: 13848
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, September 1997
A;Reference number: Z21774
A;Reference number: Z21774
A;Recession: T38148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T38148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-570 ePBA-
A;Residues: 1-570 ePBA-
A;Residues: 1-570 ePBA-
A;Residues: EMBL:299295; PIDN:CAB16578.1; GSPDB:GN00066; SPDB:SPAC22A12.08C
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <8IG>
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Pred. No. 23;
1; Mismatches
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A.Gene: SPDB:SPAC22A12.08c
A.Map Dosition: 1
A.Introns: 43/2; 62/2; 227/2; 483/1
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Best Local Similarity 66.7-
کرد 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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A;Description: The sequence of A. thaliana T12H20.
A;Reference number: 214453
A;Accession: T01906
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DA
A;Residues: 1-1074 <COT>
A;Cross-references: EMBL:AF080119; NID:g3600029; PID:g3600033
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.4
Matches 5; Conservative
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A;Accession: S76367
A;Accession: S76367
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-722 <KAN>
A;Residues: 1-722 <KAN>
A;Cross=references: EMBL:D64000; GB:AB001339; NID:g1001464; PIDN:BAA10219.1; PID:g100159
A;Cross=references: EMBL:D64000 dB:AB001339; NID:g1001464; PIDN:BAA10219.1; PID:g100159
C;Superfamily: glycine-tRNA ligase beta chain
                                                                                                                                                                                                                                                                                                                                                              C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Darcession: S76367
C;Accession: S76367
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A,Gene: SA1131
C,Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-586 «XUR»
A;Cross-references: GB:BA000018; PID:g13701089; PIDN:BAB42384.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                 hypothetical protein SA1131 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 77;
1; Mismatches 0; Indels
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Best Local Similarity 85.7%;
Matches 6; Conservative
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254 EQLVEYP 260
                                   10 QQLARYPF 17
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Best Local Similarity
Matches 6; Conserv
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A; Wolecule type: DNA
A; Residues: 1-112 < CATA
A; Experimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This sequence was isolated from a hybridoma protein that binds influenza virus he
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: hererotetramer; immunoglobulin
P;16-95/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region (H158-89H4) - mouse
(ig kappa chain V region (H158-89H4) - mouse
(igpecies: Mus musculus (house mouse)
(cjpecies: Musculus (house mouse)
(cjpecies: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
(cjpecies: 15-Dec-1988 #text
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95 QHLEYPFT 102
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853 ELIEYPF 859
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Gaps

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Length 1074;

70.8%; Score 34; DB 2; Length 107 71.4%; Pred. No. 1.2e+02; .ive 2; Mismatches 0; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141681 seqs, 52070155 residues
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CYS_MOUSE
CYS_AKOTE
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CYS_BLEUG
CYS_THOIS
SYGGS_CONTINE
CYS_THOIS
SYGGS_CONTINE
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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No.
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Q9cmb1 pasteurella P82047 cervus nipp	P82045 cervus nipp P82049 cervus nipp P82048 cervus nipp	P82046 cervus nipp Q9tlu8 cyanidium C P05332 bacillus li	Q57931 methanococc P52708 sorghum bic Q94zk8 cebus albif	
MSRB PASMU CYB CERNN	CYB_CERNT CYB_CERNA CYB_CERNH	CYB_CERNP RR5_CYACA YP20 BACLI	TYSY_METJA HNLS_SORBI CYB_CEBAL	CYB_ALCAA
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# ALIGNMENTS

SULT B_AP C	P34845; 01-FEB-1994 (Rel. 28, Created)						OX NCBL TAXID=7469; RN [1]			Crozier R.H., Crozier Y.C.;	And Siol. Biol. Byol. 9:474-482(1992).			RX MEDLINE=93114603; PubMed=8417993;	"The	sequence and genome organization.";	n genetics 133:9/-11/(1993). C -!- FUNCTION: Component of the ubjauinol-cytochrome c reductase	complex (complex III or cytochrome b-cl complex), which is		-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or	CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH CC or b566) is high-potential and absorbs at about 566 (By	similarity).	-!- SUBUNIT: The main	-!- SIMILARITY: Belongs to the cytochrome b f	This SWISS-PROT entry	between the Swiss Institute of Bioinformatics and the EMBI	the European Bioinformatics Institute. There are no restriction	use by non-promit modified and this sta	entities requires a license agreement (See http://www.isb-sib.ch	or send an email	EMBL; L06178; AAB96809.1; EMBL; M87052; -; NOT_ANNOTAT	PIR; C42622; C42622. InterPro: IPR005798;	Inte	
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Thu Sep 30 13:18:56 2004

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Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_B.HEME; 1.
PROSITE; PS00193; CYTOCHROME_B.D; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                            MEDLINE-79000273; PubMed=99160;
Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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0
                                                                                                                                 ;
0
                                                 85 IRON 1 (HEME B562 AXIAL LIGAND).
99 IRON 2 (HEME B566 AXIAL LIGAND).
184 IRON 1 (HEME B562 AXIAL LIGAND).
198 IRON 2 (HEME B566 AXIAL LIGAND).
45256 MW; A140A05E6053C2D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112; 800re 42; DB 1; Length 112; 112; 88.9%; Pred. No. 0.17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-2
                                                                                                          Score 43; DB 1; Length 383;
Pred. No. 0.36;
                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12349 MW; A58EDFD6404B9726 CRC64;
                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region MOPC 167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AA.
                                                                                                                                                                                                                         112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-1
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SMARI; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
1 23 r
                                                                                                              89.6%;
                                                                                                    Query Match
Best Local Similarity 77.8.
Conservative
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341 KQLIEYPFT, 349
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103
103
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112 AA;
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184
198
383 AA;
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nes 8; Conserv
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KV2A_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] __
SEQUENCE FROM N.A.
MEDILINE-82002223; PubMed=6791832;
Selsing E., Storb U.;
"Somatic mutation of immunoglobulin light-chain variable-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42, DB 1; Length 113;
Pred. No. 0.17;
0, Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                                                                                                                                                                                                                                                              12496 MW; EFB0DC4DA2BD3450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PO1627;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18-Appa chain V-II region VKappal67 precursor.
Mus musculus (Mouse).
         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region MOPC 511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-2
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                                                                                                                                MEDLINE=81052016; PubMed=6776396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 COLVEYPLT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σι
                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 25:47-58(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QOLVEYPFT
                                                                                               NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV2B_MOUSE
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SEQUENCE
                                                                                                                       SEQUENCE.
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Mitochondrion.
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VARIANT
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CYB AKOTB
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STRAIN=Isolate MVZ 173073, Isolate MVZ 173074, Isolate MVZ 173083, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith M.F., Patton J.L.;
"The diversification of South American murid rodents: evidence from
mitochondrial DMA sequence data for the akodontine tribe.";
Bjol. J. Linn. Soc. Lond. 50:149-177 (1993).
                                                                                                                                                                                                                                          IG KAPPA CHAIN V-II REGION VKAPPA167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith M.F., Patton J.L.,

"Variation in mitochondrial cytochrome b sequence in natural
populations of South American akodontine rodents (Muridae:
Sigmodontinae).",

Mol. Biol. Bvol. 8:85-103(1991).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-cl complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                     FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-3. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%; Score 37; DB 1; Length 120; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith M.F.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       63BB571F0E4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
Cytochrome b.
MTCYB OR COB CYTB.
MTCYB OR COB CYTB.
Micochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 AA
                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-3
            EMBL, J00562; AAA39032.1; --
EMBL, K02415; AAA39051.1; --
EMBLP, A0190; KNMS67.
HSSP: P60362; INTL.
INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR003596; Ig_v.
Fram: PP00047; ig; 1.
SWART; SM00466; IGy; 1.
FROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91163325; PubMed=2002767;
                                                                                                                                                                                                                         120. IG
43 FR
59 CO
74 FR
81 CO
113 CO
113 CO
13280 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100....
For 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 QQLVEYP 120
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r-
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 COLVEYP
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P21715;
                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON 1 (HEME BS62 AXIAL LIGAND).
IRON 2 (HEME BS66 AXIAL LIGAND).
IRON 1 (HEME BS66 AXIAL LIGAND).
IRON 2 (HEWE BS66 AXIAL LIGAND).
V -> I (in isolates MVZ 173083 and MVZ 173084).
T -> A (in isolates MVZ 173083 and MVZ 173084).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Isolate UMMZ 133965; TISSUE=Liver;
Smith M.F., Patton J.L.;
"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or E or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                          EMBL; M35714; AAA16998.2; ALT_TERM.
EMBL; M35715; AAA31630.1; --
EMBL; M35715; AAA31620.1; --
EMBL; M35716; AAA31620.1; --
InterPro; IPR005799; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b \( \bar{C}_{1} \) 1.
Pfam; PF00033; cytochrome_b \( \bar{C}_{2} \) 1.
PROSITE; PS00193; cytochrome_B \( \bar{O}_{2} \) 1.
PROSITE; PS00192; CYTOCHROME \( \bar{D}_{2} \) 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                 cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 379; Pred. No. 9.2;
                                                             similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytocomposition of and the Rieske protein (By similarity)
-!- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F9F012A46671D59A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-267 FROM N.A.
STRAIN=Isolate UMMZ 133965; TISSUE=Liver;
Smith M.F., Patton J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome b.
MTCYB OR COB OR CYTB.
Akodon toba (Chaco grass mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 AA; 42529 MW;
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87.5%;
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Best Local Similarity 87.55,
7; Conservative
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Biol. J. Linn. Soc. Lond. 50:149-177(1993)
                                                                                                               MEDLINE=91163325; PubMed=2002767;
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                                       SEQUENCE OF 1-133 FROM N.A.
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                              Isolate MVZ 174054;
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VARIANT
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       Seprentia
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                                                                                                                                         L or
(or BH
   Gaps
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Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
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Pred. No. 9.2;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smitn m.r.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U03527; AAD12554.2; -.
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam, PF00032; cytochrome_b_C, 1.
Pfam; PF00033; cytochrome_b_C, 1.
PROSITE; PS00192; CYTOCHROWE_B_HEME; 1.
PROSITE; PS00193; CYTOCHROWE_B_CO; 1.
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196 196 IF
379 AA; 42689 MW;
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87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
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CYB_AKOTO
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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IRON 2 (HEME BS66 AXIAL LIGAND).
IRON 1 (HEME BS66 AXIAL LIGAND).
IRON 2 (HEME BS66 AXIAL LIGAND).
V -> A (in isolates MVZ 174053 and MVZ 174054).
V -> I (in isolates MVZ 174053 and MVZ 174054).
STRAIN=Isolate MVZ 171720, Isolate MVZ 171721, Isolate MVZ 174053, and
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EMBL, M35701; AAA31624.1; -.
EMBL, M35702; AAA31624.1; -.
EMBL, M35702; AAA31624.1; -.
EMBL, M35705; G29725.
InterPro; IPR065798; Cytb_b6_C.
InterPro; IPR065798; Cytb_b6_C.
InterPro; IPR06379; Cytb_b6_N.
Pfam; PF00032; Cytochrome_b_C; 1.
Pfam; PF00032; Cytochrome_b_N; 1.
PROSTITE; PS00193; CYTOCHROME_B_MS; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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                                                                                                                                                Smith M.F., Patton J.L.;
"Variation in mitochondrial cytochrome b sequence in natural
"Variation in mitochondrial cytochrome b sequence in natural
populations of South American akodontine rodents (Muridae:
Sigmodontinae)."

Mol. Biol. Bvol. 8:88-103(1991).

-!-FINCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similariby).

-!-COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
bsc2) is low-potential and absorbs at about 562, and heme 2 (or in
bsc2) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cytochrome b.
MTCM B R COB OR CYTB.
Delomys sublineatus (Pallid Atlantic forest rat).
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STRAIN=Isolate MVZ 173975;
Smith M.F., Patton J.L.;
Smith M.F., Patton J.L.;
"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
J. Mammal. Evol. 6:189-1281(1999).

J. Mammal. Evol. 6:189-1281(1999).

-!- FUNCTION: Complex III or cytochrome b-cl complex), which is a complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 562, and heme 2 (or BH or Similarity).

-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
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STRAIN=Isolate MVZ 181999;
Smith M.F., Patton J.L.;
Smith M.F., Patton J.L.;
"bylogenetic relationships and the radiation of sigmodontine rodents in South America: Evidence from cytochrome b.";
J. Mammal. Evol. 6:69-128(1999).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF108698; AAD45480.1; -.
InterPro; IPR005798; Cytb b6_C.
InterPro; IPR005797; Cytb b6_C.
InterPro; IPR00379; Cytochrome b_C; I.
Pfam; PF00032; Cytochrome b_N; 1.
PROSITE; PS00192; CYTOCHROME B_D6; 1.
PROSITE; PS00193; CYTOCHROME B_Q0; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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TRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Matches 7; Conservative
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380 AA;
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InterPro: IPR005798; Cytb b6 C.
InterPro: IPR005797; Cytb b6 C.
Pfam; PF00032; cytochrome b C; 1.
Pfam; PF00033; cytochrome b N; 1.
PROSTIE; PF00192; CYTOCHROME B HEME; 1.
PROSTIE; PS00193; CYTOCHROME B Q0; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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            Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
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97 97 IRON 2 (HEME BS66 AXIAL LICAND).
182 182 182 IRON 1 (HEME BS62 AXIAL LICAND).
196 196 IRON 2 (HEME BS66 AXIAL LICAND).
380 AA; 42820 MW; DE9AOEDA1D4AE785 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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87.5%;
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Best Local Similarity 8/...
7; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                             NCBI_TaxID=89131;
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Smith M.F., Patton J.L.;
Smith M.F., Patton J.L.;
Smith M.F., Patton J.L.;
Smith America: evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
-!- FUOTION: Component of the ubiquinol-cytochrome c reductase complex (complex (complex III or cytochrome b.c.l complex), which is a respiratory chain that generates an electrochemical potential complex (A AFP Synthesis (By similarity).
-!- COTACTOR: Binds two heme groups non-covalently. Heme I (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or Br or b566).
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005798; Cytb_b6 C.
InterPro; IPR005797; Cytb_b6 N.
Pfam; PF00032; cytochrome_b C; 1.
Pfam; PF00033; cytochrome_b N; 1.
PROSITE; PS00192; CYTOCHROWE B HEME; 1.
PROSITE; PS00193; CYTOCHROWE B DO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity). COFACTOR: Binds two hem groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                          similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
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SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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97 97 IRC
182 182 IRC
196 196 IRC
380 AA; 42941 MW; D
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87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
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MTCYB OR COB OR CYTB.
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NCBI_TaxID=89122;
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METAL
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CYB_AULMI
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Isolate MVZ 182670;

A SMATH M.F. Patton J.L.;

A SMATH M.F. Patton J.L.;

A SMATH M.F. Soluth America: evidence from cytochrome b.";

J. Mammal. Evol. 6:89-128(1999).

J. Mammal. Evol. 6:89-128(1999).

C :- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a complex of thain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

CC coupled to ATP synthesis (By similarity).
                                                                                                                                                                                                                         EMBL, AF108690; AAD45472.1; -.
InterPro; IPR005798; Cytb b6_C.
InterPro; IPR005799; Cytb b6_C.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSTIE; PS00192; CYTOCHROME_B_BIEME; 1.
MACOCHROME PROSTIE; PS00193; CYTOCHROME B_DC; 1.
Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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--- SUBNUT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
--- SIMILARITY: Belongs to the cytochrome b family.
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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
7DB6BC93338DA2C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.0%; Score 36; DB 1; Length 381; Best Local Similarity 87.5%; Pred. No. 9.2; Matches 7; Conservative 0; Mismatches 1; Indels
-!- SIMILARITY: Belongs to the cytochrome b family.
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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MTCYB OR COB OR CYTB.
Eligmodoutia morgani (Morgan's gerbil mouse).
Mitochondrion.
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97 97 IRC
182 182 IRC
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381 AA; 43093 MW; 7
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or send an email to license@isb-sib.ch).
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                                             EMBL, AF108691, AAD45473.1; -.
InterPro; IPR005798; Cytb b6 C.
PitarPro; IPR005797, Cytb.b6 N.
Pfam; PR00032; cytchrone b C; 1.
Pfam; PR00033; cytchrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEMB; 1.
PROSITE; PS00192; CYTOCHROME B DO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steppan S.J.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL c b562) is low-potential and absorbs at about 562, and heme 2 (or b b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Phylogenetic relationships and species limits within Phyllotis (Rodentia: Sigmodontinae): concordance between mtDNA sequence and morphology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
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                                                                                                                                                                                                                                                                             43035 MW; D43D298BEB594E6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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381 AA;
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Q9ZZF6;
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InterPro; IPR05798; Cytb b6_C.
InterPro; IPR005798; Cytb b6_C.
Pfam; PF00032; cytochrome_b \( \brice{c}_i \) 1.
Pfam; PF00032; cytochrome_b \( \brice{c}_i \) 1.
PROSITE; PS00192; CYTOCHROME_B HERE; 1.
PROSITE; PS00193; CYTOCHROME_B \( \brice{c}_i \) 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
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IRON 2 (HEME BS66 AXIAL LIGAND)
IRON 1 (HEME BS62 AXIAL LIGAND)
IRON 2 (HEME BS66 AXIAL LIGAND)
                                                                                                                                                                                                                         Score 36; DB 1; Length 381; Pred. No. 9.2;
                                                                                                                                                                                                                                                       1; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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0; Mismatches
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InterPro; IPR005799; CYtb b6 C.
InterPro; IPR00579; CYtb b6 N.
Pfam; PF00032; cytochrome b C; 1.
Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00193; CYTOCHROME B HEME; 1.
PROSITE; PS00193; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome b.
MTCYB OR COB OR CYTB.
Sigmodon hispidus (Hispid cotton rat).
Mitochondrion.
                                                                                                                                      83 83 IR
97 97 IR
182 182 IR
196 196 IR
381 AA; 43076 MW; (
                                                                                                                                                                                                                         75.0%;
87.5%;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                           341 OPVEYPFT 348
                                                                                                                                                                                                                                                                                2 QLVEYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=42415;
                                                                                                                                                                                                                                                                                                                                                                                  SIGHI
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SEQUENCE
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CYB_SIGHI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Phylogenetic relationships and the radiation of sigmodontine rodents "phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b563) is low-potential and absorbs at about 562, and heme 2 (or BH or b563) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF108673; AAD45455.1; -.
InterPro; IPR065798; Cytb_b6_C.
InterPro; IPR065799; Cytb_b6_N.
Pfam; PF00032; Cytochrome_b_C; 1.
Pfam; PF00033; Cytochrome_b_N: 1.
PROSITE; PS00192; CYTOCHROME_B_D: 1.
PROSITE; PS00193; CYTOCHROME_B_DO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                   Gaps
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,

    similarity).
    SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
    SIMILARITY: Belongs to the cytochrome b family.

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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
3E1993B27E14502A CRC64;
                                                        IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
                                                                                                                                                                                                                                 'Match 75.0%; Score 36; DB 1; Length 381; Local Similarity 87.5%; Pred. No. 9.2; les 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                  0472259421B38284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          daphne (Daphne's oldfield mouse).
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STRAIN=Isolate MVZ 171502;
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Query Match
Best Local Similarity 87.5%; Score 36; DB 1; Length 381;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVEXPPT 9
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Db 341 QEVEXPFT 348

Search completed: September 30, 2004, 06:01:18
Job time: 7.49153 secs
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Run on:

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Q9xnw3 thipidomys
Q9mnt3 tapecomys p
Q94uz9 microtus gu
Q9mt5 andalgalomy
Q94v01 microtus oa
Q9mnt0 graomys dom
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Calvetre D., Arias M.C.;

Calvetre D., Calvetre
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saimiri sci
saimiri sci
thomasomys
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Q9mhf9 microtus lo
Q34853 lenoxus api
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CYtochrome b.
CYTE.
Mitochondrion.
Mitochondrio
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Pred. No. 5.2;
2; Mismatches 0; Indels
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Matches 6; Conservative
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Mitochondrion
SEQUENCE
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Q87rr4 vibrio para
Q8444 arabidopsis
C65550 arabidopsis
C65550 arabidopsis
Q8h816 oryza sativ
Q9b313 neoceracdu
Q9mp34 bothriomyrm
Q9xnv8 delomys dor
28m293 oxymycterus
3xnv0 reithromyrm
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Q9xnx5 6
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 QQLVEYPFT 9
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Maximum DB seq length: 200000000
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Result 80.

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Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0000160; F:DNA binding; IEA.
GO; GO:0000160; F:two-component response regulator activity; IEA.
GO; GO:0000160; F:two-component signal transduction system (p. . .; IEA.
InterPro; IPR01867; Trans_reg_C.
Pfam; PF00486; trans_reg_C.
Hypothetical protein; Complete proteome.
SEQUENCE 506 AA; 57784 MW; 7B566E691D449223 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Chen H.,
Chauk C.J. Bowser L., Japashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae. Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; et eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                               MEDLINE-22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
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0
                                                                                                                                                                     Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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Last annotation update)
                                                                                                                     Last sequence update)
Last annotation update)
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01-WAR-2002 (TrEMBLEEL. 20, Last sequenc
01-CCT-2002 (TrEMBLEEL). 22, Last annotat
Putative calmodulin-binding protein.
AT4G31000/F6118.90 OR AT4G31000.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=RIMD 2210633 / Serotype O3:K6;
                                                                                                        Created)
                                                                                                   01-JUN-2003 (TrEMBLrel, 24, 01-JUN-2003 (TrEMBLrel, 24, 01-OCT-2003 (TrEMBLrel, 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 77.8
Matches 7; Conservative
                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 QQQVEYPYT 217
              311 OMIEYPFT 318
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                                                                                                                                                                                                                 NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q8W454;
                                                                                            Q87RR4;
                                                                             087RR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                     RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             065550,
01-AUG-1998 (TERMELrel. 07, Created)
01-AUG-1998 (TERMELrel. 07, Last sequence update)
01-TON-2003 (TERMELrel. 24, Last annotation update)
Putative calmodulin-binding protein.
F6118-90 OR AT4G310Ana (Mouse-ear cress).
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids, Celrosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TAXID=3702,
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Ol.WAR-2003 (TEMBLrel. 23, Last sequence update)
Ol-OCT-2003 (TEMBLrel. 25, Last annotation update)
Hypotherical protein.
OJ1743A09.11.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryzaa.
NCBL_TAXID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Mewes H.W., Mayer K., Schueller C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX062856; AAL32934.1; -- SEQUENCE 278 AA. 31406 MW; 398DCFB65C85A836 CRC64;
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                                                                                                                                                                                                                                       77.1%; Score 37; DB 10; Length 278; 75.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitred (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO2198; CAA18193.1; --
EMBL; ALI01578; CAB79818.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A85363; A85363.
SEQUENCE 467 AA; 52831 MW; 4DB1FB318D553B3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 AA.
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PRELIMINARY;
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                                                                                                    OPVEYPFT 34
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nes 6; Conserv
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                                    QLVEYPFT
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NON TER 1
SEQUENCE 247
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                                                                                                                                                                                                                                                                                                              Q9MP34;
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a living fossil?";

conserv. Genet. (0.0010.).

COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A

COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A

EXESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY)

C --- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY

C --- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY

C --- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY

C --- SUMILARITY: BELONGS TO FC COMPLEX B-C1 ARE: CYTOCHROME B,

C CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

C STAILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

DR GO; GO:0016021); C:integral to membrane; IEA.

DR GO; GO:0005739; C:intcopnodrial electron transport chain; IEA.

DR GO; GO:0005739; C:intcochondrian; IEA.

DR GO; GO:0006118; P:electron transport; IEA.
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Frentiu F., Ovenden J.R., Street R.,
"Australian lungfish (Neoceratodus forsteri) have low genetic
diversity at allozyme and mitochondrial loci: A conservation alert for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00032; cytochrome \overline{b} \overline{C}_i 1. Electron transport; Heme; Respiratory chain; Transmembrane; Transport; Mitochondrion.
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Dipnol, Ceratodontiformes, Ceratodontidae, Neoceratodus.
NCBI_TaxID=7892,
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[1] SEQUENCE FROM N.A. Soderlund C., Kim H.-R., Rambo T., Saski C., Currie J., Collura K.;
                                                                                                                              "Rice Genomic Sequence.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ACIOSS64; AMNOS331.1. -.
GO; GO:00016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001810; P-box.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS0181; PBOX; 1.
PROSITE; PS0181; PBOX; 1.
Hypothetical procein.
SEQUENCE 609 AA; 68105 MW; AEA195731E0BF07C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 10; Length 609;
Pred. No. 40;
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Pred. No. 8.1;
0; Mismatches 1; Indels
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoceratodus forsteri (Australian lungfish).
Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.18;
77.88;
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84 AA; 9673 MW;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Matches 7; Conservative
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COBB13
AC COBB3
AC COBB COLUMN
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ACTIONAL MANUAL CARAINAL CASA AND CONTRAINAL CASA MANUAL CASA MANU
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                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
Formicidae; Dolichoderinae; Bothriomyrmex.
NCBI_TaxID=121499;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1993 (TrEMBLrel. 24, Last annotation update)
Cytochrome B (Fragment).
CYTS.
Delomys dorsalis (striped Atlantic forest rat).
                                                                               Created)
Last sequence update)
Last annotation update)
    247 AA
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PRT;
                                                                               01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24, Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                Bothriomyrmex meridionalis.
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2 QLVEYPFT 9
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NON TER
NON TER
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Q9XNV0
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                                                                                                                                                                      RA Smith M.F., Patton J.L.,

RA Smith M.F., Patton J.L.,

RT Subtobence From N.L.,

RT "Phylogenetic relationships and the radiation of sigmodontine rodents

In South America: Evidence from cytochrome b.",

L. Mammal. Evol. 6:89-128 (1999)

C. -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C. -LOPACTOR: TWO HEME SROUPS (BSCS AND BSSG) WHICH ARE NOT COVALENTLY

C. -LOPACTOR: TWO HEME ROUPS (BSC) WHICH ARE NOT COVALENTLY

C. -LOPACTOR: TWO HEME STOUPS (BSCS AND BSSG) WHICH ARE NOT COVALENTLY

C. -L. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

C. -L. SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. -L. SINILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. -L. SINILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. SO GO:0016211; SINILARITY: LAND THE CYTOCHROME B FAMILY.

C. SINILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

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C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUNITY OF COMPLEX BROWNED B FAMILY.

C. SINILARITY: THE MAIN SUBUN
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J. Mammal. 83:408-420 (2002).

J. Mammal. 83:408-420 (2002).

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROWE C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERALIES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY)
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                           Chordata, Craniata, Vertebrata; Buteleostomi;
Rodentia, Sciurognathi, Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 352
352 AA; 39631 MW; AA408DB627140D6C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2002 (TrEMBLrel, 22, 01-JUN-2003 (TrEMBLrel, 24, Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 87.5
les 7; Conservative
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                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QLVEYPFT 9
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                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=89119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
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                                                                                   Delomys.
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EXECUTION FOR THE PROPERTY OF THE UNIQUENCE FROM N.E. PAULON OF SUBMODUTION OF THE UBIQUINOL-CYTCCHROME C REDUCTASE COMPLEX (COMPLEX (COMP
BOUND TO THE PROTEIN (BY SIMILARITY).

C. 1- SUBJUNT: THE MAIN SUBNINTS OF CONFLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

C. 1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

BMBL; AF454772; AAM33839.1; -.

GO; GO: O106121; C: integral to membrane; IEA.

GO; GO: 0106739; C: mitochondrion; IEA.

GO; GO: 0106810; P: transport; IEA.

RO; GO: 0006810; P: transport; IEA.

RECTION LEARNE BENDIS; CYTOCHROME B HEME; 1.

RECTION LEARNE ROSOLS; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 371
371 AA; 41657 MW; 2BOACGBAEB2DED16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 AA.
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Best Local Similarity 87.5
Matches 7; Conservative
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Last sequence update) Last annotation update)

Created)

PRELIMINARY;

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Oxymycterus amazonicus.
Mitochondrion.
Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Bukaryota, Eutheria; Rodentia; Sciurognathi; Muridae, Sigmodontinae;
Oxymycterus.
NCBI_TaxID=196085;
                                                                                              01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24, Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q9TGL4;
                                                                         QBM2A0;
                                              QBM2A0
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Q9TGL4
RESULT 12
                     8
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SHALTH M.F., PRATURN J.L.;

SMITH M.F., PRATURN J.L.;

RI "Phylogenetic relationships and the radiation of sigmodontine rodents

RI IN SOUTH America: Evidence from cytochrome b.";

RI OWALDA G. 6:39-128 (1939)

- I MAMMAIL EVOLI 6:39-128 (1939)

- COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

CC -! CORACTOR: TWO HENG ROUDES (BS62 AND BS66) WHICH ARE NOT COVALENTLY

BOUND TO THE PROTEIN (BY SIMILARITY).

CC -! SUBBUNT: THE MAIN SUBDURTS PROTEIN (BY SIMILARITY).

CC -! SUBBUNT: THE MAIN SUBDURTS DR COMPLEX B-C1 ARE: CYTOCHROME B,

CC -! SUBBUNT: THE MAIN SUBDURTS DR COMPLEX B-C1 ARE: CYTOCHROME B,

CC -! SUBBUNT: THE MAIN SUBDURTS DR COMPLEX B-C1 ARE: CYTOCHROME B,

CC -! SUBGROUPS (BS51.1) -

SMEL, AF108669; AAD45451.1; -

CN GO: 0005746; C: mitcochondrial electron transport chain; IEA.

BO GO: 0005746; C: mitcochondrial electron transport chain; IEA.

BO GO: 0005746; C: mitcochondrial electron transport; IEA.

BO GO: 00005118; P: electron transport; IEA.

BO GO: 00005118; P: electron transport; IEA.

BO GO: 00005118; P: electron transport; IEA.

BO GO: 0000512; Cytochrome b C; I.

BROSTIE; PRO033; Cytochrome b C; I.

BROSTIE; PRO033; CYTOCHROME B HENE; 1.

BROSTIE; PRO033; CYTOCHROME B HENE; 1.

BROSTIE; PRO0193; CYTOCHROME B HENE; 1.

RW MITCOCHONDRING B HENE; 1.

RW MITCOCHONDRING B HENE; 1.

RW MITCOCHONDRING B GO: 1.
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PROSITE; PS00192; CYTOCHROME_B_HEME; 1. PROSITE; PS00193; CYTOCHROME_B_QO; 1. Electron transport; Heme; Respiratory chain; Transmembrane; Transport; Mitochondrion.
                                                                                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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75.0%; Score 36; DB 8; Length 377;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                          75.0%; Score 36; DB 8; Length 377; 87.5%; Pred. No. 39;
                                                                                                                                                                                                                                 1; Indels
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                                                                                                    NON TER 1 1 SEQUENCE 377 AA; 42533 MW; 618DB37396EE6E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AA
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scapteromys tumidus (swamp rat).
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hes 7; Conservative
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                                                                                                                                                                                                                                                                                  2 OLVEYPFT 9
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SEQUENCE FROM N.A.
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                                                                                                                                                                                   Query Match
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CONTRACTOR OF CONTRA
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  NA WAY PROS
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RT HOFfmann F.G., Lessa B.P., Smith M.F.;

RT "Systematics of Coxymycterus with description of a new species from "Systematics of Coxymycterus with description of a new species from "Systematics of Coxymycterus with description of a new species from "Turguay.";

L. Mammal. 83:408-420(2002).

C. -- FOWTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERALES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C. -- COPACTOR: TWO HENE GROUPS (BSC2 AND BSC6) WHICH ARE NOT COVALENTLY C. SUBLINIT: THE MAIN SUBDIATS OF COMPLEX B-CI ARE: CYTOCHROME B, CYTOCHROME C. CYTOCHROME IN THE RIESKE PROTEIN (BY SIMILARITY).

C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.

C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.

C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.

C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.

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C. -- SIMILARITY: THE MAIN SIMILARITY.

C. -- SIMILARITY: THE MAIN SIMILARITY.

C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.

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C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.

C. -- SIMILA
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Mitochondrion.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Cervus.
[1]
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Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379
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337 OPVEYPFT 344

2 QLVEYPFT 9

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42802 MW; BFE22C9B4F985AE1 CRC64;
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Best Local Similarity 87.5
Tr Conservative
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Mitochondrion.
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379 AA; 428
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                MEDLINE=20229580; PubMed=10764539;

A Kuwayama R., Ozawa T.;

"Whylogenetic relationships among european red deer, wapiti, and sika deer inferred from mitochondrial DNA sequences.";

Mol. Phylogenet. Evol. 15:115-123(2000).

-!- PUNCTION: CONVENDENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYMTHESIS (BY SIMILARITY).

-!- COPACTOR: TWO HEME GROUPS (18.62 AND 18.66) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL; ABROINOS TO THE CYTOCHROME B FAMILY.
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J. Mammal. 83:408-420 (2002)

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COURLED TO APP SYNTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HEME GROUDES (BS562 AND BS56) WHICH ARE NOT COVALENTLY

BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBJUILT: THE MAIN SUBJUITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AF454766; AAM33833.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ho\bar{f}\,\mathrm{fmann} F.G., Lessa B.P., Smith M.F.; ^{\prime} Systematics of Oxymycterus with description of a new species from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=29125;
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Q8M299
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ALL J. Marmall. 83:408-420(2002).

C. I. PUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C. I. COPACIOR: TWO HEME GROUPS (BSES AND BSS6) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

C. SIBLINIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

C. SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL; AF454769; AAM33836.1; ---
SIMICARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL; AF4569; AAM33836.1; ---
SIMICARITY: BELONGS TO THE CYTOCHROME B FAMILY.

CO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0016491; F: Canitochondrial electron transport chain; IEA.

GO; GO:0016491; F: Canitochondrial electron transport; IEA.

GO; GO:0016491; F: Canitochondrial Electron transport; IEA.

GO; GO:0018919; P: Canitochondrial Electron transport; IEA.

CO; GO:0018919; P: Transport; IEA.

BIT REPERO; IPR005799; Cytochrome D.C;

PERM; PP00033; Cytochrome D.C;

PERM; PP00033; Cytochrome D.C;

PROME D.C. CONDELED D.C.

BITCHER PROTEIN TRANSPORT D.C.

BITCHER PROTEIN TRANSPORT D.C.

BREAD PP00033; CYTOCHROME D.C;

BREAD PP00033; CYTOCHROME D.C.

BREAD PP00034; CYTOCHROME D.C.

BREAD PP00035465799; CHANDER D.C.

BREAD P00035465799; CHANDER D.C.

BREAD PP00035465799; CHANDER D.C.

BREAD PP00035465799; CHANDER D.C.

BREAD PP000354657999; CHANDER D.C.

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GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0005746; C:mitochondrial electron transport chain; IEA.

GO; GO:0005749; C:mitochondrian; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:001618; P:electron transport; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR005799; Cytb_b6_C.

InterPro; IPR005799; Cytb_b6_N.

Pfam; PF00032; cytochrome_b_C; 1.

Pfam; PF00032; cytochrome_b_C; 1.

PROSTIE; PS00192; CYTOCHROME_B HEMB; 1.

PROSTIE; PS00193; CYTOCHROME_B PEMB; 1.
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PROSITE; PSO0193; CYTOCHROME B QO; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Pred. No. 39;
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Query Match
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                   2 QLVEYPFT 9
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341 QPVEYPFT 348
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Search completed: September 30, 2004, 05:59:31 Job time : 32.6073 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 30, 2004, 05:55:56; Search time 43.9322 Seconds (without alignments) 57.883 Million cell updates/sec е : Run

US-09-674-716B-7 48 1 QQLVEYPFT 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### SUMMARIES

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AAG27700 AAG27699 AAG27698	AAY92171 AAY92164 AAW28154 ABU49487	ABP40069 ABM73103 AAG81648	AAR30450 ABB36950 AAG93597	ABC27404 AAR34019 AAR59513	AAY90819 AAR33951 AAR33954 AAR59509
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## ALIGNMENTS

AAY32256 standard; peptide; 9 AA. RESULT 1 AAY32256

AAY32256;

(first entry) 15-FEB-2000

Light chain CDR L3 of mouse anti-CD23 MAb Cil.

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple solerosis; Hashimoto's thyroiditis; lupus erythematosus; multiple solerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcrariue colitis; crohn's disease; slogran's syndrome; allergy, asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; 

Mus musculus.

W09958679-A1./

18-NOV-1999.

99WO-GB001434. 07-MAY-1999; 98GB-00009839. 09-MAY-1998;

(GLAX ) GLAXO GROUP LTD.

Shearin J; Rapson NT, Ellis JH, Bonnefoy JMP, Crowe SJ,

WPI; 2000-053101/04. N-PSDB; AAZ34741.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 1; Page 40; 81pp; English.

This sequence represents complementarity determinating region 3 (CDR L3) of the light chain of murine anti-CD23 (FCBRII) monoclonal antibody Cl1 (see also AAV32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain CDRs (see AAV32254-59) to

Shearin J;

Ellis JH, Rapson NT,

Crowe SJ,

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Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
                                                                                                                                                                  Claim 9; Fig 3; 81pp; English.
                                                        WPI; 2000-053101/04.
                                                                            N-PSDB; AAZ34747
                       Bonnefoy JMP,
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haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus eryhematosus. Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatilis, postidais, urticaria, nephrotic syndrome, glomerulonephritis, psoriadis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma actute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, (CDP, insulitis, bronchitis, arthcularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoco's thyroiditis; diabstes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis;, inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogram's syndrome; allergy; asthma; thinitis; eczema; insulitis; graft.versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                                                                                                                                      Score 48; DB 3; I
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "framework region 1"
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                                                                                                                                                                                                                                                                                                                         0; Mismatches
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-- "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32262 standard; protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94. .102
/note= "CDR 3"
103. .113
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.- "CDR 2"
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                                                                                                                                                                                                                                                                                      100.0%;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                       Sequence 9 AA;
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This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody Cl1, composed of a human tramework (HSIGKVII) and the light chain complementarity determining regions (see AAY3224-56) of murine antibody Cl1. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as confinence or humanised antibodies, which comprises sufficient of the amino commence of the Cl1 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II determining regions to render them capable of binding to the CD23 type II activities, lugus erythematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lugus erythematosus, Haahimoto's thyroiditis, multiple arthritis, judiabetes, uveltis, inflammatory bowel disease, ulcerative colitis, communicatory disease, ulcerative colitis, communicatory allergies, allergic asthma, cute asthmatic exacerbation, rhinitis, cozema, graffturinsic asthma, acute asthmatic exacerbation, rhinitis, cozema, graffturinsic asthma, acute asthmatic exacerbation, rhinitis, cozema, graffturinsic asthma, acute asthmatic the pronditis (particularly chronic pronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cD23; FCERII; IgB receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimocto's thyroiditis; lubus erythematosus; multiple sclerosis; urticaria; nephroiditis; diabetes; uveitis; dermatitis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
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Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse anti-CD23 MAb C11 light chain variable region.
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125. .134
/note= "CDR L3"
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/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 116 AA;
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/note= "framework region 4"

W09958679-A1

18-NOV-1999

99WO-GB001434. 98GB-00009839.

07-MAY-1999;

GROUP LID.

(GLAX ) GLAXO

This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides anti-CD23 (FCERII) monoclonal antibody C11. The invention provides CC altered antibodies, such as chimeric or humanised antibodies (see ANY32262 and AAY32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on hadmatopoietic Cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lugus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes uvelits, dermatitis, psoriasis, uriccaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative collitis, crohn's disease, Sjogren's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft: bronchitis) or diabetes (particularly type I diabetes), and B-cell mallignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents Murine, p53 protein, monoclonal antibody, mAb, PAb-421, IDI-1, IDI-1 L3, light chain variable region; VL, complementarity determining region; CDR, dematrological; immunosuppressive, antiniflammatory, autoimmune response, SLE, systemic lupus erythematosus; diagnosis, treatment; autoantigen; DNA-binding domain; anti-idiotypic antibody. Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis. Murine anti-PAb-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3 Rapson NT, Shearin J; 100.0%; Score 48; DB 3; Length 145; 100.0%; Pred. No. 0.11; ive 0; Mismatches 0; Indels Crowe SJ, Ellis JH, AAY70804 standard; peptide; 19 AA. Claim 8; Fig 2; 81pp; English. 99WO-GB001434, 99WO-US024443 98GB-00009839 31-JUL-2000 (first entry) Local Similarity 100. GROUP LID 125 QQLVEYPFT 133 o WPI; 2000-053101/04. N-PSDB; AAZ34746. QQLVEYPFT Sequence 145 AA; WO200023082-A1 (GLAX ) GLAXO Bonnefoy JMP, 19-OCT-1999; WO9958679-A1 07-MAY-1999; 18-NOV-1999. 27-APR-2000 AAY70804; Query Match Mus sp Matches ò d

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                                                                                                                                                                                                            The patent discloses a method for the treatment of systemic lupus erythematosus (SLB) by down-regulating the autoimmune response to the Creminal DNA-binding domain of p53 protein by an active compound. The present sequence is a IDI-1 L3 Septide which comprises the complementarity determining region (CDR) of the light chain of IDI-1 annoncolonal antibody (Mah). The IDI-1 mah is an anti-idiotypic antibody/Ab2 mah specific for PAb-421 which is an Ab1 mah specific to the C-terminal DNA-binding domain of murine p53 protein. The peptide corresponds to residues 92-110 of IDI-1 light chain variable region. It is an example of the active compound useful in the diagnosis, prevention and treatment of SLB in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                              Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the protein by an active compound comprising of antibodies to p53 or fragments of p53.
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/note= "Complementarity determining region"
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                                                                                                                                                                                                                                                                                                                                                                                                                          93.8%; Score 45; DB 3; Length 19; 88.9%; Pred. No. 0.051; cive 1; Mismatches 0; Indels
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                                                                                                                                                                                       Claim 78; Fig 10; 87pp; English.
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Best Local Similarity
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Gaps

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99WO-US024443

19-OCT-1999;

27-APR-2000

Herkel J;

Erez-Alon N,

Rotter V,

Cohen IR,

WPI; 2000-339512/29

(YEDA ) YEDA RES & DEV CO LID.

98US-0104816P

19-OCT-1998;

Thu Sep 30 13:18:54 2004

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Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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                                                                                                                                                                                      The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the C-terminal DNR-binding domain of p53 protein by an active compound. The present sequence is a light chain variable region of IDI-1 an anti-idiotypic antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNR-binding domain of murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on complementarity determining regions Of light and heavy chain variable regions of these antibodies, are examples of active compounds useful in the diagnosis, prevention and treatment of SLE in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric mouse human antibodies - used in treatment, diagnosis and
prophylaxis of HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                            p53
                                                                                                Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the protein by an active compound comprising of antibodies to p53 or
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0
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Pred. No. 0.38;
1; Mismatches 0; Indels
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                                                 Erez-Alon N, Herkel J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse MAb 2E12 L chain V region.
                                                                                                                                                                Claim 78; Fig 9; 87pp; English.
                        (YEDA ) YEDA RES & DEV CO LTD
98US-0104816P.
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88.9%;
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97 QQLVEYPYT 105
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Matches 8; Conserv
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(GREC ) GREEN CROS
(ZOMA-) ZOMA CORP.
                                                                                                                                         fragments of p53.
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19-OCT-1998;
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                                                 Cohen IR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR12232;
                                                                                                                                                                                                                                                                                                                                                            Query Match
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The mouse VL gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the light (kappa) - chain variable (V) region of a mouse monoclonal antibody (MAb), 2E12, and is specific for an HIV-1 viral hantigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAD 2E12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme reocgnition sites. The chimeric MADs can be used as immuno- conjugates, in association with e.g. toxins for HIV retearment. They can also be used in diagnosis of HIV. See also AAQ12057-63. (Updated on 25-WAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric mouse-human antibodies - used to detect, kill and remove {\tt HIV} -1 antigen from sample.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light (kappa) chain variable region of murine 2E12 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                              93.8%; Score 45; DB 2; Length 131;
llarity 88.9%; Pred. No. 0.41;
Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robinson R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric antibodies; immunoconjugates; HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghoshdasti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR12354 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 1; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-00433730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                               1 QQLVEYPFT 9
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                                                                                                                                                                                                                                                                Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1989;
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15-AUG-1991
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LID AAR1

AAR1

AAR1

AAR2

AAR2

AAR2

AAR3

AR3

AAR3

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0; Gaps

Score 45; DB 2; Length 132; Pred. No. 0.41; 1; Mismatches 0; Indels us-09-674-716b-7.open.rag

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Light chain of the catalytic antibody 2A10.
16-JUN-1998 (first entry)
                                                                                                                                WO9749800-A1
                                                                                                                                                                                                      25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-1998
                                                                                                                                                       31-DEC-1997,
                                                                                                                                                                                                                                                    Landry DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39804;
                                                                                                          Mus sp.
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AAW39804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW39821-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                              New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                    Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TGA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                  Light chain CDR3 of catalytic antibody 2A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 82; 147pp; English
                                                                                              AAW39823 standard; .peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                           97WO-US010965,
                                                                                                                                                                                                                                                                                                                                                  96US-00672345,
                                                                                                                                          16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                          114 QQLVEYPYT 122
            QQLVEYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-077166/07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                  25-JUN-1996;
                                                                                                                                                                                                                                                                                                                          25-JUN-1997;
                                                                                                                                                                                                                                                                            WO9749800-A1
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                                                                                                                                                                                                                                                                                                                                                                                                 Landry DW;
                                                                                                                     AAW39823;
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                                                                                                                                                                                                                                                      Mus sp.
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The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The mattbodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New catalytic antibodies able to decompose cocaine, single-chain
analogues - used to treat cocaine overdose and addiction, required in fa
smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment, overdose, addiction.
Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain of the Kappa light chain of catalytic antibody 2A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 44; DB 2; Length 113; 88.9%; Pred. No. 0.55; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW39804 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 21; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                   96US-00672345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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N-PSDB; AAV09789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113 AA;
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AAW39882 standard; protein; 113 AA

AAW39882

RESULT 9
AAW39882
ID AAW3
XX
AC AAW3

1 QQLVEYPFT 9

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31-DEC-1997.
Larosa GJ,
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                                                                                                                                      New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                            AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAS) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2M10 antibody (AAW3980) represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, humanised antibody, CC-chemokine receptor 2, CCR2; nephrotropic, neuroprotective, immunosuppressive, human immunodeficiency virus; neuroprotection, cytostatic, vasotropic, leukocyte trafficiking, allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock, multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse germline kappa light chain variable (VK) region, 167/24.
                                                                                                                                                                                                                                                                                                                                                                                                          91.7%; Score 44; DB 2; Length 113; 88.9%; Pred. No. 0.55; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                         Claim 16; Page 73-74; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE06969 standard; protein; 100 AA.
                                                               COLUMBIA NEW YORK
              97WO-US010965.
                                       96US-00672345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-2001; 2001WO-US003537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-2000; 2000US-00497625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 88.9
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                                                                                                               WPI; 1998-077166/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QQLVEYPFT
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113 AA;
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             25-JUN-1997;
                                                            (UYCO ) UNIV
                                       25-JUN-1996;
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                                                                                       Landry DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE06969;
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Matches
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fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comparising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2. They care useful for inhibiting leukocyte trafficking, for treating cCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rhemmacold arthritis and multiple sclerosis.

CCR2-mediated disorders such as inflammatory disorder, autoimmune medicament for treating cCR2-mediated disease. They are also useful for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating CCR2-mediated disease. They are also useful for inflammation, histamine and IgB- mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory sassociated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting necessive in the present of a vessel in a mammal, and inhibiting including and proper and a vessel in a mammal, preferably associated in the conting an intervention. The present sequence is mouse germline kappa
                                                                                                                                                     Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
O'keefe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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O'brien S,
Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain CDR3 of catalytic antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         light chain variable (VK) region, 167/24
                                                                                                                                                                                                                                                                                                                            Disclosure; Page 151; 183pp; English.
Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39817 standard; peptide; 9 AA.
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Best Local Similarity 100..
Horvath C,
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AAW39915-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 3B9, which is able to degrade cocaline. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                               New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39801-05 represent the amino acid sequences of the variable domain of
the Kappa light chain of catalytic antibodies which are able to degrade
cocaine. A series of cocaine transition state analogues (TSAs) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable domain of the Kappa light chain of catalytic antibody 12H1.
                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%; Score 36; DB 2; Length 9; 66.7%; Pred. No. 1.4e+06; rative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW39803 standard; protein; 113 AA.
                                                                                                          Claim 11; Page 81; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 73; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US010965.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QOLVEYPFT 9
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QHFVDYPFT 9
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P-PSDB; AAV09802.
WPI; 1998-077166/07
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prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAM39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (FSAS) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3H9 antibody (AAW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW39801 standard; protein; 113 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-1998 (first entry)
                                                                                                                                                                                            Query Match
Best Local Similarity 66...
Best Local 6; Conservative
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The present sequence is an agonist antibody clone to the human WSX receptor, which can be used to identify and purify ligands and activators. An anti-wSX receptor antibody can be used as an agonist to citivate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy to bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, can also be used demaclogical disorders, inypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSX receptor and related antibodies and ligands - used to develop products for diagnosis and therapy, e.g. for improving haematopoiesis or
                                                                                                                                                                                                                                                                                                                                                         Human; WSX receptor; clone #17; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; carteriosclerosis; coverian disease; careadoscero disease; osteoarthritis; dermatological disorder; hypertension; insuln resistance; hypertological activation; insuln resistance; cancer; cholelithiasis.
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75.0%; Score 36; DB 2; Length 241;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 2; Indels
Score 36; DB 2; Length 113;
Pred. No. 23;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matthews W;
                                                                                                                                                                                                                                                                                                                           Human WSX receptor agonist antibody clone #17.
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                                                                                                                                                                                                              AAW24063 standard; protein; 241 AA.
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75.0%;
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96US-00667197.
                                                                                                                                                                                                                                                                                      (first entry)
                                          Conservative
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                                                                                                                94 OHFVDYPFT 102
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                                                                            1 QQLVEYPFT 9
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                    Best Local Similarity
Matches 6; Conserv
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Rodrigues ML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9725425-A1.
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20-JUN-1996;
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    Query Match
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223 QQLISYPLT 231
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Search completed: September 30, 2004, 06:06:15 Job time: 46.9322 secs

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91.7%; Score 44; DB 10; Length 9; 88.9%; Pred. No. 1.2e+06; ive 0; Mismatches 1; Indels
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US-09-940-727B-8
Sequence 8, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
Conservative
Query Match
Best Local Similarity
Matches 8; Conserv
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|QFVEYPFT
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; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-27
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LENGTH:
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                                                                  0; Search time 151.017 Seconds (without alignments)
19.178 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    Published Applications AA:*

1. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
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9. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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0 US-09-840-459-32

6 US-10-766-773-32

6 US-10-766-10-32

6 US-10-437-963-104782

0 US-09-940-727B-21

0 US-09-940-727B-7

0 US-09-940-727B-100

0 US-09-940-727B-102
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                                                                 September 30, 2004, 06:01:30
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence 1310, Ap
Sequence 316, App
Sequence 936, App
Sequence 119, App
Sequence 119, App
Sequence 71736, A
Sequence 7235, A
Sequence 7235, A
Sequence 7311, Ap
Sequence 7311, Ap
Sequence 2311, Ap
Sequence 21316, App
Sequence 21368, Sequence 21368, Sequence 21368, Sequence 21368, Sequence 161157, Sequence 161157, Sequence 55, Appl
Sequence 59, Appl
Sequence 51, Appl
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| Publication No. US2003007793A1
| GENERAL INFORMATION:
| APPLICANT: Landry, Donald W
| TITLE OF INVENTION:
| FLIE FEBERGE: 0575/51400-B
| CURRENT APPLICATION NUMBER: US/09/940,727B
| FRIOR FILING DATE: 1998-12-28
| PRIOR FILING DATE: 1998-12-28
| PRIOR FILING DATE: 1998-16-25
| PRIOR FILING DATE: 1996-06-25
| PRIOR FILING DATE: 1996-06-25
| PRIOR FILING DATE: 1996-06-25
| WUMBER: OF SEQ ID NOS: 121
| SOFTWARE: Patentin version 3.1
                     US-10-293 418-1310

US-09-880-748-936

US-09-940-7278-119

6 US-09-940-7278-119

6 US-10-767-701-56894

2 US-10-425-114-77136

2 US-10-285-114-77136

2 US-10-285-114-77136

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US-10-425-114-44897

US-10-425-566-2371

US-10-424-599-280477

US-10-424-599-280477

US-10-424-599-280477

US-10-424-599-280477

US-10-424-599-280477

US-10-437-963-11557

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77.1%; Score 37; DB 16; Length 100; 100.0%; Pred. No. 17; cive 0; Mismatches 0; Indels
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17;
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Sequence 32, Application US/10766773

Sequence 32, Application US/10766773

Sequence 32, Application US/10766773

Sequence 32, Application No. US20040126851A1

SEPPLICANT: LaRcsa, Gregory J.

APPLICANT: Newman, Walter

APPLICANT: O'Reie, Tarran

APPLICANT: O'Reie, S. Tarran

APPLICANT: O'Reie, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: HUMBER: US/10/766,773

CURRENT APPLICATION NUMBER: US/20/765

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 32

LENGTH DATE: PastSEQ for Windows Version 3.0

LENGTH DATE: PastSEQ for Windows Version 3.0
TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012 CURRENT APPLICATION NUMBER: US/09/840,459 CURRENT FILING DATE: 2001-02-02 PRIOR APPLICATION NUMBER: PCT/US01/03537 PRIOR FILING DATE: 2000-02-03 PRIOR FILING DATE: 2000-02-03 PRIOR APPLICATION NUMBER: 09/497,625 PRIOR APPLICATION NUMBER: 09/497,625 PRIOR APPLICATION NUMBER: 09/359,193 PRIOR APPLICATION NUMBER: 09/121,781 PRIOR FILING DATE: 1999-07-22 NUMBER OF SEQ ID NOS: 107 SOFTWARE FASLSEQ for Windows Version 3.0 LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.1%; Score 37; DB Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-766-610-32; Sequence 32, Application US/10766610; Publication No. US20040132980Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
// ORGANISM: Mus musculus
US-09-840-459-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus US-10-766-773-32
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APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 0575/54400-8
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR PILING DATE: 1999-12-8
PRIOR PILING DATE: 1999-7-06-25
PRIOR APPLICATION NUMBER: 09/672,345
PRIOR PILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR PILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LIBRIGHT: 113
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
FRIOR APPLICATION NUMBER: 09/214,095
FRIOR APPLICATION NUMBER: 09/214,095
FRIOR FILING DATE: 1997-06-25
FRIOR FILING DATE: 1997-06-25
FRIOR FILING DATE: 1996-66-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN VEYSION 3.1
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APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Refe, Theresa
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 108, Application US/09940727B Publication No. US20030077793A1 GENERAL INFORMATION:
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; Sequence 32, Application US/09840459

; Patent No. US20020150576A1

; GENERAL INFORMATION:
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Best Local Similarity 88.9%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
, ORGANISM: mouse
US-09-940-727B-8
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ORGANISM: mouse
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US-09-940-727B-108
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                  US-10-437-963-104782

Sequence 104982, Application US/10437963

Fublication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Buckharov, Andrey A.

APPLICANT: Buckharov, Andrey A.

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)8

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 104782

LENGTH: 609
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
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| OTHER INFORMATION: Clone ID: PAT_MRT4530_102083C.1.pep
| US-10-437-963-104782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASSULTA 5 A SEQUENCE 21, Application US/09940727B

Sequence 21, Application US/09940727B

Publication No. US20030077793A1

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

CURRENT APPLICATION NUMBER: US/09/940,727B

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin Version 3.1

LENGTH. 00 21
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Pred. No. 1.2e+06;
1; Mismatches 2
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; Sequence 134, Application US/10632706
; Publication No. US20040175385A1
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Best Local Similarity 77.5-
7; Conservative
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Best Local Similarity 66...
6; Conservative
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569 QQLLEIPFT 577
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ORGANISM: Oryza sativa
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17;
                                APPLICANT: Norwan, Walter
APPLICANT: Once, S. Tarran
APPLICANT: O'BHIGH, SICHAR H.
APPLICANT: O'BHIGH, SICHAR H.
APPLICANT: O'BHIGH, SICHAR H.
APPLICANT: O'REFE, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT APPLICATION NUMBER: US/10/766,610
PRIOR APPLICATION NUMBER: DCT/US01/03537
PRIOR APPLICATION NUMBER: DCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 1909-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1000
SOFTWARE: FESTERE for Windows Version 3.0
SOFTWARE: FESTERE for Windows Version 3.0
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| Publication No. US20040151721A1
| GENERAL INFORMATION:
| APPLICANT: O'Reafe, Theresa
| APPLICANT: O'Reafe, Theresa
| APPLICANT: O'Reafe, Theresa
| TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
| TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
| TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
| TILLE REFERENCE: 10448-213001
| CURRENT APPLICATION NUMBER: US/10/73,563
| CURRENT APPLICATION NUMBER: US 60/722,899
| PRIOR FILING DATE: 2002-10-17
| PRIOR PLICATION NUMBER: US 60/350,166
| PRIOR FILING DATE: 2001-10-19
| PRIOR FILING DATE: 2001-10-19
| PRIOR PLICATION NUMBER: US 60/350,166
| PRIOR FILING DATE: 2001-10-19
| SEQII DATE: 2002-10-10-19
| SEQII DATE: 2002-10-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.1%; Score 37; DB 100.0%; Pred. No. 17; ive 0; Mismatches
LaRosa, Gregory J.
Horvath, Christopher
Newman, Walter
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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CAGANISM: Mus musculus
US-10-766-610-32
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CRGANISM: Mus musculus
US-10-733-563-32
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US-10-733-563-32
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PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR PILING DATE: 1997-06-25
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
2002-09-04
                                                                                                                                                                                                                                                                                                                                 Query Match 75.0
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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94 QHFVDYPFT 102
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                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: mouse
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US-09-940-727B-112
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US-09-940-727B-100
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                  APPLICANT: MARKS, JAMES D.
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 4077-8951200S
CURRENT EPLING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR PILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 99/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SEQ ID NOS: 278
SEQ ID NO 134
LENGTH: 9
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; Sequence 5, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
CURRENT FILING DATE: 1099-104
; PRIOR PAPLICATION NUMBER: 09/214,095
; PRIOR PAPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-625
; PRIOR APPLICATION NUMBER: 06/25
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 5: 121
; SEQ ID NO 5: 121
; LENGTH: 113
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Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.0%; Score 36; DB 16; Best Local Similarity 66.7%; Pred. No. 1.2e+06; Matches 6; Conservative 1; Mismatches 2.
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
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US-09-940-727B-7
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Score 36; DB 10; Length 113;
Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT FILING DATE: 2002-09-04
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR PLLING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-8
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LEMGTY, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR PILING DATE: 1990-12-8
PRIOR FILING DATE: 1997-06-25
PRIOR FILING DATE: 1997-06-25
NUMBER OF SEQ ID NOS: 121
SEQ ID NO: 121
SEQ ID NO: 100
                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                  Sequence 100, Application US/09940727B Publication No. US20030077793A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112, Application US/09940727B Publication No. US20030077793A1 GENERAL INFORMATION:
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75.0%; Score 36; DB 8; Length 241;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application US/08779457

Publication No. US2002193571A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Chiang, Nancy Y.

APPLICANT: Matthews, William

APPLICANT: Redrigues, Walliam

APPLICANT: Redrigues, Maria L.

TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: XSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-9881
TELEX: 910/31-7168
INFORMATION FOR EQUID NO: 50: SEQUENCE CHARACTERISTICS:
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 112
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 241 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                94 QHFVDYPFT 102
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US-08-779-457-50
                                                                                 ; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-112
                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-779-457-50
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Search completed: September 30, 2004, 06:54:52 Job time : 152.017 secs Dlank Sheet

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Sequence 20209, A
Sequence 5748, Ap
Sequence 14137, A
Sequence 25875, A
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1 Sequence 27, Application US/08672345C
Patent No. 5948658
GENERAL INTORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCES: 108
COUNTRY: USA
STREET: 1188 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036
COMPUTE: New York
COMPUTER: New York
COMPUTER: Ploppy disk
COMPUTER: Eleppy disk
COMPUTER: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGERENCE/DOCKET NUMBER: US/05/51400
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
TENDERAL OF SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-20209
US-09-328-352-5748
US-09-489-039A-14137
US-09-252-991A-25875
US-08-471-771-3

US-09-130-783-3

US-09-130-783-3

US-08-253-877C-10

US-08-253-877C-28

US-08-452-164A-10

US-08-452-164A-28

US-08-603-024-4

US-08-603-11611-2

PCT-US33-11611-2

US-08-450-809-23

US-08-450-809-23

US-08-450-809-23

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US-08-450-809-23

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88.9%; Pred. No. 3e+05;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.7
Best Local 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                           US-08-672-345C-27
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        Sequence 27, Appl Sequence 8, Appl Sequence 98, Appl Sequence 98, Appl Sequence 11, Appl Sequence 21, Appl Sequence 7, Appl Sequence 7, Appl Sequence 97, Appl Sequence 97, Appl Sequence 119, App Sequence 119, App Sequence 119, App Sequence 26, Appl Sequence 26, Appl Sequence 119, App Sequence 14, Appl Sequence 26, Appl Sequence 21, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                September 30, 2004, 06:00:45; Search time 15.2542 Seconds (without alignments) 30.459 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-214-095D-27
US-08-672-345C-98
US-08-672-345C-98
US-08-672-345C-98
US-09-214-095D-81
US-09-214-095D-21
US-08-672-345C-7
US-08-672-345C-7
US-08-672-345C-7
US-08-672-345C-7
US-08-672-345C-7
US-08-672-345C-7
US-08-672-345C-97
US-09-214-095D-112
US-09-214-095D-112
US-09-214-095D-112
US-09-214-095D-112
US-09-214-095D-112
US-09-214-095D-113
US-08-483-749A-4
US-09-214-095D-113
US-08-483-749A-4
US-09-146-6532-14
US-09-406-532-20
US-09-406-532-14
US-09-406-532-14
US-08-488-123-31
US-08-488-123-31
US-08-488-123-31
US-08-488-661-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                               1 QQLVEYPFT 9
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Match Length
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Perfect score:
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Maximum DB
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                                                                                                                                                                                           Run on:
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RESULT 4
US-08-672-345C-98
| Sequence 98, Application US/08672345C
| Patent No. 594858
| Patent No. 594858|
| The Patent No. 594858|
| APPLICANT: Landry Donald, W. TILLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS: ADDRESSE: Copper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
DEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OMPRATIGS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UW-1996
CLASSIFICATION NUMBER: 26,678
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 26,678
REGISTRATION NUMBER: 26,678
TELEPHONE: 212-279-0400
TELEPHONE: 212-279-0400
TELEFORM: 212-279-0400
TELEPHONE: CLASSIFICS:
INPORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
TENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09214095D
Patent No. 6280937
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 QOFVEYPFT 102
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SEQ ID NO 8
LENGTH: 113
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                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 3; Length 9; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280097;
GENERAL INFORMATION:
; APPLICANT: Landary, Donald
; TILLE OF INVENTION:
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT PAPLICATION NUMBER: US/09/214,095D
; CURRENT PILIOR DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 27
; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: TOUS OF THE SEAD ABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELERERAE: 212-78-0400
TELERERAE: 212-78-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE SINCESSIONESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2;
Pred. No. 0.25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-672-345C-8
; Sequence 8, Application US/08672345C
Patent No. 5948658
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         91.7%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acidi
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                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27
                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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MOLECULE TYPE: protein
US-08-672-345C-8
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Best Local Similarity
Matches 8; Conserv
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91.7%; Score 44; DB 2; Length 113; 88.9%; Pred. No. 0.25;
                                               1; Indels
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Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches
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amino acid
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Murinae gen.sp. US-09-214-095D-21
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                                                                                                            1 QHEVDYPFT 9
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                               RESULT 8
US-09-214-095D-21
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                                                                                                                                    US-09-214-095D-108
; Sequence 108, Application US/09214095D
; Patent No. 628087
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; CURRENT PRILICE DATE:
; CURRENT FILING DATE:
; CURRENT FILING DATE:
; SOFTWARE:
; SEC ID NO:
; SEC ID NO 108
; SEC ID NO 108
; LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPUTER: 24-JUN-1996
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 0575/51400
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-672-345C-21
Sequence 21, Application US/08672345C
Patent No. 5948658
CENTERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 3;
Pred. No. 0.25;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative-
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TYPE: amino acid
STRANDEDNESS: single
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                                                    QOFVEYPFT 102
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-108
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ARDRESSER: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
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APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONINY AGENT INFORMATION:
NAME: White, Ohn PRESIDENCE POOCKET NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REPRENCE/POCKET NUMBER: 0575/51400
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                   Sequence 21, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
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Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO: 97
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
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94 QHFVDYPFT 102
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           COUNTRY:
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                                                                      75.0%; Score 36; DB 2; Length 113; 66.7%; Pred. No. 8.5;
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                                                                                                                                            2; Indels
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US-08-672-345C-95

Sequence 95, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:

APPLICANT: Landary Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPENDENCE ADDRESS:

ADDRESSE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
CORRESPONDENCE ADDRESS:
ADDRESSED: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 10036

COMPUTER: 10039 disk

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTONNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 212-39-0400

TELEPHONE: 212-39-0400

TYPE: Amino acids

TYPE: Amino A
                                                                                                                                            1; Mismatches
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Best Local Similarity 66.7%;
Matches 6; Conservative :
                                                                                                   Best Local Similarity 66.7
Matches 6; Conservative
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94 QHFVDYPFT 102
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JS-08-672-345C-5
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                                                                      Query Match
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COMPUTER: READBAGE FORM:
MEDITAN TYPE: ROADBAGE FORM:
MEDITAN TYPE: ROADBAGE FORM:
MEDITAN TYPE: ROADBAGE FORM:
MEDITAN TYPE: PROPRY disk
COMPUTER: IRM FOR Compatible
OPERATION SYSTEM: No. 80-705/M-0.05
GENERAL PARTICIATION NAME: 00772/345C
CLASSITEATION NAME: 00772/345C
TELEGROWN: 12.22-70-700
MANE: WALLOADER TYPE: Amino acid
MEDITALION NAME: 00775/51400
TELEGROWN: 12.22-70-700
MANE: WALLOADER TYPE: Amino acid
MEDITALION NAME: 00775/51400
TELEGROWN: 12.22-70-700
MANE: WALLOADER TYPE: Amino acid
MEDITALION NAME: 00775/51400
MANE: WALLOADER TYPE: Amino acid
MEDITALION NAME: WALLOADER TYPE: Amino acid
MATCHES CONSTRUCTION NAME: 00774/M-DOS
MATCHES CONSTRUCTION NAME: 00774/M-DOS
MATCHES CONSTRUCTION NAME: 00774/M-DOS
MATCHES CONSTRUCTION NAME: 00774/M-DOS
MATCHES CONSTRUCTION NAME: 00775/M-DOS
MATCHES MATCHES MATCH NAME: 007774/M-DON NAME: WALLOADER TYPE: Amino NAME: WALLOADER TYPE: Amino NAME: WALLOADER TYPE: 007774/M-DON NAME: NAME: 007774/M-DON NAME: 0077777/M-DON NAME: 0077777/M-DON NAME: 0077777/M-DON NAME: 0077777/M-DON NAME: 0077777/M-DON
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                                                 Score 36; DB 2; Length 113;
Pred. No. 8.5;
1; Mismatches 2; Indels
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8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09214095D

Patent No. 6280987

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION:

FILE REFERENCE: 51400-A-PCT-US

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
10S-09-114-095D-100
1 Sequence 100, Application US/09214095D
1 Patent No. 6280987
1 GENERAL INFORMATION:
2 APPLICANT: Lendry, Donald
1 TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Landry, Donald
APPLICANT: Landry, Donald
TITLE OF INVENTION:
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
LENGTH: 113
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US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987.
                                                   75.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
; ORGANISM: Murinae gen. Sp.
US-09-214-095D-5
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Murinae gen. sp
; MOLECULE TYPE: peptide US-08-672-345C-97
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94 QHFVDYPFT 102
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94 QHFVDYPFT 102
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                                                                                                                           1 QQLVEYPFT 9
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US-09-214-095D-7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 30, 2004, 05:55:56; Search time 5.42373 Seconds (without alignments) 88.677 Million cell updates/sec

US-09-674-716B-9 33 1 GYWMS 5

Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	hypothetical prote	<u>.</u>	D)	hypothetical prote	conserved hypothet	hypothetical prote	AbiD phage protein	carbamate kinase (	GDP-D-mannose dehy	hypothetical prote		hypothetical prote		conserved hypothet	undecaprenyl-phosp	hypothetical prote	arginine/ornithine	probable membrane		PTS system, sucros	arginine/ornitine	multidrug-efflux t	D-ribulokinase (EC	probable glycyl-tR		hypothetical prote		env polyprotein pr	
Ω	A84376	GZMSUI	809681	F97302	T42185	AE1752	AH1728	H86836	G69142	H83554	E83163	T08724	B95249	G98113	T00113	T28818	T46745	D84505	539978	D90038	C86879	G69804	878598	C72544	IKEBCA	T15600	JQ1462	VCLJGL	JC4836
Length DB	67. 2																												
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Query Match
100.0%; Score 33; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels

hypothetical prote cation efflux syst		amily	helicase, Snf2/Rad	multidrug resistan	hypothetical prote	Ig heavy chain V r	hypothetical prote	Ig heavy chain V r	hypothetical prote	Ig heavy chain pre	hypothetical prote			
T47495 A33830	JC4700	A86595	B72029	T42216	AF0683	S13692	B72742	S13693	S13690	S13694	S13691	A83756	803326	D84436
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851	063	215	215	502	71	101	102	111	112	115	116	122	137	152
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90.06					87.9	87.9	87.9					87.9	87.9	87.9
6.06		6.06	6.06	6.06				87.9		87.9	87.9			

## ALIGNMENTS

RESULT 1 A84376 hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Accession: A84376 R;My W.V; Kennedy, S.P; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. R;My W.V; Kennedy, S.P; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. Jung, K.H.; Alam, M.; Jung, D. Jung, M.J.; Hough, D.W.; Jung, D. Jung, Match Baset Local Similarity, Jung, Pred, No. 15; Baset Local Similarity, D. 100.0%; Pred, No. 15; Baset Local Similarity, D. O. 0%; Pred, No. 15; Baset Local Similarity, D. O. 0%; Pred, No. 15; Baset Local Similarity, D. O. 0%; Pred, No. 15; Baset Local Similarity, D. D. 00.0%; Pred, No. 15; Baset Local Similarity, D. 00.0%; Pred, No. 15; Baset Local Simil	QY 1 GYMMS 5
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; 0

Gaps

.; 0

0; Indels

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Score 30; DB 2; Length 86; Pred. No. 69;
A;Reference number: Z22068; MUID:98391744; PMID:9722640
A;Accession: T42185
A;Status: pressionsry; translated from GB/EMBL/DDBJ
A;Acledus: type: DNA
A;Residus: 1-86 < SURA
A;Cross-references: EMBL:AP074613; PIDN:AAC70153.1
A;Experimental source: strain EDL933; serotype 0157:H7
A;Genome: plasmid po157
A;Note: L7085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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Best Local Similarity 80.v.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein L7085 - Escherichia coli plasmid po157
(Species: Bscherichia coli
(Species: Bscherichia coli
(Species: Bscherichia coli
(Scherichia coli)
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A;Cross-references: GB:AE001437; PIDN:AAK81209.1; PID:g15026351; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                            NiAlternate names: citrate carrier
C;Species: Klebsiella pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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R. van der Rest, M. B.; Schwarz, E.; Oesterhelt, D.; Konings, W.N.

Eur. J. Biochem. 189, 401-407, 199.

A. Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.

A. Reference number: S09681; MUD: 90249385; PMID: 2186908

A. Accession: S09681

A. Molecule type: DNA

A. Residues: 1-444 < RES>

A. Cross-references: EMBL: X51479; NID: 943800; PIDN: CAA35844.1; PID: 943801
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Similarity 100.0%; Score 33; DB 2; Length 444;
5; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                           citrate transport protein - Klebsiella pneumoniae plasmid pESI
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C;Superfamily: citrate utilization determinant
C;Keywords: membrane protein
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                        31 GYWMS 35
                                             GYWMS 5
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Matches
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hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Accession: AE1752
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
A;Relence number: AB1077; MulD:21537279; PMID:11679669
A;Accession: AE1752
A;Status: preliminary
A;Residues: 1-298 A;Glas
A;Cross-references: GB:AL592022; PIDN:CAC97789.1; PID:g16415084; GSPDB:GN00178
A;Residues: 1-298 A;Glas
A;Genetics:
C;Genetics:
A;Genetics:
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Rydlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominger-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat Ok. C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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AbiD phage protein homolog lin2373 [imported] - Listeria innocua (strain Clip11262)
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A;Molecule type: DNA
A;Rosidues: 1-238 «GLA>
A;Cross_references: GB:AL592022; PIDN:CAC97600.1; PID:gl6414896; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .Species: Listeria innocua
.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative

A,Gene: lin2373

|||:| GYWLS 49

1 GYWMS 5

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M.J.; Bri
K.; Lim,
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A,Molecule type: DNA
A,Moscule type: DNA
A,Residues: 1-375 <STO>
A,Gross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07250.1; GSPDB:GN0013
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: H83554
A;Status: preliminary
A;Nolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-358 <STO>
A;Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN001:
A;Experimental source: strain PA01
A;Grosics: PA0736
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A;Accession: E83163
"Species: Pseudomonas aeruginosa ('Species: Pseudomonas aeruginosa (strain PAO1) ('Species: Pseudomonas aeruginosa ('Species: Pseudomonas aeruginosa ('Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C'Accesion: H83554 ('Accesion: H83554 ('Accesion: H83554 ('Accesion: H83554 ('Accesion: H83554 ('Accesion: H83554 ('Accesion: H83564 ('Accesion: H83564 ('Accesion: Harbid, 'A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ', Lory, S., Olson, M.V.

Nature 406, 959-964, 2000
A,7itle: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A,Reference number: A82950; MUID:20437337; PMID:10384043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Species: Pseudomonas aeruginosa
C'Species: Describo #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C'Accession: E83163
R'Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, S.Stover, C.Y.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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Pred. No. 2.7e+02;
1; Mismatches 0; Indels
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A;Experimental source: fetal kidney; clone DKFZp566D213
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Best Local Similarity 80.v-
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Best Local Similarity 80.03
Matches 4; Conservative
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203 GYWLS 207
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19 GYWLS 23
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A,Residues: 1-348 <MTH>
A;Cross-references: GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AAB84839.1; PID:g262138
A;Experimental source: strain Delta H
C;Genetics:
A,Gene: MTH333
C;Superfamily: GDP-D-mannose dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14 C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: H86836 Fs. Bolotin, A: Wincker, P: Mauger, S: Jaillon, O: Malarme, K:; Weissenbach, J: Ehrli Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis say Reference number: A86625; MUID:21235186; PMID:11337471
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J; Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Retersion: G69142
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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DP-D-mannose dehydratase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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A;Residues: CB:ABB005176; PID:g12724712; PIDN:AAK05794.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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                                                               Score 30; DB 2; Length 298;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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Pred. No. 2.4e+02;
1; Mismatches 0; Indels
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A,Gene: arcC3 C,Superfamily: carbamate kinase C,Keywords: phosphotransferase

Genetics:

Status: preliminary Molecule type: DNA

Accession: H86836

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A, Residues: 1-452 <NAK>
A, Residues: 1-452 <NAK>
A, Cross-references: BMBL:AB010415; NID:g3132248; PIDN:BAA28142.1; PID:g3132265
A, Experimental source: strain NCTC 9710
C; Superfamily: xps2A protein
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G98113
conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001
GAccession: G98113
GAccession: G98113
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.; P.; Muthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G98113
A;Molecule type: DNA
A; And Constant Application Constant A;Accession: G98113
A;Molecule type: DNA
A; Accession: G98113
A;Molecule type: DNA
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A;Molecule type: DNA
A; Accession: G98113
A;Accession: G981
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A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE005672; PIDN:AAK76187.1; PID:g14973641; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
A;Genetical Source: strain TIGR4
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C;Genetics:
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1; Mismatches 0; Indels
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                                                                                                                                     Score 30; DB 2; Length 417
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
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C;Genetics:
A;Note: DKFZp566D213.1
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                                                                                                                                          September 30, 2004, 05:55:56; Search time 3.05085 Seconds (without alignments) 85.337 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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CIT1 KLEPN
CAPA KLULA
AMPR PROST
ARCU LACSK
ARCD LACSK
ARCD CLOPE
PTSB STAXY
SYG AERPE
CEA CITFR
PPCK NEOFR
ENV GALV
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CCAP RHOMR
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MRP6 HWAT
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MRP10 ARBIT
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Auffaat C., Sikorav J.L., Ollo R., Rougeon F.;
Auffaat C., Sikorav J.L., Ollo R., Rougeon F.;
Aucrelation between D region structure and antigen-binding specificity: evidences from the comparison of closely related immunoglobulin VH sequences.";
Ann. Immunol. (Paris) 132D:77-88(1981).
-!- MINCELLANEOUS: THIS CHIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOWA PROTEIN BINDING 2,6-LEVAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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10-CTT-2003 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region UPC10.
1g heavy chain V receive Chordon UPC10.
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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P57057 P
P53099 8
P25297 8
P94532 P
P08393 B
P081117 I
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                                                                                                                                             GLPT HUMAN
YGT6 YEAST
PH64 YEAST
CSTA BACSU
SPPA HAEIN
SPPA ECOLI
AMYILLIPKO
XII19 MYCTU
GAOA DACDE
                                               DEBOC
ECOLI
HUMAN
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PIR; A02081; G2MSU1.
HSSP; P01810, 2FBJ.
INTERPO; IPR007110; Ig-like.
INTERPO; IPR003596; Ig-V.
PRART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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Best Local Similarity 100.
Matches 5; Conservative
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444 CYTOPLASMIC (POTENTIAL).
48142 MW; D431F732EEDA3EC2 CRC64;
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069772;
30-MAY-2000 (Rel. 39, Created)
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                                           Local Similarity 100.
les 5; Conservative
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444 AA;
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Best Local Similarity
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074232;
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                                                                                                                                 RESULT 3
CAPA_KLULA
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                                                                                                                                                                                                                                          carbon and energy.
--- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
--- SIMILARITY: TO CIT IN TN3411 AND PWR60 FOUND IN E.COLI AND TO CIT IN CITROBACTER AMLONATICUS.
--- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ATCC 13882;
MEDLINE=90249385; PubMed=2186908;
van der Rest W.E., Schwarz E., Oesterhelt D., Konings W.N.;
"DNA sequence of a citrate carrier of Klebsiella pneumoniae.";
Bur. J. Blochem. 189:401-407(1990).
-!- FUNCTION: UPTAKE OF CITRATE AFORS THE BOUNDARY MEMBRANE WITH
THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-!- PATHWAY: Allows the utilization of citrate as a sole source of
                                                               CITH OR CIT.
Klebsiella pneumoniae.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Klebsiella.
     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
02-8FEB-2003 (Rel. 41, Last annotation update)
Citrate-proton symporter (Citrate transporter) (Citrate carrier protein).
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EXTRACELLULAR (POTENTIAL).
12 (POTENTIAL).
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PROSITE; PS00216; SUGAR TRANSPORT 1; 2.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004736; Cit H symport.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR00883; ZA0106; 1.
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 STANDARD;
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318
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P16482;
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
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100.0%; Score 33; DB 1; Length 444; 100.0%; Pred. No. 45; 0; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
F-actin capping protein alpha subunit (Fragment).
                                                                                                                                                                                                                                                                                                          214 AA
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InterPro; IPR02189; Fractin_cap_A.
Pfan; PF01267; F-actin_cap_A; 1.
PRINTS; PR00191; FACTINAPA; 1.
ProDom; PD006960; F-actin_cap_A; 1.
PROSTITE; PS00749; F-ACTIN_CAPPING A 1; 1.
PROSTITE; PS00749; F-ACTIN_CAPPING A 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1998) to the EWBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS A POSITIVE REGULATOR OF GENE EXPRESSION
-!- FUNCTION: ALCTAMASE (AMPC).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
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P35831;
00-071-2001 (Rel. 29, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last Engle En
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Koeck J.L., Basmaciogullari S., Parzy D., Barnaud G., Teyssou R., Buisson Y., Philippon A., Arlet G.J.,
"Cloning and sequencing of ampC and ampR genes from Providencia
                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales,
Enterobacteriaceae, Providencia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.9%; Score 30; DB 1; Length 292; 80.0%; Pred. No. 1.1e+02; ative 1; Mismatches 0; Indels
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EMBL, Y17315, CDA76738 1; -.
InterPro; IPR000847; HTH LysR.
InterPro; IPR001919; LysR subst.
& Pfam; PF00126; HTH 1; 1.
& Pfam; PF0039; HTHLYSR.
R PRINTS; PR00039; HTHLYSR, 1.
R PROSITE; PS0931; HTH LYSR, 1.
M Transcription regulation; DNA-binding; Activator.
M Transcription 26 45 HTH LYSR-TYPE.
Thus RIND 26 45 HTH LYSR-TYPE.
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   30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional activator ampR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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292 AA; 32741 MW;
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Best Local Similarity 80...
A; Conservative
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                                                                                                                             Providencia stuartii
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ID ARCIL E
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DT 01-JUN
DT 10-OCT
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SPECIMES FROM N. STAINSANCE 2912;

X NEULINE-ZEGGALIS, STRAINSANCE 2912;

X NEULINE-ZEGGALIS, PROMESLISOS STAINSANCE 2912;

X NEULINE-ZEGGALIS, PROMESLISOS STAINSANCE 2912;

X NEULINE-ZEGGALIS STAINSANCE 30. WARTHAN N. WEDGESCOUR Escalis;

X NEULINE-ZEGGALIS STAINSANCE 30. WARTHAN N. WEDGESCOUR Escalis;

X NEULINE-ZEGGALIS STAINSANCE 30. WARTHAN N. WEDGESCOUR Escalis;

X NEULINE-ZEGGALIS, STAINSANCE 30. WARTHAN N. WESTON N
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                                                                                                                    E->A: NO CHANGE IN ACTIVITY, WHEN ASSOCIATED WITH A-137, A-139 AND A-140.
E->A: NO CHANGE IN ACTIVITY, WHEN ASSOCIATED WITH A-135, A-139 AND A-140.
K->A: NO CHANGE IN ACTIVITY; WHEN ASSOCIATED WITH A-135, A-137 AND A-140.
E->A: NO CHANGE IN ACTIVITY; WHEN ASSOCIATED WITH A-135, A-137 AND A-130.
D->A: ALWOST NO ACTIVITY; WHEN ASSOCIATED WITH A-135, WHEN ASSOCIATED WITH A-135, A-137 AND A-139.
                                                                                                                                                                                                                                                                                            D->A: ALMOST NO ACTIVITY; WHEN ASSOCIATED WITH A-207 .

I -> D (IN REF. 4).

S014514A7FEBE290 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **EDLINE=98861904; PubMed=9696761; Zuniga M., Champomier-Verges M., Zagorec M., Perez-Martinez G.; Zuniga M., Champomier-Verges M., Zagorec M., Perez-Martinez G.; Structural and functional analysis of the gene cluster encoding the enzymes of the arginine deiminase pathway of Lactobacillus sake."; J. Bacteriol. 180:4154-4159(1998).

-!- FUNCTION: Catalyzes an electroneutral exchange between arginine and ornithine to allow high-efficiency energy conversion in the arginine deiminase pathway (By similarity).

-!- SUBCELLIAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: Belongs to the amino acid permease family.

ArcD/cadB/lysI subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                       Transferase; Kinase; Arginine metabolism; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                              WITH A-209
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PIR; T46745; T46745.
InterPro: IPR002293; AA/rel_permeasel.
InterPro: IPR00481; Permease_region.
InterPro: IPR004754; R/C antiport.
Pfam; PF00324; aa_permease; 1.
TIGRPAMS; TIGR00905; 2A0302; 1.
InterPro, IPR003964; Bac_carb_kinase.
Pfam; PF00696; aakinase; 1.
PRINTS; PR01469; CARBMTKINASE.
                                                                                                                                                                                                                                                                                                                                                 32795 MW;
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                                               TIGRFAMS; TIGR00746; arcC;
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MUTAĞEN 135
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053092;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Catalyzes an electroneutral exchange between arginine and ornithine to allow high-efficiency energy conversion in the arginine deiminase pathway (By similarity).
-!- SUBCRITULAR LOCATION: Integral membrane protein (Potential).
-!- SINGRITY: Belongs to the amino acid permease family.
ArcD/cadB/lys! subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=13 / Type A, bubmed=11792842; bubbilnus=21664373; bubmed=11792842; bibmizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 1.7e+02;
; Mismatches 0; Indels
     transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                     8E91A01F6A2203CC CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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InterPro, IPR002293, AA/rel_permeasel.
InterPro, IPR004841; Permease_region.
  Amino-acid
                                                                                                                                                                                                                                                                                                                                                     51881 MW;
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ARCD OR CPE0170.
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361
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475 AA;
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Best Local Similarity
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01-0CT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
PTS system, sucrose-specific IIBC component (BIIBC-SCR) (Sucrose-permane IIBC component) (Phosphotransferase enzyme II, BC component) (EC 2.7.1.69) (BII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate.
-!- SUBCELLUAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
-!- SIMILARITY: Contains 1 PTS EIIC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DSM 20267 / Isolate C2A;
MEDLINE=94049686; PubMed=8232209;
Magner E., Goetz F., Brueckner R.;
"Cloning and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system from
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       .;
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          Pfam, PF00324; aa permeases; I.
TIGRFAMS; TIGR00905; 2A0302; I.
Transport; Antiport; Amino-acid transport; Transmembrane;
                                             POTENTIAL.
MISSING (IN REF. 1).
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1288;
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  IPR004754; R/O antiport.
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478 AA;
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GYWLS 100
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS)
GLYS OR APE1639.
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80.0%; Pred. No. 1.7e+02;
ive 1; Mismatches 0; Indels
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Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                 Transferase;
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                                                                                             EMBL, X68800; CAA49461.1; -
PIR; S39978; S39978.
InterPro; IPRO01396; Prrans_EIIB.
InterPro; IPRO03322; Prrans_EIIC.
Pfam; PF002378; PTS_EIIB; 1.
Propom; PD001476; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_01; 1.
PROSITE; PS01035; PTS_EIIB_07; 1.
PROSITE; PS01035; PTS_EIIB_075; 1.
PROSITE; PS01035; PTS_EIIB_075; 1.
PROSITE; PS01035; PTS_EIIB_075; 1.
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=99310339; PubMed=10382966;
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NCBI TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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HSSP; P56206; 1ATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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PIR; 140744; IREECA.
PDB; 1COL; 15-UL-93.
InterPro; 1F5-UL-93.
Finish PF01024; Colicin, 1.
PRINTS; PROBO280; CHANLOCOLICIN; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
Antiblotic; Bacteriocin; Flagmend; Transmembrane; 3D-structure.
TRANSMEM 528 548
POTENTIAL.
TRANSMEM 555 575
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80.0%; Pred. No. 2.1e+02;
ive 1; Mismatches 0; Indels
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Matches 4; Conservative
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PPCK NEOFR
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-I- FUNCTION: This colicin is a channel-forming colicin. This class of transmembrane toxins depolarize the cytoplasmic membrane, leading to dissipation of cellular energy.
-I- FUNCTION: COLICINS ARE POLYPERTIDE TOXINS PRODUCED BY AND ACTIVE AGAINST. ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.
-I- SIMILARITY: Belongs to the channel forming colicin family.
               InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002315; tRNA-synt_2b.
InterPro; IPR006195; tRNA-synt_gly.
InterPro; IPR006195; tRNA-synt_gly.
InterPro; IPR006195; tRNA-synt_2b; 1.
Pfam; PF00587; tRNA-synt_2b; 1.
PRINTS; PR01043; TRNA-SYNTHGLY.
ITGRPAM; TIGR00389; gly& dimeric; 1.
PROSITE; PS50862; AA TRNA_LIGASE II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=84036205; PubMed=6313941;
Morlon J., Lloubes R., Varenne S., Chartier M., Lazdunski C.;
"Complete nucleotide sequence of the structural gene for colicin A, a gene translated at non-uniform rate.";
J. Mol. Biol. 170:271-285(1983).
                                                                                                                                                                                                                                                                                                                   Gaps
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Morlon J., Chartier M., Bidaud M., Lazdunski C.;
"The complete nucleotide sequence of the colicinogenic plasmid ColA.
High extent of homology with ColE!.";
Mol. Gen. Genet. 211:231-243 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92235820; PubMed-1373773;
Parker M.W., Postma J.P.M., Pattus F., Tucker A.D., Tsernoglou D.;
"Refined structure of the pore-forming domain of colicin A at 2.4-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
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0
                                                                                                                                                                                                                                                                     90.9%; Score 30; DB 1; Length 583; 80.0%; Pred. No. 2.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                              583 AA; 66395 MW; 7D75DE7B5AA3F999 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 389~592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Colicin A.
InterPro; IPR004154; HGTP anticodon
                                                                                                                                                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Citrobacter freundii.
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                            Complete proteome.
SEQUENCE 583 AA
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P04480;
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MEDLINE-92184115; PubMed=1339359;

MEDLINE-92184115; PubMed=1339359;

Reymond P., Geourjnon C., Roux B., Durand R., Fevre M.;

Reymond P., Geourjnon C., Roux B., Durand R., Fevre M.;

Sequence of the phosphoenolpyruvate carboxykinase-encoding cDNA from "Sequence of the phosphoenolpyruvate carboxykinase-encoding converse the runen anaerobic fungus Neocallimastix frontalis: comparison of the amino as sequence with animals and yeast.";

Gene 110:57-63 (1992).

-! - CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate

    + CO(2).
    -!- ATHWAY: Rate-limiting gluconeogenic enzyme.
    -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP] family.

                                                                                                                                      (Phosphoenolpyruvate carboxylase) (PEPCK).
Neocallimastix frontalis (Rumen fungus).
Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Neocallimastix.
                    P22130;
01-AUG-1991 (Rel. 19, Created)
14-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
608 AA.
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EMBL; X01008; CAA25503.1; -.

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Gaps

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Length 667;

90.9%; Score 30; DB 1; Le 80.0%; Pred. No. 2.4e+02; .ive 1; Mismatches 0;

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4; Conservative
Query Match
Best Local Similarity
Matches 4; Conserv
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CARBOHYD
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  oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor [Contains: Knob protein GP70; Spike protein
P15E].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
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PIR; C32595; VCLJGL.
HSSP, P03385; IMOF.
InterPro; IPR002050; Env polyprotein.
InterPro; IPR008981; F_MULV_bind.
Pfam; PF00429; ENV polyprotein; 1.
Coat protein; dlycoprotein; Polyprotein; Transmembrane; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.9%; Score 30; DB 1; Length 608; 80.0%; Pred. No. 2.2e+02; ative 1; Mismatches 0; Indels
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W, SFFB32F00D8631BE: CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibbon ape leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=11840;
                                                                 EMBL, MS9372; AAA33553.1; -.
EMBL, MS9372; AAA33553.1; -.
EMBL, MS9372; AAA33553.1; -.
EMBL, MS9372; AAA33553.1; -.
R InterPro; IPR008210; PEPC X.N.
R InterPro; IPR008210; PEPC X.N.
DR Pfam; PF00831; PEPC X.N.
DR PROSITE; PS00505; PEPC X.N.
DR ROSITE; PS00505; PEPC X.N.
DR Gluconeogenesis; Lyase; Decarboxylase; GTP-binding.
The matter of the matter o
                                                                                                                                                                                                                                                                                                                                                                                                 C4D2B249A92B7D26 CRC64;
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MEDLINE=90051069; PubMed=2683360;
Delassus S., Sonigo P., Wain-Hobson S.;
"Genetic organization of gibbon ape leukemia virus.";
Virology 173:205-213(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNOB PROTEIN GP70.
SPIKE PROTEIN P15E.
POTENTIAL.
POTENTIAL.
     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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421 N-
433 N-
453 N-
73729 MW;
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Best Local Similarity 80..
4; Conservative
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ENV GALV
AC P21415;
DT O1-MAY-199
DT OARBOHYD
ENV OOAL DYORE
DE DE DISSURS
RY MEDLINE=90
RA MEDLINE=90
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                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase)
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PIR, JC4836; JC4836.
InterPro; IPR005154; Glyco hydro_67.
Pfam; PF03648; Glyco_hydro_67; 1.
Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.signAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=QM9414 / Rut C-30;
MEDLINE=96257277; PubMed=8654984;
Margolles-Clark E., Saloheimo M., Slika-Aho M., Penttilae M.;
"The alpha-glucuronidase-encoding gene of Trichoderma reesei.";
Gene 172:171-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichoderma reesei (Hypocrea jecorina).
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + D-glucuronate.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity 80.0%; Pred. No. 38+02;
4; Conservative 1; Mismatches 0; Indels
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N-LINKED (GLCNAC. N-LINKED 
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                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
180 GYWLS 184
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CAPP RHOMR
ID CAPP RHOM
AC QS9757;
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Alcaligenes eutrophus (Ralstonia eutropha).
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                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                              L-aspartate and L-malate.
-!- PATHARY: Tricarboxylic acid cycle.
-!- SUBUNIT: Honoterramer.
-!- MISCELLANEOUS: The optimum temperature for activity is 75 degrees Celsius. The enzyme exhibits a pH optimum of 8.0.
-!- SIMILARITY: Belongs to the PEPCase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CZCA ALCEU STANDARD; PRT; 1063 AA.
P13511; P94142;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cobalt-zinc-cadmium resistance protein czcA (Cation efflux system
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-Rel. 31, Last amodation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                              Rhodothermus marinus (Rhodothermus obamensis).
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Crenotrichaceae; Rhodothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, NE 0059; 1.1.
InterPro; IPR01449; PEPcase.
Pfam; PF00111; PEPcase; 1.
PR0150; PEPCAREXIASE.
PR0SITE; PS00793; PEPCASE 2; 1.
PROSITE; PS00781; PEPCASE 1; 1.
Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 1; Length 930
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 BY SIMILARITY.
595 BY SIMILARITY.
107886 MW; C9AA94C3F26C345A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.9%;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X99379; CAA67760.1; -. HSSP; P00864; 1FIY.
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595
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Best Local Similarity
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allosteric enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 GYWMA 602
                                                                            NCBI_TaxID=29549;
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595
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CZCA.
                                                                                                         STRAIN=OKD7
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CZCA ALCEU
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                                                                                                                                                         STRAIN=CH34;
MEDLINE=901477; PubMed=2678100;
MEDLINE=901477; PubMed=2678100;
MEDLINE B., Nies A., Chu L., Silver S.;
"Expression and nucleotide sequence of a plasmid-determined divalent cation efflux system from Alcaligenes eutrophus.";
Proc. Natl. Acad. Sci. U.S.A. 86:7351-7355(1989).
                                                                                                                                                                                                                                                                                                                                                                                               van der Leije D., Schwuchow T., Wuertz S., Schwidetzky U.,
Bacyens W., Scheel P.O., Nies D.H.;
Bacyens W., Scheel P.O., Nies D.H.;
Bacyens W., Scheel P.O., Nies D.H.;
Schmitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HAS A LOW CATION TRANSPORT ACTIVITY FOR CO(2+), IT IS
BESSENTALE FOR THE EXPRESSION OF COBALT, ZNIC, AND CADMIUM
RESISTANCE. CZCA AND CZCB TOGETHER WOULD ACT IN ZN(2+) EFFLUX
NEARLY AS EFFECTIVELY AS THE COMPLETE CZC EFFLUX SYSTEM (CZCABC)
-!- SOBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- INDUCTION: By cadmium, copper and zinc.
-!- SIMILARITY: BELONGS TO THE ACRE/ACRD/ACRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Plasmid pWOL30.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
NCBI_TaxID=510;
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1063 AA; 115668 MW; 1E95B7923996AEBC CRC64;
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Pred. No. 3.7e+02;
1; Mismatches 0;
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BIR; A33820; A33830.
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004763; CzcA.
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Plasmid; Transport; Zinc; Cobalt;
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PRINTS; PR00702; ACRIFLAVINRP.
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MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MARIA H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dang H.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Rabardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

M. Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

MEBL; A84376.

SEQUENCE 67 AA; 6601 MW, A6BAF23FCBBBB648 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 33; DB 17; Length 67; 100.0%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaecta; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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01-MAR-2001 (TrEMBirel. 16, Last sequence update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
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091AD9
091AH0
091AAG4
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Q9S4W3
Q9WTF7
   5; Conservative
   Local Similarity
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                                                                                                        September 30, 2004, 05:55:56; Search time 16.3559 Seconds (without alignments) 96.454 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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Q8FR71
Q8FB4
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sp_unclassified:*
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sp. organele:*
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Match Length
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Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali B.C., Machado M.A., Madeira A.M.B.N., Martines-Rossi N.M., Martine B.C., Machado M.A., Madeira A.B.N., Martines-Rossi N.M., Martine B.C., Mardanis J., Menck C.F.M., Myaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Sosai A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."
                                                                                                                                                                                                                                                   100.0%; Score 33; DB 16; Length 85; 100.0%; Pred. No. 69; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       85 AA; 9609 MW; CGFDC29D07155274 CRC64;
                                                                                                                                                                    Nature 417:459-463(2002).
EMBL; AE012100; AAM39386.1; -.
Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integral membrane protein.
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5, Conservative
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Lactobacillus plantarum,
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SEQUENCE FROM N.A.

SEQUENCE 202145; PubMed=12024217;

MEDINIE=20202145; PubMed=12024217;

A LVC 3. Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A LVC 5. Ganarao L.E.A.,

Camarotte G. Cannavan F., Cardozo J., Chambergo E.E.A.,

Camarotte G. Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A LVC 5. Ganarotte G. Cardozo J., Cursino-Santos J.R., El-Dorry H.,

Paria J.B., Ferrelar A.J.S., Ferreira R.C.C., Furbor M.I.T.,

Ratsuyama A.M., Kishi L.T., Careggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Madeira B.C., Gruber A.,

Ratsuyama A.M., Mishi L.Y., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Setubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing

thost specificities.",

Nature 417459-463 (2002).
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STRAINATCS 33913 / NCPPB 528;
MEDLINE-22022145; PubMed=1204217;
MEDLINE-22022145; PubMed=1204217;
MEDLINE-22022145; PubMed=1204217;
Ga Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,
                                                                                                                                                                       Bacteria, Proteobacteria; Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome. SEQUENCE 73 AA; 8296 MW; 89C3771680F46C3D CRC64;
                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Hypothetical protein XAC0095.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                    Xanthomonas axonopodis (pv. citri)
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                                                 PRELIMINARY;
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Best Local S
Matches 5
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Klearebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Klipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Mierop Groof M.N., Kerkhoven R., De Vries M., Ursing De Vos W.M., Siezen R.J.;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel 25, Last annotation update)
10-OCT-2003 (TrEMBLrel 25, Last annotation update)
10-OCT-2003 (TrEMBLrel 25, Last annotation update)
10-OCT-2000 (TrEMBLrel 25, Last annotate)
10-OCT-2000 (TrEMBLrel 25, Last annotate)
10-OCT-2000 (TrEMBLrel 25, Last annotate)
11-OCT-2000 (TrEMBLrel 25, Last annotate)
11-OCT-2000 (TrEMBLrel 25, Last annotate)
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Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
BMBL, AL935.27; CAD64219.1; -
InterPro; IPR007163; DUF368.
Pfam; PF04018; DUF368, 1.
Complete proteome.
SEQUENCE 285 As. 30888 MW; D93DB9353EA9D881 CRC64;
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                                                                                                                                                                                                                                          Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae,
Lactobacillus.
NCBI_TaxID=1590;
(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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MEDLINE=20115608; PubMed=10648209;

AS 3011/van J.P., Lavoue S., Hopkins C.D.;

Molecular systematics of the Airican electric fishes (Mormyroidea:
Teleostei) and a model for the evolution of their electric organs.";

I. D. Exp. Balol. 203:665-683(2000).

B. Balol. AF201644; AAF43355.1.

B. Ball. AF201644; AAF43355.1.

B. GO, GO:0005634; C:nucleus; IEA.

GO, GO:0005310; P:DNA binding; IEA.

R. GO; GO:0005310; P:DNA recombination; IEA.

R. D. GO:0005310; P:DNA recombination; IE
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

X MEDIANE-20115608; PubMed=10648209;
ANDLINE-20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(200).
R EMBL; AR201618; AAR43329.1;
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0005631; P:DNA recembination; IEA.
R GO; GO:0006310; P:DNA recembination; IEA.
R TherPro; IPR004321; RAG2.
R PFan; PF03089; RAG2; I.
R NON TER.
T NON TER.
T NON TER.
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                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neoperygii, Teleostei, Osteoglossomorpha, Osteoglossiformes, Mormyridae, Brienomyrus.
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels C
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Recombination-activating protein 2 (Fragment).
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100.0%; Score 33; DB 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=112141;
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X Sullivan J.E., Lavoue S., Hopkins C.D.;

Sullivan J.E., Lavoue S., Hopkins C.D.;

If "Molecular systematics of the African electric fishes (Mormyroidea: Teleoster) and a model for the evolution of their electric organs.";

If Teleosteri) and a model for the evolution of their electric organs.";

If EMBL; AP201645; AAF43356.1;

IR EMBL; AP201645; AAF43356.1;

IR EMBL; AP201645; AAF43356.1;

IR GO; GO:0005310; PiDMA binding; IEA.

R GO; GO:0005310; PiDMA recombination; IEA.

IR PFGM; PFGM; PFGM;

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MEDLINE=20115608; PubMed=10648209;
Sullivan J.P., Lavouce S., Hopkins C.D.;
Sullivan J.P., Lavouce S., Hopkins C.D.;
Molecular systematics of the African electric fishes (Mormyroidea:
"Molecular systematics of the African electric organs.";
J. Exp. Biol. 203:665-683(2000).
G.S. Barb. AR-201635; AAR-43346.1; -
GO, GO:0005634; C:nucleus; IEA.
GO; GO:000577; F:DNA binding; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
PFG03089; RAG22: 1.
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Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Mormyrus.
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              Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha; Osteoglossiformes; Mormyridae; Ivindomyrus.
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NON TER 377 377
SEQUENCE 377 AA; 41428 MW; B60EDE613EA0FDBE CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
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Best Local Similarity 100..
Page 5; Conservative
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Best Local Similarity
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                                                                        Osteoglossiformes
NCBL_TaxID=91727;
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RESULT 6 Q91AE9

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RESULT 7 Q91AH4 ID Q91AJ AC Q91AJ DT 01-O

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Query Match
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Q9IAG1;
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Q9IAG1
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MEDLINE=20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.,
"Molecular systematics of the African electric fishes (Mormyroidea:
Teleostei) and a model for the evolution of their electric organs.",
J. Exp. Biol. 203:665-683(2000).
BMBL, AF201620; AAF43311; --
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005637; F:DIA binding; IEA.
GO; GO:0006310; P:DIA binding; IEA.
InterPro; IPR004321; RAG2.
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Sullivan J.P., Lavoue S., Hopkins C.D.;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the African electric organs.";
J. Exp. Biol. 203:665-683(2000).
Exp. Biol. 203:665-683(2000).
EMBL; AF201625; AAF43335.1; -..
GO: GO:000534; AAF43335.1; -..
GO: GO:000534; Cinucleus; IEA.
GO: GO:0005310; P:DNA binding; IEA.
GO: GO:0005310; P:DNA binding; IEA.
InterPro; IPR004321; RAG2.
NOW_TER
                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha,
Osteoglossiformes, Mormyridae, Brienomyrus.
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377 377
377 AA; 41522 MW; 2E93DC79A8B6EC4A CRC64;
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                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
101-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment)
Campylomormyrus tamandua
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100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
                                                   377 AA.
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                                                     PRT;
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Best Local Similarity 100.0
                                                     PRELIMINARY;
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NON TER 1 1
NON_TER 377 377
SEQUENCE 377 AA; 41
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377 AA;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=42637;
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SEQUENCE
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RESULT 9
Q9IAH2
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WEDLINE=20115608; PubMed=10648209;

A Sullivan J.P., Lavoue S., Hopkins C.D.;

A Sullivan J.P., Lavoue S., Hopkins C.D.;

Explain and a model for the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";

Explain AF20163; AAF4344.1;

EMBL, AF201633; AAF4344.1;

CO, GO:0005634; C:nucleus, IEA.

CO, GO:000534; C:nucleus, IEA.

CO, GO:000517; F:DNA binding; IEA.

CO, GO:000517; F:DNA binding; IEA.

CO, GO:000367; F:DNA binding; IEA.

CO, GO:000367; F:DNA binding; IEA.

CO, GO:000367; F:DNA binding; IEA.

CO, GO:000317; F:DNA binding; IEA.
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MEDLINE=20115608; PubMed=10648209;

MEDLINE=20115608; PubMed=10648209;

Sullivan J.P., Lavoue S., Hopkins
Sullivan J.P., Lavoue S., Hopkins
T. "Molecular systematics of the African electric fishes (Mormyroidea:
T. "Molecular systematics of the African electric organs.";
J. Exp. 10.2 13:65-665-683(2000).

I. Exp. 10.2 13:65-665-683(2000).

R. Exp. 10.2 10.3 16.5 16.5 16.5 16.5

R. GO: GO:0003674; F:DNA binding; IEA.

R. GO: GO:0003671; F:DNA recombination; IEA.

R. TherPro; IPR004321; RAG2.

R. Pfan; FF03089; RAG2; I.

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Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Hyperopisus.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
Marcusenius senegalensis.
Marcusenius senegalensis.
Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha;
Osteoglossifonmes, Mormyridae, Marcusenius.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
Hyperopisus bebe.
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Matches 5; Conservative
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                                                     368 GYWMS 372
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1 GYWMS 5
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368 GYWMS 372
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MEDLINE=20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Teleostei) and a model for the African electric fishes (Mormyroidea:
Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(2000).
EMBL, AF201621; AR43332.1;
EMBL, AF201621; AR43332.1;
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
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J. Exp. Biol. 203:665-683(2000).

GO; GO:0005654; AR43367.1; -..
GO; GO:0005677; F:DNA binding; IEA.
GO; GO:00056710; P:DNA binding; IEA.
FILTEFPC, IPRO04221; RAG2.
PFGM; PF03089; RAG2; 1.
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                                                                        Score 33; DB 13; Length 377;
Pred. No. 3.1e+02;
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41393 MW; A33A11B903FE33C7 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Recombination-activating protein 2 (Fragment).
Stomatorhinus walkeri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 AA.
                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 3.16
Matches 5; Conservative 0; Mismatches
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SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SUllivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

"Molecular systematics of the African electric fishes (Mormyroidea:

"Molecular systematics of the African electric organs.";

Teleostei) and a model for the evolution of their electric organs.";

J. Exp. Biol. 203:665-683(2000).

EMBL, AF201654; AAF43365.1;

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005631; F:DNA binding; IEA.

GO; GO:00056310; P:DNA recombination; IEA.
                                                                                                                                                                                                                                                         O; Gaps
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01-0CT-2000 (TTENBLrel. 15, Last sequence update)
01-0CT-2003 (TTENBLrel. 25, Last amontation update)
Recombination-activating protein 2 (Fragment).
Pollimyrus isidori.
Pollimyrus isidori.
Pollimyrus isidori.
Actinopterygii, Neoperygii, Teleostei, Osteoglossomorpha;
Actinopterygii, Neoperygii, Teleostei, Osteoglossomorpha;
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
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                                                                                                                   377 377 377 377 AM; 735853EEA67408FE CRC64;
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100.0%; Pred. No. 3.1e+02;
ative 0; Mismatches 0;
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GO; GO:0006310; P:DNA recombination; IEA.
InterPro; IPR004321; RAG2.
Pfam; PF03089; RAG2; 1.
NON_TER 377 377
SEQUENCE 377 AA; 41475 MW; 735853EEA6
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Pfam; PF03089; RAG2; 1.
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les 5; Conservative
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Dime Sheet

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September 30, 2004, 05:55:56; Search time 24.4068 Seconds (without alignments) 57.883 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                              1586107 seqs, 282547505 residues
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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33
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Perfect score:
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Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

A Geneseq 29Jan04:\* .: geneseqp1980s:\* :: geneseqp1990s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Light cha Mouse ant DNA clone DNA clone Humanised V39, mono Human sec Human gen Human sec Chlamydia Novel sig Human nov Staphyloc Enterococ GALV retr Drosophil Novel hum Human sec Human sec prote prote prote Rat HT gl Skin cell Staphyloc Rat HRat HRat Description Abr48102 B Abr00271 B Adb91793 B Adc74531 B Aay07813 B Aay35482 Aay1327 B Adb94035 B Aab94035 B Aab56053 Aab56053 Abb72253 Abb72290 Abb72290 Abm72990 Aam72990 Aau35317 Aay32263 Abb62006 Abg07533 Aar95472 SUMMARIES AAY07813 AAY35482 AAU17327 ADB94035 AAR95472 ABR48102 ABR00271 ADC74531 Query Match Length DB 100.0 Score Result . S

Abu29423 Protein e			Aab19870 Activatin	Aag31981 Arabidops	Aab38394 Human sec	Ada41195 Human sec	Abr48101 Human sec	Abr00270 Human gen	Adb91792 Human sec	Adc74530 Human sec	Adc74397 Human sec	Adc97365 E. faeciu	-H	Aay13362 Amino aci	Human	Aab24396 Human PRO	Adc78429 Human PRO	Aab80230 Human PRO	Aab27228 Human EXM
ABU29423	ABB55045	AAG31982	AAB19870	AAG31981	AAB38394	ADA41195	ABR48101	ABR00270	ADB91792	ADC74530	ADC74397	ADC97365	AAY05281	AAY13362	AAY88569	AAB24396	ADC78429	AAB80230	AAB27228
310 6	315 5	359 3	374 4			392 6	392 6	_	392 7	392 7	392 7	408 7	420 2	420 2	420 3	420 3	420 3	420 4	420 4
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## ALIGNMENTS

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; confluenterity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; Light chain CDR H1 of mouse anti-CD23 MAb C11. AAY32257 standard; peptide; 5 AA. 15-FEB-2000 (first entry) AAY32257; 

urticaria, nephrotic syndrome; glomerulonephritis; urticaria, nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

Mus musculus. 07-MAY-1999; WO9958679-A1 18-NOV-1999.

99WO-GB001434. 98GB-00009839. GLAX ) GLAXO GROUP LTD 09-MAY-1998;

Shearin J; Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT,

WPI; 2000-053101/04. N-PSDB; AAZ34742.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 1; Page 40; 81pp; English

This sequence represents complementarity determinating region 1 (CDR H1) of the heavy chain of murine anti-CD23 (FCBRII) monoclonal antibody C11 (see also AAY32253). The invention provides altered antibodies, such as chiencic or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

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render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus eryhematosus. Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, frianmatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma authentic exacerbation, rhinitis, eczema, graft-versus-host disease, (OPD), insulitis, bronchitis (particularly chronic bronchitis) or diabetes are also useful for studying interactions between CD23 and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD23; FCERII; IgE receptor; monoclonal antibody; CII; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region, CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria, nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogrem's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
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/note= "CDR H3"
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129. .1
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Matches 5; Conserv
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This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides anti-CD23 (FCERII) monoclonal antibody C11. The invention provides carefront and havales, such as chimeric or humanised antibodies, such as chimeric or humanised antibodies (see AAY32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on hamancopietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematicus, Hashimoto's thyroiditis, multiple of arthritis, lupus erythematics, dermatics, sporiasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Siggren's syndrom, allergies althma, acute asthmatic exacerbation, rhinitis, eczema, graftvorintrinsic asthma, acute asthmatics, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and Brcell mallignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA clone originating in barley containing SNP sequence #377.
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100.0%; Pred. No. 1.2e+02;
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Claim 8; Fig 1; 81pp; English.
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20-DEC-2001, 2001JP-00487131.
20-DEC-2001, 2001JP-00403299.
20-DEC-2001, 2001JP-00403309.
27-SEP-2002, 2002JP-00327515.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003057877-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characteristics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM73967;
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ABM73967
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Length 345

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The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonuclectide clone sequence featured in the specification. The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published-pct-sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired characteristics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA clone originating in barley containing SNP sequence #66.
                                                                                                                                                                                                          Length 163;
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Similarity 100.0%; Score 33; DB 7; Length 16
Similarity 100.0%; Pred. No. 1.5e+02;
5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published-pct-sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                        ABM73656 standard; protein; 345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2001; 2001JP-00387059.
20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403309.
27-SEP-2002; 2002JP-00327515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kohara Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2002; 2002WO-IB005403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNI-) UNIV JAPAN OKAYAMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                            84 GYWMS 88
                                                                                                                                                                                                                                                                                        1 GYWMS 5
                                                                                                                                                                            Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare.
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Best Local S:
Matches 5
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Sequence 345 AA;

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                                                                                                                                                                                                                  CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; inflammatory bowel disease; ulcerative collitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft.versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This amino acid sequence represents the heavy chain of humanised anti-
CD23 (FCERII) monoclonal antibody C11, composed of a human framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis,
                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell receptor specific antibodies useful for treating e.g. diabetes, multiple sclerosis and psoriasis.
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Query Match
100.0%; Score 33; DB 7; I
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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'note= "framework region 1"
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/note= "constant region"
                                                                                                                                                                                                Humanised anti-CD23 MAb C11 heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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101. .103
                                                                                                                               AAY32263 standard; protein; 444 AA
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/note= "framework
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...35
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note= "CDR 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonnefoy JMP, Crowe SJ,
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N-PSDB; AAZ34748.
                                                                      GYWMS 270
                                                 1 GYWMS 5
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                      AAY32263;
                                                                                                                                                                                                                                                                                                                                  therapy.
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Region
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CHSIGKVII) and the heavy chain complementarity determining regions (see AA732257-59) of murine antibody CII. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, which comprises sufficient of the amino acid or humanised antibodies, which comprise sufficient of the amino acid sequences of the CII light and heavy chain complementarity determining regions to render them capable of binding to the CD31 type II molecule expressed on haematopoletic cells. The antibodies are used to block soluble CD33 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's throiditis, multiple sclerosis, calabetes, uvertis, dermatitis, psoriasis, utticaria, nephrotic syndrome, complementolomphritis, inflammatory bowel disease, ulcerative colitis, crown, s disease, Sjogren's syndrome, allergic asthma, acute asthmatic exacerbation, thinitis, eczema, graftcores. Oversus-host disease, COPD, insulitis, bronchitis (particularly type I diabetes) and B-cell malignancies (claimed). They are also useful for studying interactions of the colline of the present also useful for studying interactions of the colline of the particularly choose of the colline of the particular of the present colline of the present colline of the particular of the present colline of the present coll
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0
100.0%; Score 33; DB 3; Length 444; 100.0%; Pred. No. 4.1e+02; ive 0; Mismatches 0; Indels
  Query Match
Best Local Similarity 100.
Matches 5, Conservative
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RESULT 6 ABB62006

ABB62006 standard; protein; 1254 AA.

ABB62006;

26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 12810.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US009231.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE ) PE CORP NY.

solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell Myers EW; Li PWD, Venter JC, Adams M, WPI; 2001-656860/75. N-PSDB; ABL06109 New isolated

Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.

interactions.

geneg

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737- $\mathbf{x}_{\mathsf{C}} \mathbf{x}_{\mathsf{C}} \mathbf{x}$ 

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recarbinates, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed city control in gene therapy techniques to restore normal activity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. Abg00010-Ab330377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                  100.0%; Score 33; DB 4; Length 1254; 100.0%; Pred. No. 1.2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #7524.
                                                                                                                                                                                                                                                                                                                               ABG07533 standard; protein; 40 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                  Local Similarity 100.
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                                                                                                                                                                                                                                  1139 GYWMS 1143
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                                                                             Seguence 1254 AA;
                                                                                                                                                                                           1 GYWMS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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New isolated peptide(s) with specific binding activities - obtd. by screening random peptide libraries, for use in diagnostic and therapeutic
                                                                                                                                                                                                                                                                                 Abtide, prostate specific mucin antigen; human prostate cancer; LNCaP; diagnostic; detection; imaging; tumour; phage; peptide library; breast; polymorphic; epithelial.
                                                                                                                                                                                                                                                                V39, monoclonal antibody SM-3 derived antigen binding peptide.
                                                                                              Length 40;
                                                                                             90.9%; Score 30; DB 4; Length 40;
80.0%; Pred. No. 1.3e+02;
.ive 1; Mismatches 0; Indels
                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 38; Page 75; 106pp; English.
                                                                                                                                                                                                        AAR95472 standard; peptide; 43 AA.
Sep 30 13:18:58 2004
                                                                                                                                                                                                                                                                                                                                                                                                          94US-00310192.
95US-00488161.
                                                                                                                                                                                                                                                                                                                                                                                       95WO-US011934
                                                                                                                                                                                                                                                05-NOV-1996 (first entry)
                                                                                                       Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-188471/19.
                                                                                                                                                        33 GYWLS 37
                                                                                                                                    1 GYWMS 5
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monoclonal antibody SM-3 which recognises a specific polymorphic epithelial mucin tumour antigen found on human breast cancer cells. The ebithelial mucin tumour antigen found on human breast cancer cells. The abtides are identified from random peptide libraries using specific ligand binding. Abtides minic the binding specificity of large molecules such as antibodies and receptors but have a much smaller size allowing timmunogenicity aiding in vivo delivery. The abbides are useful for the diagnosis, detection, imaging and treatment of disease, e.g. tumours, prostate cancer and breast cancer

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Score 30; DB 2; Length 43;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                              1; Mismatches
 90.9%;
                               4; Conservative
     Query Match
Best Local Similarity
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|||:| 6 GYWLS 10

RESULT 9

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The present invention relates to novel human secreted proteins (ABR47633-CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences (ACC50344-ACC50856). The proteins cor pharmaceutical composition for diagnosing or treating a cardiovascular disorder; arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, misorders, pulmonary disorders, reproductive disorders, immune gastrointestinal disorders, pulmonary disorders, renal disorders, immune proliferative disorders and/or cancerous diseases and conditions, for commenced and entire and proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue cransplants or bone grafte, to prevent skin aging or hair loss, to transplants or bone grafte, to prevent skin aging or hair loss, to crans before transplantation of haematopoietic cells and bone carrow calls when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in celectronic format and is available from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                       Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
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80.0%; Pred. No. 2e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID NO 993; 1881pp; English
                                                                                                                                       Human secreted protein, SEQ ID 993.
                   ABR48102 standard; protein; 63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                           .9-MAR-2002; 2002WO-US009785
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Best Local Similarity Bu...
4; Conservative
                                                                                                 12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Ruben SM;
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RESULT 10

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ADB91793 standard; protein; 63 AA.

RESULT 11

ADB91793

ADB91793;

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Drotein genes, and ABP00011-ABP00299 represent the proteins they encode.

ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted

Drotein genes, and ABP00011-ABP00299 represent the proteins they encode.

ABZ711540 represent human secreted proteins they encode.

Convention also encompasses antibodies specific for the secreted proteins.

The use of the secreted proteins in drug screening, and recombinant vectors and host cells comparising a mucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing activity are useful for diagnosing, treating, ameliorating or preventing of sophagus, stomach, small intestine, large intestine, liver, billary treatment of immune disorders in flammation, infection, oscophagus, stomach, and include cancers of these organs and tissues. The recented proteins and their mucleic acids may also be used in the treatment of immune disorders, inflammation, infection, hyperproliferative disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute propers. The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                              Human, secreted protein; digestive disorder, gastrointestinal disorder, mouth, oesophagus; stomach, small intestine, large intestine, liver; billary tract, pancreas, cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; hyperciton, wound healing; drug screening; chromosome identification, chromosome mapping, cytostatic; gene therapy; antiinflammatory; immunosuppressive; vulnerary; chromosome 3p25.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
                                                                                                                                                         Human gene 139 encoded secreted protein HPRAL78, SEQ ID NO:560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.9%; Score 30; DB 6; Length 63; 80.0%; Pred. No. 2e+02; 1.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 1107; 1216pp; English.
                       ABR00271 standard; protein; 63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-029900/02
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                                                                                                                                                                                                                                                                                                                                                                                                 WO200276488-A1.
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                             03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002.
                                                                 ABR00271;
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Matches
ABR00271
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The invention relates to isolated nucleic acid molecules ADB91065-ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449.

ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-ADB91449.

ADB91344. Also disclosed is a recombinant vector comprising a pulparate of the invention, and a recombinant host cell comprising the recombinant vector. The polypeptide of the invention is useful in identifying a binding partner by contacting the polypeptide with a binding partner, and determining whether the binding partner increases or decreases activity of the polypeptide. The polypeptide, polynucleotide, antibody or its fragment, agonist or antagonist are useful for preparing a pharmaceutical composition for diagnosing or treating diabetes or conditions related to diabetes. The present sequence is that of the human immunoglobulin Fc portion used to generate fusion proteins, increasing the stability of the fused protein as compared to the secreted protein only. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding a human secreted protein is useful in diagnosing or treating diabetes or conditions related to diabetes.
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                                                                                                                        Secreted protein; gene therapy; antidiabetic; diabetes; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 739; 1537pp; English.
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                                                                                      Human secreted protein #SEQ ID 739.
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                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                              19-MAR-2002; 2002WO-US008124;
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                                                   (first entry)
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Best Local Similarity 80.0.
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                                                                                                                                                                                         WO2003004622-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 63 AA;
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                                                                                                                                                         Homo sapiens.
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                                                   04-DEC-2003
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SEXPXFXEX
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45 GYWLS 49

1 GYWMS 5

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Human secreted protein fragment encoded from gene 70.

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New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
            antidiabetic; immunosuppressive; dermatological; nephrotropic; antiparkinsonian; neuroprotective; nootropic; antiparterial; virucide; fungicide; antiparastitic; antiateriosclerotic; vulnerary; cytostatic; haemopoietic; haematologic; antentia; autoimmune disorder; rheumatoid arthritis; inflammation; drave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's, wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parastitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; SEQ ID NO 1164; 2272pp; English.
                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                        19-MAR-2002; 2002WO-US008277
                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-430516/40.
N-PSDB; ADC73916.
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                                                                                                                                                                                WO2003038063-A2.
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                             08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                   Rosen CA,
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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haematologic disorder such as anaemia, autoimmune disorders such as rhemmation, farave's disease, disorders such as rhemmation, farave's disease, controlled arthritis, inflammation, farave's disease, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene therapy procedures and for identifying a binding partner by contacting the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. invention.

Gaps ö 90.9%; Score 30; DB 7; Length 63; 80.0%; Pred. No. 2e+02; 1ve 1; Mismatches 0; Indels Query Match Query Match Best Local Similarity 80.vv, Best Local Similarity Sequence 63 AA;

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|||:| GYWLS 49 1 GYWMS 5 à 셤

AAY07813 standard, protein; 64 AA. AAY07813; RESULT 13
AAY07813
ID AAY07
XX
AC AAY07
XX
DT 06-JU

(first entry) 06-JUL-1999

Human; secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosts; cancer; tumour; neurodogenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; alleray; astima; sepsis; diabetes; AIDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection. 97US-0056369P. 97US-0056535P. 97US-0056555P. 97US-0056628P. 97US-0056629P. 97US-0056726P. 97US-0056726P. 98WO-US017044 98US-0092956P. (HUMA-) HUMAN GENOME SCI INC. Homo sapiens. WO9909155-A1. 18-AUG-1998; 25-FEB-1999. 19-AUG-1997; 19-AUG-1997) 19-AUG-1997, 19-AUG-1997, 16-JUN-1998 15-JUL-1998; 19-AUG-1997 19-AUG-1997 

Florence Ruben SM, Young PE, Brewer LA, Ebner R, Olsen HS, Florence Rosen CA, Duan R, Moore PA, Shi Y, Lafleur DW, Florence C, Soppet DR, Endress GA, Feng P, Komatsoulis GA;

WPI; 1999-190160/16. N-PSDB; AAX37438. New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

Claim 1b; Page 264; 280pp; English.

This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or amaliorating medical conditions es.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or absence of mutations in the new polymucleotides. Specific uses are described for each of the 70 polymucleotides. Specific uses are described for each of the 70 polymucleotides based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foctal deficiencies, blood disorders, leukemias, diseases of the inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and cognitive disorders schizophrenia osteoporosis, arthritis, psoriasis, inflammation, allergies, infections and renal disease, lymphomas, of dispessive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/enclassive/

Sequence 64 AA;

Gaps .; 0 90.9%; Score 30; DB 2; Length 64; 80.0%; Pred. No. 2e+02; cive 1; Mismatches 0; Indels Local Similarity 80.0 es 4, Conservative Query Match Best Loc Matches

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Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae. (Updated on 17 -2003 to standardise OS fitch)
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Pred. No. 5.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel signal transduction pathway protein, Seq ID 892.
                                                                                                                                Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 1244; Disclosure; 1912pp; English
                            AAY35482 standard; protein; 181 AA.
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Matches 4; Conservative
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GYWLS 52
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13-SEP-1999
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RESULT 14
               AAY35482
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organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; enrodedenzative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                                                                                                                                                                        2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
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2000US-0216647P
2000US-0217487P
2000US-0217487P
2000US-0217496P
2000US-0217496P
2000US-0220964P
2000US-0220964P
2000US-0220964P
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2000US-0226279P.
2000US-0226681P.
2000US-0226868P.
2000US-0227182P.
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2000US-0229343P.
2000US-0229344P.
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2000US-0225214P.
2000US-0225266P.
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2000US-0225757P
2000US-0225758P
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2000US-0229509P.
2000US-0229513P.
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2000US-0231244P.
2000US-0231413P.
                                                                                            WO200154733-A1.
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17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
28-JUN-2000;
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23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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06-SEP-2000;
                                                                            Homo sapiens.
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08-SEP-2000;
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2000US-0232401P

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200004S-023423P.
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200004S-0234997P.
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200004S-0234997P.
200004S-02358344P.
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200004S-02358349P.
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200004S-0235834P.
200004S-023493P.
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2000US-0249299P.
2000US-0249300P.
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17-NOV-2000;
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25 - SEP - 2000;
26 - SEP - 2000;
27 - SEP - 2000;
27 - SEP - 2000;
29 - SEP - 2000;
20 - SEP - 2000;
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17-NOV-2000;
17-NOV-2000;
14-SEP-2000;
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14-SEP-2000;
21-SEP-2000;
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4; Conservative

|||:| 68 GYWLS 72 1 GYWMS 5

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completed: September 30, 2004, 06:06:20 ne : 29.4068 secs

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The invention relates to novel isolated polypeptides (1), and

C polymucleotides (II). (II) and the antibody to (I) are useful for

C diagnosing, preventing and treating diseases including immune system

disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

disorders (e.g. rongenital arthritis), inflammatory conditions, organ

transplant rejections and graft versus host disease, infectious diseases

CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and

cher blood-related disorders (sickle cell anaemia), myeloproliferative

cother blood-related disorders (sickle cell anaemia), myeloproliferative

CC quench: disease, Parkinson's disease), hyperproliferative disorders

CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC Alzheimer's disease, Parkinson's disease), chromosomal disorders (e.g.

Chown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.

Glomerulorephritis), cardiovascular disorders (e.g. arrhythmia),

crepiratory disorders, dermatological disorders (e.g. Addison's

clinflammatory disorders, liver disorders, gastrointestinal disorder

C (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

B-cell responsiveness to pathogens, activators of T-cells, to induce

CC higher affinity antibodies, and as a means to induce tumour proliferation

chapter affinity antibodies, and as a means to induce tumour proliferation

chapter affinity antibodies, and as a means to induce (unour proliferation

chapter affinity antibodies, and as a means to induce (myours)

con pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-

con pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-

con pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-

con pathologies of the invention
                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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80.0%; Pred. No. 6.8e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 892; 880pp; English.
                                                                                                                                                                                                                                                  Ruben SM
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-025199P.
08-DEC-2000; 2000US-025199P.
11-DEC-2000; 2000US-025499P.
05-UAN-2001; 2001US-0254097P.
                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                  Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                 WPI; 2001-465460/50.
N-PSDB; AAS27244.
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Best Local Similarity
Matches 4; Conserv
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Dank Shelf

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  September 30, 2004, 06:01:30; Search time 83.8983 Seconds (without alignments) 19:178 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                       1351062 seqs, 321799191 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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33
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                                                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                                                                                              Sequence:
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Description	Sequence 450, App	Sequence 57, Appl	Sequence 178878,	Sequence 128079,	Sequence 144813,		Sequence 162, App	Sequence 231107,	Sequence 41902, A	Sequence 53836, A	Sequence 178190,	Sequence 900, App	Sequence 892, App	Sequence 210785,	Seguence 393, App
QΙ	US-10-327-598-450	US-10-418-861B-57	US-10-437-963-178878	US-10-437-963-128079	US-10-437-963-144813	US-10-144-929-162	US-10-144-929-162	US-10-424-599-231107	US-10-767-701-41902	US-10-767-701-53836	US-10-424-599-178190	US-10-289-762-900	US-09-764-868-892	US-10-424-599-210785	US-09-866-050A-393
DB	16	72	16	16	16	14	15	12	16	16	12	15	σ	12	70
% Query Match Length DB	10	73	103	504	721	64	64	77	88	95	167	181	210	229	242
% Query Match	100:0	100.0	100.0	100.0	100.0	90.0	90.9	90.9	90.0	90.9	90.9	90.9	6.06	6.06	6.06
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	Seguence 625, App	ò	Sequence 57347, A	Sequence 18477, A	Seguence 1130, Ap	1495	180,	156,		Sequence 180, App	828,	e 141	109,	109,	109,	109,	_	_	Sequence 109, App	109	Sequence 109, App	109	Sequence 109, App	84,	86,	109	109	109	Seguence 109, App
10 US-09-866-050A-502	10 US-09-866-050A-625	9 US-09-815-242-10910	US-10-282-12	US-10-369	US-10-369-493-113	US-10-437	US-10-050-704-18	US-10-144-929-1	US-10-144	16 US-10-798-512-180	US-10-087		US-09-909-320-10	OR-08-309-088B-109		9 US-09-902-853-109	9 US-09-907-824-109	9 US-09-907-841-109		0-SD	US-09-906-83	10 US-09-907-613-109	US-09-907-942		US-09-796	US-09-904-85	-606-60-SN	10 US-09-904-820-109	10 US-09-904-786-109
242	242	310	310	315	348	381	392	392	392	392	414	419	420	420	420	420	420	420	420	420	420	420	420	420	420	420	420	420	420
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16 3	17 3	18 3	19 3	20 3	21 3	22 3	23 3	. 24	25 3	26 3	27 3	28 3	29 3	30	31 3	32 3	33	34 3	35	36	37 3	38	39	40 3			43 3	44	45 3

# ALIGNMENTS

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Sequence 450, Application US/10327598

Sequence 450, Application US/10327598

Publication No. US20040181039A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Alyappa, Ashok
APPLICANT: Alyappa, Ashok
TITLE OF INVENTION: Comine Immunoglobulin Variable Domains, Caninized Antibodies, and
TITLE OF INVENTION: for Making and Using Them
TITLE OF INVENTION: 101799-A
TITLE OF INVENTION: 10202-12-20
FILE REPRENCE: 2002-12-20
PRIOR PELLING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR PLING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 35;
cive 0; Mismatches 0;
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Sequence 57, Application US/1041B861B

; Publication No. US20040010131A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: canis familiaris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
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LENGTH: 10
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Voculic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 128079
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144811, Application US/10437963

Publication No. US2004012334341

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Application Cao, Youna

APPLICANT: Mu, Wei

APPLICANT: Mu, Wei

APPLICANT: Mu, Wei

APPLICANT: Barbauk, Brad

APPLICANT: Barbauk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PLING DATE: 2003-05-14

NOTHER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_30468C.1.pep
US-10-437-963-128079
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US-10-437-963-144813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 33; DB 16;
100.0%; Pred. No. 9.8e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(504)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                               ; Sequence 128079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa
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                          JS-10-437-963-128079
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US-10-437-963-144813
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LENGTH: 721
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                                                                                       APPLICANT: Ferro, Jesus Aparecido
APPLICANT: De Oliveiro, Julio Cezar Franco
APPLICANT: De Laia, Marcelo Luiz
APPLICANT: De Laia, Marcelo Luiz
APPLICANT: Setubal Joao C.
APPLICANT: Setubal Joao C.
APPLICANT: Furlan, Luiz Roberto
TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded the
TITLE OF INVENTION: 1804 Let Setupal CONTREMY APPLICATION NUMBER: US/10/418,861B
CURRENT APPLICATION NUMBER: US/10/418,861B
PRIOR APPLICATION NUMBER: US 60/374,620
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 85
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Eac, Vilua
APPLICANT: Cao, Vongwei
APPLICANT: W. Wei
APPLICANT: W. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 178878
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US-10-437-963-178878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(103)
OTHER INFORMATION: unsure at all Xaa locations
PERATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                       Farah, Shaker Chuck
Quaggio, Ronaldo Bento
Reinach, Fernando de Castro
da Silva, Ana Claudia Rasera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 178878, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GYWWS 10
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US-10-437-963-178878
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APPLICANT:
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Sequence 231107, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEO ID NOS: 285684
SEQ ID NO 231107
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US20040172694A1

Publication No. US20040172694A1

Publication No. US20040172694A1

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Clone ID: PAT_MRT3847_50710C.1.pep
US-10-424-599-231107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; CTHER INFORMATION: Clone ID: LIB3478-024-P1-K1-F2.pep
US-10-767-701-41902
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max
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RESULT 8
US-10-424-599-231107
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US-10-767-701-41902
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US-10-767-701-53836
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LENGTH: 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 162, Application US/10144929
Publication No US2004001495499
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PSO14P1
CURRENT APPLICATION NUMBER: US/10/144,929
CURRENT APPLICATION NUMBER: US/09/251,329
FRIOR APPLICATION NUMBER: PSO2005-15
FRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 162
LENGTH: 64
                                                                                                                                                                                                     APPLICANT: Ruben et al.
ITILE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ014P1.
CURRENT APPLICATION NUMBER: US/10/144,929
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/251,329
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (64)

; OTHER INFORMATION: Xaa equals stop translation

US-10-144-929-162
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OTHER INFORMATION: Xaa equals stop translation
                                                                                                                              ; Sequence 162, Application US/10144929; Publication No. US20030069405A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
319 GYWMS 323
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45 GYWLS 49
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                                                                          RESULT 6
US-10-144-929~162
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US-10-144-929-162
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LENGTH: 64
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US-10-424-99-210765

US-10-424-599-210765

Sequence 210785, Application US/10424599

Publication No. US20040031072A1

SEQUENCE 210785, Application Wo. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: APPLICANT: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 210785

LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                Sequence 892, Application US/09764868
Sequence 892, Application US/09764868
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT PILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                       Query Match 90.9%; Score 30; DB 15; Length 181; Best Local Similarity 80.0%; Pred. No. 1.3e+03; Matches 4; Conservative 1; Mismatches 0; Indels
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90.9%; Score 30; DB 12; Length 229;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.9%; Score 30; DB 9; Length 210
80.0%; Pred. No. 1.5e+03;
ive 1; Mismatches 0; Indels
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OTHER INFORMATION: Clone ID: PAT_MRT3847_32366C.1.pep

US-10-424-599-210785
                                FEATURE:

NAME/REI:

LOCATION: 1...181

OTHER INFORMATION: Xaa=unknown or other
US-10-289-762-900
             ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-868-892
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                                                                                                                                                                                                                                                                                  48 GYWLS 52
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US-09-764-868-892
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LENGIH: 210
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Publication No. US20040006218A1
GENERAL INFORMATION:
FILE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: Thereof and uses thereof, in particular for the diagnosis, prevering PTILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION WOMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
SEQ ID NOS: 63128
LENGTH: 95
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                                                                                                                                                                                                                                                                                                                                        Length 95;
                                                                                                                                                                                                                                                                                                                                    h Score 30; DB 16; Length 95 Similarity 80.0%; Pred. No. 7.5e+02; 4; Conservative 1; Mismatches 0; Indels
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US-10-424-599-178190
                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 13586731.pep
US-10-767-701-53836
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Best Local Similarity 80.07
-204 4; Conservative
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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89 GYWLS 93
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LENGTH: 181
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109 GYWLS 113

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RESULT 15
US-09-86-050A-393
is-09-86-050A-393
is-09-86-050A-30-3
is-09-86-050A-30-3
is-09-86-050A-30-3
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Search completed: September 30, 2004, 06:54:52 Job time : 83.8983 secs

1 GYWMS 5 |||:| 224 GYWLS 228

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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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US-09-489-039A-14325
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                                                                   September 30, 2004, 06:00:45; Search time 8.47458 Seconds (without alignments) 30.459 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                        389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                    US-09-674-716B-9
33
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Match Length DB
                                                                                                                                              1 GYWMS 5
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Perfect score:
                                                                                                                                                                      Scoring table:
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Maximum DB
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                                                                                                                                               Sequence:
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Sequence 1111, 212, Application US/09489039A

Paquent No. 6610836

GENERAL INFORMATION:
APPLICANT: GARY BRECON et., al
APPLICANT: GARY BRECON ET., al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER: OF SEQ ID NOS: 14342

SEQ ID NO 14325

LENGTH: 466
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Sequence 11, Appl Sequence 114, App Sequence 125, Appl Sequence 29, Appl Sequence 18, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 32, Appl Sequence 23128, Appl Sequence 6217, Appl Sequence 62175, Appl Sequence 6217, Appl 621897, Appl 6218997, Appl 6218997,
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1 Sequence 39, Application US/08488161

1 Patent No. 5885577:

GENERAL INFORMATION:

APPLICANT: Alvarez, Vernon L.

TITLE OF INVENTION: Peptide Libraries

CORRESPONDENCES: 103

CORRESPONDENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: 1155 Avenue of the Americas

CITY: New York

STREET: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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100.0%; Score 33; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
US-08-467-831-11
US-08-053-451B-114
US-08-053-451B-125
US-08-480-434-18
US-08-480-434-18
US-08-480-434-18
US-08-480-434-18
US-08-480-434-18
US-08-480-434-18
US-09-431-19
US-09-431-887-32
US-09-431-887-32
US-09-431-887-32
US-09-431-887-32
US-09-489-482
US-09-489-482
US-09-489-482
US-09-489-482
US-09-252-991A-23328
US-09-107-532A-6217
US-09-252-991A-18697
US-09-252-991A-18697
US-09-252-991A-18697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT / ORGANISM: Klebsiella pneumoniae US-09-489-039A-14325
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US-05-198-452A-900
US-05-198-452A-900
US-05-198-452A-900
Sequence 900, Application US/09198452A
Patent No. 655924
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
FILE PERERENCE: 9710-003-999
FILE PERERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
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0
                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CINI: New York
STATE: New York
COUNTRY: USA
                                                    90.9%; Score 30; DB 3; Length 43; 80.0%; Pred. No. 68; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.9%; Score 30; DB 5; Length 43; 80.0%; Pred. No. 68;
                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FLING DATE: 20-SEP-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MASTOCK, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-196-228

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9741/8864

TELEFAX: (212) 790-9741/8864

TELEFAX: (212) 869-9741/8864

TELEFAX: (212) 869-9741/8864
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                                                                                                                                                                                                                                                                                  PCT-US95-11934-39; Sequence 39, Application PC/TUS9511934; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 80.0
Matches 4; Conservative
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MOLECULE TYPE: peptide
PCT-US95-11934-39
                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                         6 GYWLS 10
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            US-09-273-685-39
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APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Patigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%; Score 30; DB 2; Length 43; 80.0%; Pred. No. 68; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,685
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,161
FILING DATE: 07-UUN-1995
CLASSIFFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Miscock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09273685
Patent No. 6015561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,161
FILING DATE:
                                                                                                                                                                                                              IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENOTH: 43 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-161-39
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6 GYWLS 10
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Sequence 29457, Application US/09252991A
Sequence 29457, Application US/09252991A
Sequence 29457, Application US/09252991A
Sequence 29457, Application US/09252991A
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANTON: WCLEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: UNCLECT ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                 Sequence 6029, Application US/09134000C

Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT RILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
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                                                90.9%; Score 30; DB 4; Length 243;
80.0%; Pred. No. 3.5e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.9%; Score 30; DB 4; Length 334; 80.0%; Pred. No. 4.6e+02; tive 1; Mismatches 0; Indels
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Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6029
LENGTH: 334
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Best Local Similarity 80.09
Matches 4; Conservative
                                                Query Match
Best Local Similarity 80.03
Matches 4; Conservative
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US-09-252-991A-29457
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       US-09-134-001C-4114
                                                                                                                                                                                                                                                                                          US-09-134-000C-6029
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SEQUENCEST INFORMATION:
SEQUENCE APPLICATION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
STILE PERRENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/054,964
SELOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
SELOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
LENGTH: 243
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Patent No. 8573095

GENERAL INFORMATION:
APPLICANT: Witson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Minison, James G.
BOTTWARE: 1999-05-14

NUMBER OF SEQ ID NOS: 425

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 393

LENGTH: 242
                                                                                                                                                                                                                                                                90.9%; Score 30; DB 4; Length 181; 80.0%; Pred. No. 2.6e+02; vative. 1; Mismatches 0; Indels
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80.0%; Pred. No. 3.40+02;
tive 1; Mismatches 0; Indels
                                                                                                                                               ; LUCATION: 1...181
; OTHER INFORMATION: Xaa-unknown or other
US-09-198-452A-900
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                                                                       TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 900
LENGTH: 181
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Best Local Similarity
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-134-001C-4114
                                                                                                                                          NAME/KEY: SITE
LOCATION: 1...1
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US-09-312-283C-393
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
                                                                                                                                                                                                                                                ;
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                                                       , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...408
; SEQUENCE DESCRIPTION: SEQ ID NO: 6992:
US-09-107-532A-6992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 9C7/US00/04414
PRIOR APPLICATION NUMBER: PC7/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PC7/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109, Application US/09907794A Patent No. 6635468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gow, Wei-Olang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Geneticoh, Inc.
APPLICANT: Geneticoh, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Eaton, Dan L.
  ORIGINAL SOURCE:
                                             FEATURE:
NAME/KEY:
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                      263 GYWMT 267
                                                                                                                                                                                                                                                                                         1 GYWMS 5
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Sequence 20063, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AGRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
TITLE OF INVENTION: AGRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-107-512A-6992
US-09-107-512A-6992
I Sequence 6992, Application US/09107532A
| Sequence 6992, Application US/09107532A
| Patent No. 6583275
| GENERAL INFORMATION:
| APPLICANT: Lynn A Doucette-Stamm and David Bush
| APPLICANT: Lynn A Doucette-Stamm and David Bush
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 5.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GTC-012
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: <Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 408 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6992:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.98;
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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APPLICANT
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PPLICANT: Tumas, Daniel

PPLICANT: Williams, P. Mickey

PPLICANT: Wood, William, I.

TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TILE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 420
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Patent No. 6664376
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-109
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US-09-905-125A-109
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APPLICANT:
APPLICANT:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Pred. No. 5.8e+02;
1; Mismatches 0;
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 2000-01-05
PRIOR RELING DATE: 2000-01-05
PRIOR RELING DATE: 2000-01-05
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Patent No. 6686451
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bettetin, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Blen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 80.0%;
Matches 4; Conservative 1
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 GYWLS 406
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US-09-902-775A-109
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LENGTH: 420
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Sequence 6868, Application US/09107532A
Patent No. 6583275
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                   CUCRRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 2000-02-2

PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-18
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PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
PRIOR P
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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Best Local Similarity 80.0
Matches 4; Conservative
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US-09-902-775A-109
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION DATA:

PRINT APPLICATION DATA:

PRINT APPLICATION NUMBER: 00/085,598

FILING DATE: 14, May 1998

APPLICATION NUMBER: 60/05171

FILING DATE: 14, May 1998

APPLICATION NUMBER: 60/05171

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Famela Deneke

REGISTRATION NUMBER: 40,489

FELESCOMMUNICATION NUMBER: 40.489

INDORMATION TO SECTION NUMBER: 40.007

FELESCOMMUNICATION NUMBER: 40.007

INDORMATION ROR SEQ ID NO: 6868:

SEQUENCE TRARACTERISTICS:

INTORNETICAL: YES

ONLOLIVAL SOURCE:

MANE/KEY: misc feature

MANE/KEY:
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19 heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Accession: S38714
R;Cimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Reference number: S38714
A;Reference number: S38714
A;Status: preliminary
A;Molecule type: ACIM:
A;Residues: 1-115 ACIM:
A;Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroteramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                       Je heavy chain V region - mouse
CjSpecies: Mus musculus (house mouse)
CjSpecies: Mus musculus (house mouse)
CjSpecies: Mus musculus (house mouse)
CjAccession: S26660
R;Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Reference number: S26460
A;Reference number: S26460
A;Reference Hushary
A;Molecule type: mRNA
A;Residues: 1-101 < KAV>
CjSuperfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin immunoglobulin homology
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Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                 ALIGNMENTS
$46466
$410122
$410122
$410289
$410289
$4319380
$434903
$734903
$734903
$74903
$74003
$760981
$760981
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1100
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                                                                                                       September 30, 2004, 05:55:56; Search time 20.6102 Seconds (without alignments) 88.677 Million cell updates/sec
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                   US-09-674-716B-11
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1 EIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1: pir1:*
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Rikaartinen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24490
A;Accession: S24521
A;Accession: preliminary
A;Gatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 < KAA>

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Aymory chain V-III region (U61) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Decies: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: B93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins. A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: B93818
A;Molecule type: protein
A;Residues: 1-113 < VRA>
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < IPMN>
F;15-100/Domain: immunoglobulin homology < IPMN>
F;22-98/Disulfide bonds: #status predicted
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C;Species: Mus muscrilus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Acession: A90400; A02072
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                                                   Score 91; DB 1; Length 113;
Pred. No. 1.7e-07;
0; Mismatches 1; Indels
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Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                0; Mismatches
F;22-98/Disulfide bonds: #status predicted
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                                                                                                                                                                          1 EIRLKSDNYATHYAESVKG 19
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                                                   92.98;
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Best Local Similarity 94.7'
Matches 18; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: C92811; A02072
R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
T. Immunol. 128, 302-307, 1982
A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein A;Reference number: A92811; MulD:82099361; PMID:6798111
A;Accession: C92811
A;Molecule type: protein
A;Residuas: 1-115 cyOH>
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Comment: Immunoglobulin to region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted
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C:Species: Me musculus (house mouse)
C:Species: Me musculus (house mouse)
C;Accesion: A91818; A02072
R;Vrana, M: Rudikoff, S:; Potter, M.
Proc. Natl. Acad. Sci. U:SA. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins. A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: A93818
A;Molecule type: protein
A;Residues: 1-113 <VRA>
C;Comment: This chain was isolated from a myeloma protein that binds inulin. C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
.;F:15-100/Domain: immunoglobulin homology <IMM>
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                                          $24521
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S24521
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94.9%; Score 93; DB 2; Length 106
Best Local Similarity 94.7%; Pred. No. 7.4e-08;
Matches 18; Conservative 1; Mismatches 0; Indels
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ch 1 Similarity 94.7%; Pred. No. 8.1e-08; 18; Conservative 1; Mismatches 0

Query Match Best Local Similarity Matches 18; Conserv

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EIRLKSNNYATHYAESVKG 68 1 EIRLKSDNYATHYAESVKG 19

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Tigheavy chain V-III region (T957) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: A92810; A02072
R;Rudikoff, S.; Potter, M.
J. Immunol. 127, 191-194, 1981
A;Referrence Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a net A;Referrence number: A92810; MUID:81216632; PMID:6787122
A;Accession: A92810
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7. Immunol. 127, 191-194, 1981
A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a ne
A;Reference number: A92810; MUD:81216632; PMID:6787122
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Adression: A02074
R;Bernard, O.; Gough, N.M.
R;Bernard, O.; Gough, N.M.
A;Title: Nucleotide sequence of immunoglobulin heavy chain joining segments between trans A;Reference number: A02074; MUD:81013937; PMID:6251474
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C)Comment: This chain was isolated from a myeloma protein that binds inulin. C)Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin P:15-100/Domain: immunoglobulin homology < IMM>
F:15-100/Domain: immunoglobulin homology < IMM>
F:22-98/Disulfide bonds: #status predicted
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A.Residues: 1-113 <RUD>
C.Comment: This chain was isolated from a myeloma protein that binds inulin.
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin
B.15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997
C;Accession: A02073
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A;Residues: 1-111 <BER>
A;Note: the sequence was also determined from the differentiated gene
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Pred, No. 1.6e-06;
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Pred. No. 1.1e-06;
0; Mismatches 2; Indels
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              50 QIRLASDNYATHYAESVKG 68
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1 Similarity 89.5%;
17; Conservative
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Local Similarity 89.5%;
les 17; Conservative
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Biochemistry 16, 1170-1175, 1977
A;Title: Heavy-chain variable-region sequence from an inulin-binding myeloma protein. A;Feference number: A90400, MUID:77134726; PMID:402936
A;Accession: A90400
A;Molecule type: protein
A;Residues: 1-113 <VRA>
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin nomology
F;15-100/Domain: immunoglobulin predicted
F;22-98/bisulfide bonds: #status predicted
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Pred. No. 1.7e-07;
0; Mismatches 1; Indels
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A;Residues: 1-115 <HER>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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89.5%; Pred. No. 3.6e-07;
tive 1; Mismatches 1; Indels
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94.7%; Pred. No. 1...
0; Mismatches
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R;Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, 318-315, 1992
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc A;Reference number: PC1213; MUID:93077049; PMID:14466822
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Abl. Cell. Biol. 11, 5660-5670, 1991
A:Title: Non-homologous recombination/deletion at sites within the mouse JH-Cdelta locus
A:Reference number: IS7520; MUID:92017847; PMID:1922069
A:Recession: I77394
A,Note: the sequence of the first 197 residues of the C region was also determined and C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;10-94/Domain: immunoglobulin homology < MM>> F;10-94/Domain: immunoglobulin homology < MM>> F;17-92/Disulfide bonds: #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
C;Accession: PC1213
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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: I77394
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A; Residues: 1-139 <-HON>
A; Residues: 1-139 <-HON>
A; Cross-references: Gs: M98041; NID: g195092; PIDN: AAA38159.1; PID: g195093
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <sIG>
F;20-139/Product: IG heavy chain V region #status predicted <MAT>
F;34-119/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-64 <RES.
A;Cross_references: GB:M64568; NID:g198472; PIDN:AAA39341.1; PID:g198473
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                 Query Match
77.0%; Score 75.5; DB 1; Length 111;
Best Local Similarity 89.5%; Pred. No. 5.3e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 1
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74.5%; Score 73; DB 2; Length 139;
Best Local Similarity 73.7%; Pred. No. 0.00017;
Matches 14; Conservative 4; Mismatches 1; Indels
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9 ITVKSDNYGANYAESVKG 26
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bacillus su

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P01783 mus musculu
P49417 vibrio angu
P23524 escherichia
P32704 escherichia
Q92111 helicobacte
Q92947 bacillus ha
P1265 human parai
C67301 aguifex aeo
Q89311 xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=82099361; PubMed=6798111;
Johnson N., Slankard J., Paul L., Hood L.;
Johnson N., Slankard J., Paul L., Hood L.;
The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.;
J. Immunol. 128:302-307(1982).
-!- NISCELIANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; PO1789; IMCP.
INTEFPC; IPRO07110; Ig-like.
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P01756;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 phavy chain V-III region A4.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                  Ig heavy chain VIII region diffection appared.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
 P39118
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Pred. No. 2e-08;
1; Mismatches 0; Indels
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12810 MW; B67AD6638A121A5F CRC64;
                                                                                                                                                                                                                               IG-LIKE.
BY SIMILARITY.
                                                                                                                                                                                               ALIGNMENTS
             HV05_CARAU
HV16_MOUSE
CAT_VIBAN
GRKZ_ECOLI
YJCF_ECOLI
SYEZ_HELPY
MQO_BACHD
                                                                                                                      VGLF_PIIHC
YC62_AQUAE
ACSA_XANCP
 GLGB_BACSU
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PRAM: PROGUST; 19_V.

PROSTIE: PSS0835; 10_LIKE; 1.

PROMIN | V region. | 10

DOMAIN | 1 114. IG

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NON TER | 115 AA; 12810 MW;
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                             September 30, 2004, 05:55:56; Search time 11.5932 Seconds (without alignments) 85.337 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                     141681 segs, 52070155 residues
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HV17 MOTISE
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HV21_MOUSE
HV18_MOUSE
HV19_MOUSE
HV22_MOUSE
HV25_MOUSE
HV26_MOUSE
HV26_MOUSE
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YS76 ANASP
Y186 MYCGE
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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                                                                                                                                                                              1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                   US-09-674-716B-11
98
                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
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Match Length
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Gaps

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50 EIRLKSHNYATHYAESVKG

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                             RESULT 4
HV29 MOUSE
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HV30 MOUSE
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                        Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
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[1]
SEQUENCE.
MEDLINE-78158406; PubMed=417344;
MEDLINE-78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
"Sequence variation among heavy chains from inulin-binding myeloma
"Sequence variation among heavy 75:1957-1961 (1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
proceins.";
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                        Score 91; DB 1; Length 113;
Pred. No. 4.2e-08;
0; Mismatches 1; Indels
                                                                                  -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A93818; AVMSAB.
HSSP; P01810; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
Pfam; PR0047; ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
19 heavy chain V-III region U61.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                   113 AA.
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BY SIMILARITY.
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                                                                                                                                                                                                                           92.9%;
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                    Query Match
Best Local Similarity 94,7%
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                                                                                                                                                                                               113 AA;
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HV28 MOUSE
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1 EIRLKSDNYATHYAESVKG 19

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Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

INTECELANEOUS. THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.

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-!- MISCELLANDEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A90400; AVMSB7.

HISCPP. PO1810; 2FBJ.

ILLCPPC.; IPR007110; IG-like.

InterPro; IPR007180; IG-V.
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Vrana M., Rudikoff S., Potter M.;
"Heavy-chain variable-region sequence from an inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=78156406; PubMed=417344;
MEDLINE=78156406; S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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HV29_MOUSE STANDARD; PRT; 113 AA. P01799 | 113 AA. P01799 | 113 AA. P01799 | 113 AA. P01791 | 113 AA. P01791 | 114 AA. P01791 | 115 AA. P01791 | 116 AA. P01791 | 116 AA. P01791 | 116 AA. P01791 | 116 AA. P01791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 11791 | 1
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1 EIRLKSDNYATHYAESVKG 19
          NCBI_TaxID=10090;
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                                                                   SEQUENCE
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; D92811; AVMS82.
HSSP; PO1810; 2FBJ.
InterPro; IPR07110; Ig-like.
InterPro; IPR07110; Ig-like.
FRAM: PR00047; ig. 1.
PRAM: PR00047; ig. 1.
PRAM: PR00047; ig. 1.
PROSITE; PS50835; IG LIKE; 1.
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P0180;
21-JUL-1908 (Rel. 01, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE-8209361; PubMed-6798111;
MEDLINE-8209361; PubMed-6798111;
Midneon W., Slamkard J., Paul L., Hood L.;
"The complete V domain amino acid sequences of two myeloma inulinbinding proteins.";
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                                                                                                                                                                                                                                                                                 Query Match 92.9%; Score 91; DB 1; Length 113; Best Local Similarity 94.7%; Pred. No. 4.2e-08; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                       DISULFID 22 98 BY SIMILARITY.

NON TER 113 113

SEQUENCE 113 AA, 12675 WW, 76658C16C779845E CRC64;
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NON TER 115 115
SEQUENCE 115 AA; 12887 MW; 984517648C121C5A CRC64;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 EIRLKSHNYATHYAESVKG 68
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Pfam; PF00047; ig; 1.
SMAAR; SMOAGO; IGV; 1.
PROSITE; PS50815; IG LIKE; 1.
Immunoglobulin V region.
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Matches
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      REAR TITES
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SEQUENCE.

REDILINE=81216612; PubMed=6787122;

Rudikoff S., Potter M.;

Rudikoff S., Potter M.;

Rudikoff S., Potter M.;

Immunoglobulin heavy chains from anti-inulin myeloma proteins:

To vidence for a new heavy chain joining segment.";

U. Immunol. 127:191-194(1981).

SINDELIANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN:

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN:

C-I- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A92810; ANMS57.

RIGHT, PRO07110; IG-like.

RIGHT, PRO07110; IG-like.

RIGHT, PRO07110; IG-like.

REMART; SM00406; IG-1.

REMART; RM00406; IG-1.

RIGHT, PROSITE; PS50835; IG_LIKE; I.

FROM IMMUNOGlobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rudikoff S., Potter M.;

"Immunoglobulin heavy chains from anti-inulin myeloma proteins:

"Immunoglobulin heavy chains from anti-inulin myeloma proteins:

"Immunol. 127:191-194(1981).

"Immunol. 127:191-194(1981).

"Immunol. 127:191-194(1981).

"Immunol. 127:191-194(1981).

"Immunol. 127:191-194(1981).

"Immunol. 127:191-194(1981).

"Immunoglobulin-like domain.

"Immunoglobulin-like domain.

"Impuroglobulin ig-like.

"Impunoglobulin V region.

"Immunoglobulin V region.

"Immunoglobulin V region.
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ID HV34_MOUSE

Tyle Mouse

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DS Ig heavy chain V region AMPC1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 101_TaxID=10090;
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Best Local Similarity 89.5%; Pred. No. 4.1e-07;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%; Score 86; DB 1; Length 113;
89.5%; Pred. No. 2.8e-07;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID 22 98 BY SIMILARITY.

NON TER 113 113

SEQUENCE 113 AA, 12732 MW, 26618F626B59B59E CRC64;
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NON TER 113 113

SEQUENCE 113 AA, 12691 MW, 7A6D906AAA966E9E CRC64;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
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FROM THE
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Bernard O., Gough N.M.;

"Nuclectide sequence of immunoglobulin heavy chain joining segments

"Nuclectide sequence of immunoglobulin heavy chain joining segments

between translocated VH and mu constant regions genes.";

Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).

"INCENLIANBOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C

REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM TH

CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.

"INTIMARITY: Contains 1 immunoglobulin-like domain.

PILS, A02074, MMMS76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=83064537; PubMed=6292865; Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.; "Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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-!- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RAIS.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02075; EVRTC.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.0%; Score 75.5; DB 1; Length 111; Best Local Similarity 89.5%; Pred. No. 1.5e-05; Matches 17; Conservative 0; Mismatches 1; Indels
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111 111
111 AA; 12304 MW; 0EDE98EC7348056A CRC64;
                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region HPC76 (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rattus norvegicus (Rat).
                                                                                 111 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
NON TER < 1 110 IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P01789, 1MCP.
InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig_v.
                                                                          STANDARD;
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                                                                   HV35 MOUSE
P01804;
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HV01_RAT
ID HV01_RAT
AC P01805;
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Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
-!- MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; P01789; 1MCP.
InterPro; 1PR007110; Ig-like.
InterPro; 1PR007596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Robinson E.A., Appella E.;
"Complete amino acid sequence of a mouse immunoglobulin alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=16090;
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20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7787, 20.7
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                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION IR2. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;
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21-UUL-1986 (Rel. 01, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ans musculus (Mouse).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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69 EIRNKANNYVAYYGKSLKG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIRLKSDNYATHYAESVKG 19
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SMART; SMO0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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P01790;
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DOMAIN
NON TER
SEQUENCE
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SEQUENCE
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HV21_MOUSE
HV21_MOUSE
DT 21-UUL-
DT 21-UUL-
DT 10-OCT-
DE IG heav
OC EUKBARYC
OC Mammal:
OC EUKBARYC
OC MARMY | 1]
RP SEQUENC
RT (COMPLING
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Ig heavy chain V region H8.

Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) PRT; 123 AA.> 52 RNKANDYTTEYSASVKG 68 STANDARD; RESULT 13
HV19 MOUSE
AC PO178;
DT 21-4UL-1986
DT 21-4UL-1986
DT 10-OCT-2003
DE IG heavy cha.
OC Eukaryota; Mammalia; Eu.
OX NCBI TAXID=11
RN [1]
RA BARSAGELAM
CC H-1-8KS EUROELAM
CC H-1g

Bafstad P.; Thesis (1975), California Institute of Technology / Pasadena, U.S.A. -!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.

MEDLINE=81197602; PubMed=7231520;

A Gearhart P. J., Johnson N.D., Douglas R., Hood D.;

Gearhart P. J., Johnson N.D., Douglas R., Hood D.;

"Igg antibodies to phosphorylcholine exhibit more diversity than
"Igg antibodies to phosphorylcholine exhibit more diversity than
"Igg antibodies to phosphorylcholine exhibit more diversity than
"In their IgM counterparts".

"In Mature 29:129-14(1981).

"In MILARITY: Contains I immunoglobulin-like domain.

"In DS PHOSPHORYLCHOLINE."

"In PROPESS, AWMEN."

"In PROPESS, AWMEN."

"In PROPESS, PO1789; IMVP.

"In TherPro' IPR007110; Ig-like."

"In SMART; SM00407; Ig': 1.

"MED PERSON IN TOTAL Gaps 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region HPCM6.
If heavy chain V regionse).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus. NGELTAXID=10090; .; 0 ; 49.0%; Score 48; DB 1; Length 123; 52.9%; Pred. No. 0.59; tive 4; Mismatches 4; Indels 49.0%; Score 48; DB 1; Length 123; 52.9%; Pred. No. 0.59; ive 4; Mismatches 4; Indels 123 123 123 AA, 13895 MW, 81361892ECBF7000 CRC64; 123 AA; 13805 MW; 9D581401912F7000 CRC64; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ig heavy chain V region HPCG14. IG-LIKE. HSSP; P01789; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
FMSITE; PS50835; IG\_LIKE; 1.
Immunoglobulin V region. IG 3 RLKSDNYATHYAESVKG 19 3 RLKSDNYATHYAESVKG 19 | |:::| | |: |||||
RNKANDYTTEYSASVKG 68 52 RNKANDYTTEYSASVKG 68 Query Match
Best Local Similarity 52.9
Matches 9; Conservative Query Match
Best Local Similarity 52.9
Matches 9; Conservative STANDARD; STANDARD; HV25 MOUSE P01794; NON TER SEQUENCE HV25\_MOUSE ID HV25\_MC AC P01794; DT 21-UUL DT 10-OCT-DE IG hear RESULT 15 SO THE PRESENCE OF THE PROPERTY OF THE PROPERT

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MEDLINE=81197602; PubWed=7231520;

MALURE 291:29-34(1981).

MALURE 291:29-34(1981).

MALURE 291:29-34(1981).

MEDLINE=81197603.

MARICAL SHOEMPHORY CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PROSPERIAN PROTEIN THAT Immunoglobulin-like domain.

MEDLINE=81197602; MEDLINE=811976.

MEDLINE=81197602; MEDLINE=81197602; MEDLINE=811976.

MEDLINE=81197602; MEDLIN
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Best Local Similarity 52.9%; Pred. No. 0.59;
Matches 9; Conservative 4; Mismatches 4; Indels
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NON TER 123 123
SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;
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Search completed: September 30, 2004, 06:01:21 Job time : 12.5932 secs

3 RLKSDNYATHYAESVKG 19

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56; search time 62.1525 Seconds (without alignments)

Perfect score: 98
Sequence: US-09-674-716B-11
Sequence: 1 EIRLKSDNYATHYAESVKG 19
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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SPIREMBL 25:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

# Score Match Length DB ID Match Length DB ID 9 91.8 47 11 Q80217 68 69.4 64 11 Q61750 57 58.2 479 11 Q80217 68 10 469 11 Q81829 69 11 Q81829 69 11 Q81829 69 12 48 61 10 Q91821 69 12 0 Q81829 69 12 48 61 10 Q91821 69 12 0 Q81829 60 12 0 Q81829 60

84597887978439

Q8d219 streptococc Q7V1x9 haemophilus Q45962 clostridium Q7V1x5 candidatus G8dux1 oceanobacil Q8dwn2 streptococc Q7W829 onion yello 035037 archaeoglob Q85227 mycobacteri Q86227 mycobacteri Q86227 mycobacteri Q86728 streptococc Q89485 bradyrhizob Q89481 bradyrhizob Q89481 bradyrhizob Q89485 bradyrhizob Q89485 bradyrhizob Q89485 bradyrhizob Q89485 bradyrhizob Q89485 bradyrhizob Q89485 bradyrhizob Q8950 bradyrhizob Q8950 bradyrhizob Q8950 bradyrhizob Q8951 bradyrhizob Q8951 bradyrhizob Q8951 bradyrhizob Q8951 bradyrhizob Q8951 bradyrhizob Q87075 bracella me Q8287 bracella me Q87085 braceroides Q930C mycococcus P82987 homo sapien Q9510 braceria can Q9510 bradyrhizob Q87096 linaria mar Q84189 linaria can Q84187 linaria can Q84187 linaria can	are) ate, dae, Eu	O CRC64; Length 487; i Indels 0; Gaps 0;
Q8DZT9 Q7VLX3 Q45962 Q7VLX3 Q45962 Q8CUX1 Q8DWN2 Q8DWN2 Q852Z7 Q852Z7 Q852Z7 Q897B5 Q897B5 Q897B5 Q897B5 Q897B1 Q87ZK5 Q87CK5	PRT; 487 AA.  Created) Last sequence update Last annotation upd .; Craniata; Vertebr .; Sciurognathi; Mur.	31F2C893900A4D8 Score 90; DB 11; Pred: No. 2.4e-06 19
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	7; 24, 24, 25, 25, 010n;	13.1; 13.1; 13.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10.1; 10
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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REPLINE-2388257; PubMed=12477932;

RECURSEDER R.D., Feingold E.A., Grouse L.H., Derge J.G.,

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Ricusper R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A hischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Rahe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

Raha S.S., Worley K.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Raha V.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Willing M. Madan A., Young A.C., Shevchenke Y., Boutfard G.G.,

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Mol. Cell. Biol. 115660-570(1991).
EMBL, M64569; AAA39341.1;
PIR: 177394.
HSSP; P01789; IMCP.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 0.0011;
2; Mismatches 3; Indels
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
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MEDLINE=92017847; PubMed=1922069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
NON TER 1 1 1
SEQUENCE 64 AA; 7594 MW; I
                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, JH-Cdelta locus (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ITVKSDNYGANYAESVKG
                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                              Q61750
Q61750;
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                                                           RESULT 2
2061750
ID AC 06177
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DE MASH
OC MAMM
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Gaps
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OLDEC-2001 (TrEMBLrel. 19, Created)

OLDEC-2001 (TrEMBLrel. 19, Last sequence update)

OLOCT-2003 (TrEMBLrel. 25, Last sequence update)

Hypothetical protein (Fragment).

Hypothetical protein (Fragment).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Ms. TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                    Match 58.2%; Score 57; DB 11; Length 479; Local Similarity 57.9%; Pred. No. 0.69; es 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 11; Length 469;
Pred. No. 6.6;
                                                               Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-205905, AAH55905.1; -. Hypochetical protein. SEQUENCE 479 AA; 52209 MW; 532DED9D46D0AEED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ll protein.
469 AA; 51976 MW; 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
[2]
SEQUENCE, FROM N.A.
STRAIN-C57BL/6J; TISSUB=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                 69 QIRNKPYNYETYYSDSVKG 87
                                                                                                                                                                                                                                                                                                      1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MER, B45837, B45837.
MGD: MGI:96446, IGh-4.
InterPro; IPR00710, IG-like.
InterPro; IPR003596, IGMHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC024405; AAH24405.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.67
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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DB 11; Length 754;
Choi I., Cho C.;

"Cloning and characterization of ADAM6.";

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AN158689; AANN7878.1; --

R PIR, PT0706; PT0706;

R GO; GO:0006508; PT0706

GO; GO:0006508; P: Protecolysis and peptidolysis; IEA.

GO; GO:0006508; P: Protecolysis and peptidolysis; IEA.

R InterPro; IPR001762; Disintegrin.

R InterPro; IPR001599; Peptidase_M12B.

R InterPro; IPR002879; PEPT like.

R InterPro; IPR002870; Peptidase_M12B.

R Pfam; PF01421; Reprolysin; 1.

P Ffam; PF01421; Reprolysin; 1.

R PRAMT; SM00608; ADAM MEPRO; 1.

R SMART; SM00608; ADAM MEPRO; 1.

R PROSITE; PS50214; DISIN; 1.

R PROSITE; PS50214; DISINFERIN; 2; 1.

R PROSITE; PS50214; DISINFERIN; 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.5%; Score 47.5; D
64.7%; Pred. No. 43;
:ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas syringae (pv. glycinea).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 RLSSKNYATHPA-AIKG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IRLKSDNYATHYAESVK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.73
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Q88ZK4
ID Q88ZF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
Q9RBZ3
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MEDLINE-20015131; PubMed=10545263;
Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrich M., Bender C.L.;
"Characterization of plasmids encoding the phytotoxin coronatine in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazaa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%; Score 51; DB 11; Length 480; 50.0%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 49; DB 2; Length 361; 52.6%; Pred. No. 11; 7; Indels tive 2; Mismatches 7; Indels
                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO10798; AAH10798.1; -.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003106; Ig-MHC.
InterPro; IPR003306; Ig-V.
Pfam; PF00447; ig: 4.
PR001TE; SM00440; IG-NE; IG-N
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
1S870-like transposase.
Pseudomonas syringae (pv. glycinea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas syringae.";
Plasmid 42:210-220(1999).
EMBL; AF170066; AAD50977.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonadaceae; Pseudomonas
NCBI_TaxID=318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBCGQ1,
01-MAR-2003 (TEEMBLrel. 23,
01-MAR-2003 (TEEMBLrel. 23,
01-OCT-2003 (TEEMBLrel. 25,
ADAM6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ICR; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 50.09
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                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
NON_TER 1
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Matches
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0805
0805
0805
0805
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0805
01-00
01-00
01-00
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05 buka
06 buka
07 buka
08 buka
08 buka
08 buka
08 buka
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208 BZ2
10 C O O RE
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DE PSSU
OC PSSU
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Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrích M., Bender C.L.;
Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrích M., Bender C.L.;
Pidracterization of plasmids encoding the phytotoxin coronatine in Pseudomonas syringae.";
Plasmid 42:210-220(1999).
EMBL, AR169828; Anab50908.1; -.
EMBL, AR169828; Anab50908.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0004601; P:DNA recombination; IEA.
InterPro; IPR001584; Rve.
Pfam; PP00665; rve; 1.
                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceee; Pseudomonas.
NCBI_TaxID=318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 48.0%; Score 47; DB 2; Length 357; Local Similarity 58.8%; Pred. No. 22; local Since 10; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 AA; 40339 MW; F21B4028AA5A9BD2 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Gaps

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

XA SEQUENCE 5234683; PubMed=12466851;

XA The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

REMBL; AK029742; BAC26593.1; -.

DR MGJ; MGJ; A444636; 493062301; -.

REMBL; AK029742; BAC26593.1; -.

ROJ, GO:0006508; P: Freetalloendopeptidase activity; IEA.

GO; GO:0006508; P: Freetalloendopeptidase ML2B.

RICEPPO; IPR006280; Peptidase ML2B.

RICEPPO; IPR006280; Peptidase ML2B.

RICEPPO; IPR006280; Peptidase ML2B.

RICEPPO; IPR006280; Peptidase ML2B.

REMB; PEODON; PEDFOLYSIN; 1.

PREMB; PEODON; PEDFOLYSIN; 1.

PREMB; PEODON; PEDFOLYSIN; 1.

REMART; SM00606; DISINITEGRIN; 1.

REMART; SM00606; DISINITEGRIN; 1.

REMOSITE; PS50214; DISINITEGRIN.2; 1.

REMOSITE; PS50214; DISINITEGRIN.2; 1.

REMORED PROSITE; PS50214; DISINITEGRIN.2; 1.

PREMB; PROSITE; PS50214; DISINITEGRIN.2; 1.

REMORED PROSITE; PS50214; DISINITEGRIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.4%; Score 45.5; DB 11; Length 703; 58.8%; Pred. No. 85;
         46.9%; Score 46; DB 10; Length 2910; 60.0%; Pred. No. 3.5e+02; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL71, PRELIMINARY, PRT, 121 AA. 019UL71, C1 MA. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2003 (TrEMBLrel. 25, Last annotation update) Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Similar to TMDC IV protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703 AA.
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204 RISSKNYATHPA-AIKG 219
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                                                                                                                                                                                                                                                                    297 LKEDNHQEEYAESVE 311
                                                                                                                                                                                         4 LKSDNYATHYAESVK 18
                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                   Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 10; Conserv
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SEQUENCE
         Query Match
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Q8C0V3;
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Q8C0V3
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Q9UL71
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A Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
A Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Ler K., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W. B.J., Sterkema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.;
Complete genome sequence of Lactobacillus plantarum WCFS1.";
Froc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
EMBL; AL935252 Candscase all A. 100:1990-1995 (2003).
R GO: GO:0008522; Cintracellular; IEA.
R GO: GO:0008522; Cintracellular; IEA.
R GO: GO:0008152; P:metabolism; IEA.
R GO: GO:0008152; P:metabolism; IEA.
R GO: GO:0008152; P:metabolism; IEA.
R GO: GO:0016740; F:transferase activity; IEA.
R FO: GO:0016740; F:transferase activity; IEA.
R FO: GO:0016740; F:transferase activity; IEA.
R FO: FERM: PFO:00871; Acetate_kinase; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MON-2003 (TrEMBLrel. 24, Last annotation update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
Similarity to heat shock protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
NCBI_TAXID=3702;
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Sequence features of the regions of 1,044,062 bp covered by thirteen
physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006702; BAB11602.1; -..
EMBL; AB017062; BAB11602.1; -..
GO; GO:0003773; F:heat shock protein activity; IEA.
Heat shock.
SEQUENCE 2910 AA; 325351 MW; A847EC3FB1427DF7 CRC64;
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STRAIN=Columbia;
MEDLINE=98068011; PubMed=9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
Tabata S.;
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                                                                                                                                                                                                                                                           Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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PROSITE; PS01075; ACETATE KINASE 1; 1.
PROSITE; PS01076; ACETATE KINASE 2; 1.
SROSITE; PS01076; ACETATE KINASE 2; 1.
                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                            Acetate kinase (EC 2.7.2.1)
ACK2 OR LP_0310.
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STRAIN=NCIMB 8826 / WCFS1;
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Best Local Similarity 6x...
Pest Local Similarity 6x...
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1590;
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Q9FND5;
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OX RRN RA RA RA RA RA RA DA DA DA DA DA DA FTT SQ SQ SQ SQ SQ

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MEDLINE=21608550; PubMed=11743193; MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul H., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Pallmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreeppan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome of the natural genetic engineer Agrobacterium tumefaciens
558.";
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Lymantria dispar (Gypsy moth).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea,
Lymantriidae, Lymantria.
                                                                                                               SEQUENCE FROM N.A. Denlinger D.L., Lee K.-Y., Horodyski F.M., Valaitis A.P., Molecular characterization of the insect immune protein hemolin and the high induction during embryonic diapause in the gypsy moth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 45; DB 5; Length 422; 53.3%; Pred. No. 58;
                                                                                                                                                                                                Lymantria dispar.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF453868; AAL49765.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR00598; Ig-c2.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                    SWART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 4.
Immunoglobulin domain.
SEQUENCE 422 AA; 47234 MW; 0DC52EC4BF142617 CRC64;
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Agrobacterium Tumefaciens (strain C58 / ATCC 33970)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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01-0TM-2002 (TrEMBLrel. 21, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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EMBL; AE009427; AAL46320.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 EVRFKADNYSTALLE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
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                                                                         NCBI_TaxID=13123;
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Q8U651
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Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,

Harris B., Lennard N., Hall N., Atkin K., Chillingworth C., Doggett J.,

Derminan M., Pain A., Hall S., Cuail M., Barrell B.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AL844509; CAD52741.1; -.

EMBL, AL84509; CAD52741.1; -.

EMBL, PRO001099; Fiprotein domain specific binding; IEA.

InterPro; IPR000308; 14-3-3; 1.

PRINTS; PR000305; 14-3-3; 1.

ProDom; PD000600; 14-3-3; 1.

Hypothetical protein.

SEQUENCE 300 AA; 35090 MW; B1E678EC606D2B63 CRC64;
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                                   SEQUENCE FROM N.A.
MEDILINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin_reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.9%; Score 45; DB 5; Length 300; 50.0%; Pred. No. 39; 6; Indels ative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 45; DB 4; Length 121; 50.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                          121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035G43; AAD56279.1; -
HSSP; P01772; ZF84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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EKSMKSYSYALHYANKMK 198
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(TrEMBLrel. 20, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
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51 ISGDGGSTYYADSVKG 66
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Best Local Similarity 50.0%
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  NCBI_TaxID=9606;
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Hemolin.
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RESULT 14 Q8WR61

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DR EMBL; AE007935; AAK91044.1; -.

DR PIR; AB3238; AB3238

GO; GO:0048621; C:extrachromosomal DNA; IEA.

DR GO; GO:0048497; E:monocxygenase activity; IEA.

DR GO; GO:0004497; E:monocxygenase activity; IEA.

DR GO; GO:0004412; P:protein Diosynthesis; IEA.

DR InterPro; IPR00103; Bac_luciferase.

DR InterPro; IPR00103; Bac_luciferase.

DR InterPro; IPR00103; Bac_luciferase.

DR PROSTTE; PS00962; RIBOSOMAL S2 1; 1.

KW Monocxygenase; Plasmid; Complete proteome.

SQ SEQUENCE 450 AA; 50163 WW; D3ADB8261D68C026 CRC64;

Query Match

Best Local Similarity 58.3%; Pred. No. 62;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps

QY 7 DNYATHYABSVK 18

DD 57 DNYGQHPADTVK 68
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Search completed: September 30, 2004, 05:59:36 Job time : 65.3192 secs

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September 30, 2004, 05:55:56; Search time 92.7458 Seconds (without alignments) 57.883 Million cell updates/sec.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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98
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp201s:\* qeneseqp2003as:\* geneseqp2003as:\* A\_Geneseq\_29Jan04:\* 1: qeneseqp1980s:\* geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	t C	100.0	100.0	0	0	0	100.0	96.9	96.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	٠	94.9	94.9	94.9	94.9	94.9	94.9	94.9	92.8
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Aab35292 Murine PS Abc10743 Consensus Abr44687 Murine J4 Aar70829 WAb 4197X Aar70829 WAb 4197X Aar26810 Heavy cha Aar25410 Heavy cha Aav28748 Heavy cha Aav80188 Lead bind Aab30033 Scaffold Abol10709 Murine J4 Abr44653 Murine J4 Abr44653 Murine J4 Abr44653 Murine J4 Abr10734 Consensus	
AAB35292 ABC10743 ABC10743 AAR70829 AAR70827 AAR25410 AAR258748 AAY90816 AAY01588 AAB010709 ABC10709 ABC10709 ABC10709 ABC10734	ABO10725 ABO10733 ABR44672 ABR44670 ABR44678 ABR44678
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# ALIGNMENTS

RESULT 1

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcrarive colitis; Crohn's disease; signaria syndrome; allergy, asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; Light chain CDR H2 of mouse anti-CD23 MAb C11. Ä. 2258 AAY32258 standard, peptide, 19 (first entry) 15-FEB-2000 AAY32258; therapy. 

Mus musculus. WO9958679-A1.

99WO-GB001434. 07-MAY-1999; 18-NOV-1999.

98GB-00009839 09-MAY-1998;

Ellis JH, Bonnefoy JMP, Crowe SJ, (GLAX ) GLAXO GROUP LTD.

WPI; 2000-053101/04. N-PSDB; AAZ34743.

Shearin J;

Rapson NT,

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 1; Page 40; 81pp; English.

This sequence represents complementarity determinating region 2 (CDR H2) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody Cl1 (See also AAY32254). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain CDRs (see AAY32254-59) to

Aau76696 Mouse hea

AAU76696

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92.9

91

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haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uvaitis, dermatitis, inticaria, nephrotic syndrome, glomerulonephritis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma actue asthmatic exacerbation, rhinis, eczema, graft-versus-host disease, (CDP), insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
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# Sequence 19 AA;

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Gaps
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0
      Length 19;
      100.0%; Score 98; DB 3; Length 19
100.0%; Pred. No. 2.5e-09;
iive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
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### 1 EIRLKSDNYATHYAESVKG 19 EIRLKSDNYATHYAESVKG 19 ò 임

ABO10742 standard; protein; 123 AA ABO10742; RESULT 2 ABO10742 

Variable region of murine antibody MuVHIIIC.

(first entry)

20-AUG-2003

Modified antibody, deimmunised antibody, anti-PMSA antibody; prostate specific membrane antigen; immunogenic; CDR; murine; complementarity determining region, 1951; 0415; 0533; B99; mouse; prostatic disorder; cancerus disorder; genitourinary inflammation; prostatitis; benign enlargement; prostatic cancer; testicular cancer; solid tumour; soft tissue tumour; metastetic lesion; pain; analgesic; antiinflammatory; cytostatic; framework region; variable heavy chain, variable light chain; VH; VL; variable region.

Mus musculus.

WO200298897-A2.

12-DEC-2002,

30-MAY-2002; 2002WO-US017068.

01-JUN-2001; 2001US-0295214P. 20-SEP-2001; 2001US-0323585P. 08-MAR-2002; 2002US-0362810P.

(CORR ) CORNELL RES FOUND INC

Hamilton A; Carr FJ, Bander N,

WPI; 2003-156839/15.

New modified anti-prostate specific membrane antigen (PSMA) immunoglobulins, useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatitis, or prostatic or testicular cancer.

Disclosure; Fig 7C; 254pp; English.

The present invention relates to modified (e.g. deimmunised) antibodies to prostate specific membrane antigen (PSMA). The modified anti-PSMA antibodies are less immunogenic compared to the unmodified anti-PMSA antibodies. The modified antibodies comprise complementarity determining regions (CDRs) from a non-human antibody (e.g. murine antibody J591,J415,

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US33 or E99), and framework sequences that are less immunogenic in humans (e.g. less antigenic than the murine frameworks in which a murine CDR naturally occurs). The modified antibodies bind with PMSA, preferably human PMSA, with high affinity and specificity. The anti-PMSA antibodies are useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatitis, benign enlargement, prostatic cancer or testicular cancer, or solid tumours, soft tissue tumours or metastatic lesions, and its associated pain. The present sequence represents a variable region from a murine antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; murine; antibody; skin disorder; binding agent; PSWA; cytostatic; prostate specific membrane antigen; antipsoriatic; antiarthritic; emanatory; antiallergic; vaccine; dermal disorder; epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis; neoplastic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ablating/killing aberrant prostate specific membrane antigen-expressing cells for treating skin disorders, by contacting the cell with an antibody that binds to the extracellular domain of prostate specific
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                               100.0%; Score 98; DB 6; Length 123; 100.0%; Pred. No. 2.3e-08; Eive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine MuVHIIIC amino acid sequence SEQ ID NO:69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR44686 standard; protein; 123 AA
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08-MAR-2002; 2002US-0362612P.
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                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                            Sequence 123 AA;
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The skin disorder is a dermal or an epidermal disorder, and is selected from psoriasis (preferably chronic stationary psoriasis, psoriasis vulgaris, eruptive (gluttate) psoriasis, psoriatic erythroderma, generalised pustular psoriasis, psoriatis erythroderma, psoriasis, and localised pustular psoriasis, province carthritis, exfoliative dermatitis, pityriasis rubra planis, pityriasis rosacea, parapsoriasis, ptrylasis lichenoiders, lichen planus, lichen nitidus, lichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis, preferably psoriasis. Mi is useful for treating a skin disorder such as an inflammatory or neoplastic disorder of the epidermis or dermis, preferably an epidermal precancerous or cancerous lesion. Mi is also useful to treat or prevent disorder involving aberrant activity of PSMA-expressing cell, e.g. kidney, liver or brain cell. Acc68816 to Acc68817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD23; FCBRII; IgE receptor; monoclonal antibody; CII; mouse, monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region, CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erythematosus; multiple sclerosis; urticaria; nephrotic syndrome; glomerulonaphritis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; sjogren's syndrome; allergy, aethma: rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse anti-CD23 MAb C11 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note= "CDR H2"
129. .131
/note= "CDR H3"
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                              of the present invention
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N-PSDB; AAZ34745.
                                                                                                                                                                                                                                                                                                             Local Similarity
les 19; Conser
                                                                                                                                                                                                                                                               Sequence 123 AA;
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This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see ANY32262 and AAY32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 (Type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Habhimoto's thyroiditis, multiple cof arthritis, lupus erythematosus, Habhimoto's thyroiditis, multiple solerosis, diabetes, uveitis, dermatitis, psociasis, uricaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Slogren's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly type I diabetes), and Brcell mallignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence may be used in the activation of new ketone prodrug compounds containing active agents. The ketone derivatives are useful as carriers for antitumour agents such as cyrotoxic agents, where the antitumour agent is a microtubule stabilising agent such as paclitaxel,
Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 98; DB 3; Length 137; 100.0%; Pred. No. 2.6e-08; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lerner RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB50426 standard; protein; 286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody 33F12 catalytic fragment.
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                                                           Claim 8; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2000; 2000WO-US014366.
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Best Local Similarity 100.0
Matches 19; Conservative
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N-PSDB; AAC90472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 137 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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epothilone or its therapeutically active analogue or an anthracycline antibiotic such as doxorubicin or its therapeutically active analogue. The ketone derivatives are useful for targeted drug delivery. The inactive molecules in the ketone compounds are converted to active molecules by retro-Michael reaction. The antibody has bifunctional activity and specifically immunoreacts with cell surface antigen of a target cell. The active ingredients can be mixed effectively with excipients as per desired amount along with the buffering agent to enhance the effectiveness and activity of the compound
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                                                                                                                                                               100.0%; Score 98; DB 4; Length 286; 100.0%; Pred. No. 6.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-CD23 MAb C11 heavy chain.
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.CDR 2"
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104. .111
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/note= "CDR 1"
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/note= "
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                                                                                                                                                                          Local Similarity 100.
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                                                                                                                                        Sequence 286 AA;
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Synthetic.
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                                                                                                                                                                  Query Match
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This amino acid sequence represents the heavy chain of humanised anticops (PERII) monoclonal antibody C11, composed of a human framework (EGEKYII) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric cor humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus expthematosus, Hashimoto's thyroiditis, multiple scierosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, colon, s disease, Sjogren's syndrome, allergies, allergic asthma, acute asthmatic exacerbation, rhinitis, eczema, graftversus-host disease, (DOP), insulitis, bronchitis (particularly dyroid interactions malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention, neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                    Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse germline heavy chain variable (VH) region, V(H)22.1.
Rapson NT,
  Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE06973 standard; protein; 100 AA.
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                                                                                                                                                                      Claim 9; Fig 4; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 19; Conservative
  Crowe SJ,
                                           WPI: 2000-053101/04.
                                                                  N-PSDB; AAZ34748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157226-A1.
  Bonnefoy JMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
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(MILL-) MILLENNIUM PHARM INC.

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Jones ST, O'brien S, O'keefe T;

Newman W,

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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), CC comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They care useful for inhibiting leukocyte trafficking, for treating cCR2-mediated disorders such as inflammatory disorder, autoimmune invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as rheumatoid arthritis and multiple sclerosis, carberogenesis and atherosclerosis, and in the manufacture of a cuestul in therapy or diagnosis, and in the manufacture of a cuestul in therapy or diagnosis, and in the manufacture of a cuedicament for treating CCR-2 mediated disease. They are also useful for treating allersy, anaphylaxis, malignancy, chronic and acute confinitammation, histamine and IGB-mediated allersic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory confinitammatory associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting continual hyperplasia of a vessel in a mammal, and inhibiting continuinal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline heavy continuing and variable (VH) region, V(H)22.1
                                                                                                      Humanized immunoglobulin for treating a CC-chemokine receptor 2-media disorder in a patient, comprises a binding specificity for CCR2, and non-human antigen binding region and human immunoglobulin.
                                                                                                                                                                                                                         Disclosure; Page 152-153; 183pp; English
Horvath C,
                                                      WPI; 2001-488888/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 100 AA;
Larosa GJ,
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Length 100; 96.9%; Score 95; DB 4; Length 100 94.7%; Pred. No. 5.6e-08; tive 1; Mismatches 0; Indels Conservative Local Similarity es 18; Conser Query Match Matches

68

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Gaps

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Mouse antibody 38C2 catalytic fragment AAB50425 standard; protein; 299 AA 1 EIRLKSDNYATHYAESVKG 19 QIRLKSDNYATHYAESVKG 13-MAR-2001 (first entry) AAB50425; 20 RESULT 8 <u>D</u> à

Mouse; antibody 38C2; ketone compound; antitumour; cytotoxic; targeted drug delivery.

WO200071556-A1 Mus sp.

30-NOV-2000.

24-MAY-2000; 2000WO-US014366.

99US-00318661 25-MAY-1999;

(SCRI ) SCRIPPS RES INST.

Lerner RA; List B, Rader C, Barbas CF, Shabat D,

WPI; 2001-061339/07. N-PSDB; AAC90471.

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The present sequence may be used in the activation of new ketone prodrug compounds containing active agents. The ketone derivatives are useful as carriers for antitumour agents such as cytotoxic agents, where the antitumour agent is a microtuble stabilising agent such as pacificaxel, epothilone or its therapeutically active analogue or an anthracycline antibiotic such as doxorubicin or its therapeutically active analogue. The ketone derivatives are useful for targeted drug delivery. The influetive molecules in the ketone compounds are converted to active molecules by retro-Michael reaction. The antibody has bifunctional activity and specifically immunoreacts with cell surface antigen of a target cell. The active ingredients can be mixed effectively with excipients as par desired amount along with the buffering agent to enhance the effectiveness and activity of the compound
           carriers for e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New monoclonal antibody BW835 specific for tumour antigens - useful for diagnosis and treatment of tumours affecting the breasts, ovaries,
                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 2.1e-07;
1; Mismatches 0; Indels
           New ketone compounds containing active agents useful as antitumor agents, antibiotics or fluorescent molecules.
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                                                       Disclosure, Fig 9; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            205 EIRLRSDNYATHYAESVKG 223
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(first entry)
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                   Sequence 299 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Monoclonal antibody BW 835 is produced by hybridoma cell line BW 835. The antibody strongly reacts with lung adenocarcinomas and human mammary-, ovary- and prostate carcinomas. It additionally reacts with polymorphic epithelial mucin (PEM) but does not react with normal human tissue. (Updated on 25-MAR-2003 to correct PN field.) Disclosure; Fig la; 24pp; German.

prostate and lungs.

Query Match

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XX SS

AAY03869;

RESULT 10 AAY03869

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CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a branched mucin type synthetic glycolipid, A gene fragment encoding the V region of the heavy chain an antibody recognising the present protein is claimed. The antibody fragment is useful for the development of cancer treatments and
                                                                                                                                               Amino acid sequence of a synthetic branched mucin type glycolipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recognising branched mucin type synthetic glycolipid - using gene fragment of an antibody, useful in cancer treatment and diagnosis
                                                                                                                                                                            Branched mucin type glycolipid; V region; heavy chain; antibody; cancer treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.9%; Score 93; DB 2; Length 119; 94.7%; Pred. No. 1.5e-07; ive 1; Mismatches 0; Indels
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                                  AAW46958 standard; protein; 119 AA.
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21-OCT-2002; 2002US-0420472P.
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Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-264850/24.
N-PSDB; AAV22331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 119 AA;
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                                                                                                                                                                                                                                                                                       JP10084963-A.
                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1996;
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                                                                                                               06-JUL-1998
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                                                                       AAW46958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a process for preparing a crystal using cadmium. Structure factors or structural coordinates obtained from the crystal of Structure factors or structural coordinates obtained from the crystal of SMM antibody bound to an epitope can be used to design minics of the binding fragment of the SMM antibody bound to a peptide recognised by the epitope binding site of SMM. The products and methods can be used to epitope binding site of SMM. The products and methods can be used to tumours. Much epitope mimics can also be used to prevent or decrease an immune response, e.g. in the therapy of diseases caused by autoimmune response, e.g. in the therapy of diseases caused by autoimmune response, inflammatory disorders or transplant rejections such as graft versus host disease. The present sequence represents the amino acid sequence of a heavy chain variable region of SMM antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New SM3 antibody crystal structures - used to develop agents for treating e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or
                                                                                                                                                                                                                                                                                                                                                                                                        SM3 antibody, epitope, mimic, crystal; tumour, MUC1 epitope; allergy; immune response, arthritis; multiple sclerosis; asthma; diabetes; inflammatory disorder; transplant rejection; graft versus host disease.
                                                                          Gaps
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                                  Score 93; DB 2; Length 115;
Pred. No. 1.4e-07;
L; Mismatches 0; Indels
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                      94.9%; Scor.
94.7%; Pred. No. 1...
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sternberg MJE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                  AAY03869 standard; protein; 116
                                                                                                                                                                                                                                                                                                                                                                   SM3 heavy chain variable region.
                                                                                                               1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                    46 EIRLKSNNYATHYAESVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-GB002542
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                                                       Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. tumors, autoimmu
transplant rejection.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX31971.
Sequence 115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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The invention relates to treating a human patient diagnosed with a B-cell malignancy. The method involves (a) administering to the human patient a blocking anti-CD22 monoclonal antibody binding to the first two Ig-like domains, or to an epitope within the first two Ig-like domains of native human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the mailgnancy to the treatment. The method is useful for treating a human patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma, Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy the amino acid sequence for heavy chain Vh-D-Jh junction for anti-CD22 antibody from hybridoma HB22-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating an autoimmune disease or a B-cell malignancy in a human patient comprises administering an amount of an anti-CD22 monoclonal antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD22; autoimmune disease; anti-CD22 antibody; ilmmunosuppressive; cytostratic; nephrotropic; dermatological; antihiflammatory; anti-ulcer; antirheumatic; antiarthritic; antiporiatic; thyromimetic; antianemic; antidiabetic; antiallergic; gene therapy; HB22-23.
                                                                                                                                     Treating a human patient diagnosed with a B-cell malignancy by administering a blocking anti-CD22 monoclonal antibody binding to the first two Ig-like domains of native human CD22 (hCD22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybridoma HB22-23 anti-CD22 MAb heavy chain (VH) fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93;
Pred. No.
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                                                                                                                                                                                                    Claim 31; Fig 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.9%;
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2002US-0420472P
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Best Local Similarity 94.7
Matches 18, Conservative
             (UYDU-) UNIV DUKE.
(REGC ) UNIV CALIFORNIA.
                                                             Tuscano J;
                                                                                          2003-712652/67.
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                                                                                         WPI; 2003-712652/
N-PSDB; ACF36425.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 119 AA;
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21-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                           redder T,
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                                                            The invention relates to treating a human patient diagnosed with an autoimmune disease. The method involves administering to the patient an amount of a blocking anti-CD22 monoclonal antibody and monitoring the response of the autoimmune disease to the treatment. The method is useful in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis, Hashimoto's thyroiditis, autoimmune haemolytic anemass, diabetes or allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The present sequence represents the amino acid sequence for heavy chain Vh-D-Jhiuction for anti-CD22 antibody from hybridoma HB22-23
the patient and monitoring the response of the disease to the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; Fd fragment, lead cation, perfume, cosmetic; pharmaceutical; health care, skin treatment; pesticide; herbicide;
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                                                                                                                                                                                                                                                                                           Length 119;
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Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW01589 standard; protein; 120
                                                                                                                                                                                                                                                                                                                                                                1 EIRLKSDNYATHYAESVKG 19
                                 Claim 1; Fig 14; 69pp; English.
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95US-00541373.
                                                                                                                                                                                                                                                                                           94.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-043140/04
                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                             Sequence 119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy metal.
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in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; muchin; cancer; cyrostatic; hybridoma; specific binding assay; affinity purification; drug targeting; toxin targeting; imaging; genetic; therapeutic.
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                                                                                                Query Match 94.9%; Score 93; DB 2; Length 120; Best Local Similarity 94.7%; Pred. No. 1.5e-07; Matches 18; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      2G3 hybridoma VH domain SEQ ID NO:2.
                                                                                                                                                                                                                                                                                      AAY90812 standard; protein; 122 AA.
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                                                                                                                                                                                                      50 EIRLKSNNYATHYAESVKG 68
                                                                                                                                                                    1 EIRLKSDNYATHYAESVKG 19
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85US-00690750.
86US-00842476.
88US-00190778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA38896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 122 AA;
                                                                   Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating cancer.
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21-MAR-1986;
08-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-1984;
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                                                                                                                                                                                                                                                      RESULT 15
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1 EIRLKSDNYATHYAESVKG 19

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Search completed: September 30, 2004, 06:06:22 Job time : 94.7458 secs

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Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 69, Appl Sequence 77, Appl Sequence 15, Appl
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19:178 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_MBW PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/PCT_MBW PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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11: \cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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6 US-10-449-379-69
6 US-10-688-15-69
US-09-883-758-4
US-09-80-475-36
6 US-10-766-61-36
6 US-10-766-61-36
0S-10-733-563-36
US-10-733-563-15
US-10-372-481-15
5 US-10-371-797-15
5 US-10-239-656-69
2 US-10-239-656-69
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 200000000
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Match Length DB
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Appl Appl Appl Appl Appl	App] App] App]	App App	Appl Appl Appl Appl Appl	Appl Appl Appl Appl Appl	App   App
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9-855-153-15 9-854-811-15 9-934-773-15 9-963-620-15	10-225-784- 10-224-720- 10-225-779- 10-374-381-	10-446-542-1 10-160-506-7 10-449-379-7 10-688-015-7	10-422-049-1 10-422-049-1 10-277-471A- 10-160-506-3 10-449-379-3	.10-688-015- .10-160-506- .10-160-506- .10-160-506- .10-160-506-	10-449-379-4 10-449-379-6 10-449-379-6 10-688-015-4 10-688-015-4
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## ALIGNMENTS

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Sequence 69, Application US/10160506
| Publication No. US20030161832A1
| GENERAL INFORMATION:
| APPLICANT: Bander, Neil H.
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING;
| TITLE OF INVENTION: SKIN DISCRDERS USING BINDING AGENTS SPECIFIC FOR;
| TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN;
| TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN;
| FILE REPERENCE: 10448-162001
| CURRENT FILING DATE: 2002-05-30
| PRIOR PILING DATE: 2001-09-20
| PRIOR PILING DATE: 2001-09-20
| PRIOR PILING DATE: 2001-09-20
| PRIOR PILING DATE: 2001-09-30
| PRIOR PILING DATE: 2002-03-08
| NUMBER OF SEQ ID NOS: 128
| SOFTWARE: FastSEQ for Windows Version 4.0
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0
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100.0%; Score 98; DB 14;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 69, Application US/10449379; Publication No. US20040120958A1; GENERAL INFORMATION:
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RESULT 1
US-10-160-506-69
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US-10-449-379-69
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US-09-564-329A-15

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Gaps

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0; Indels

Length 285;

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
COTHER INFORMATION: residue sequence of catalytic fragment
US-09-883-758-4
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 98, DB 9, I
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 19; Conservative 0; Mismatches 0;
FILE REFERENCE: PLF0011S
CURRENT APPLICATION NUMBER: US/09/883,758
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US/09/318,661
PRIOR PLING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2:1
SEQ ID NO 4
LENGTH: 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 EIRLIGDNYATHYAESVKG 221
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                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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CRGANISM: Mus musculus
US-09-840-459-36
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US-10-766-773-36
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US-09-840-459-36
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Sequence 69, Application US/10688015

Sequence 69, Application WS/10688015

Publication No. US20040136998A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING

TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN

TITLE OF INVENTION NUMBER: 60/422,396

PRIOR FILING DATE: 2002-10-30

NUMBER OF SEQ ID NOS: 128

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 123
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Patent No. US20020058804A1
Patent No. US20120058804A1
Patent No. US20120058804A1
APPLICANT: Barbat, Doron
APPLICANT: Rader, Christoph
APPLICANT: Lerne, Richard A
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
  APPLICANT: Bander, Neil H.

TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF FILE REFERENCE: 10448-163002.
CURRENT APPLICATION NUMBER: US/10/449,379
CURRENT FILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-09-08
PRIOR PRILING DATE: 2002-09-08
PRIOR APPLICATION NUMBER: 60/362,810
PRIOR FILING DATE: 2002-09-08
PRIOR FILING DATE: 2001-09-01
NUMBER OF SEQ ID NOS: 128
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 123;
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ilarity 100.0%; Pred. No. 9.3e-08;
Conservative 0; Mismatches 0;
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Matches 19; Conservative
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CORGANISM: Mus musculus
US-10-688-015-69
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ORGANISM: Mus musculus
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Best Local Similarity
Matches 19; Conserv
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US-09-883-758-4
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Gaps
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96.9%; Score 95; DB 9; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels
US-09-840-4559-56

Sequence 36, Application US/09840459

Patent No. US2002015057641

GENERAL INPORMATION:
APPLICANT: LARGOS, Gregory J.
APPLICANT: LARGOS, Gregory J.
APPLICANT: Ownen, Walter
APPLICANT: O'SHIEN, SIGNAN H.
APPLICANT: O'SHIEN, SIGNAN H.
APPLICANT: O'SHIEN, SIGNAN H.
APPLICANT: O'SHIEN, SIGNAN H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: O9/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
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RESULT 9
US-09-883-758-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LAGOSA, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Reie, S. Taxran
APPLICANT: O'Refe, Tharesa
APPLICANT: O'Reefe, Tharesa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: MUMBER: US/10/766,610
CURRENT APPLICATION NUMBER: US/40,459
PRIOR APPLICATION NUMBER: O9/840,459
PRIOR PILING DATE: 2001-04-23
PRIOR PELING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PELING DATE: 1909-07-23
PRIOR PELING DATE: 1999-07-23
PRIOR PELING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ. ID NOS: 107
APPLICANT: Newman, Walter
APPLICANT: O'DES, S. Tarran
APPLICANT: O'DES, S. Tarran
APPLICANT: O'REF, Theresa
TITLE O'RINGHING HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REPERENCE: 1855.1052-028
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR PILING DATE: 1999-07-22
PRIOR PILING DATE: 1999-07-22
SPIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
SOFTWARE OF SEQ ID NOS: 106
SEQ ID NOS: 106
SEQ ID NOS: 106
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB 16;
Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 95; DB 16;
Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIRLKSDNYATHYAESVKG 19
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity 94.7%;
Matches 18; Conservative
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CORGANISM: Mus musculus
US-10-766-610-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
COGANISM: Mus musculus
US-10-766-773-36
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50 OIRLKSDNYATHYAESVKG 68

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Sequence 61, Application US/10239656

Sequence 61, Application No. US20040038339A1

Sequence 61, Application No. US20040038339A1

APPLICANT: KUER, PETER

APPLICANT: LOTTERBUSE, RALF

APPLICANT: BORSCHERT, KATRIN

APPLICANT: BORSCHERT, KATRIN

APPLICANT: BORSCHERT, ROBERT

APPLICANT: BORSCHERT, ROBERT

APPLICANT: HOFMEISTER, ROBERT

TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE

TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPLEX

FILE REFERENCE: 029976/0106

CURRENT APPLICATION NUMBER: 2003-06

PRIOR APPLICATION NUMBER: PCI/EP01/03414

PRIOR APPLICATION NUMBER: EP 00106467.4

PRIOR FILING DATE: 2000-03-24

NUMBER: OF SEQ IN NOS: 20.

NUMBER: DO SEQ IN NOS: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-11 single ; OTHER INFORMATION: chain Fv US-10-239-656-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-2 single; OTHER INFORMATION: chain FV
US-10-239-656-61
                    APPLICANT: MAYER, MONIKA
APPLICANT: HOFWEISTER, ROBERT
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPLEX
FILE REFERENCE: 029976/0106
CURRENT PAPLICATION NUMBER: US/10/239,656
CURRENT FILING DATE: 2003-03-06
PRIOR FILING DATE: 2001-03-26
PRIOR PAPLICATION NUMBER: EP 00106467.4
PRIOR APPLICATION NUMBER: EP 00106467.4
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SEQ ID NO 69
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%; Score 93; DB 12; Length 256; ilarity 94.7%; Pred. No. 1.3e-06; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.9%; Score 93; DB 12; Length 25 Best Local Similarity 94.7%; Pred. No. 1.3e-06; Matches 18; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 256
  KISCHEL, ROMAN
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Best Local Similarity
Matches 18; Conserva
  APPLICANT:
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              GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
ITILE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 5405.306
CURRENT APPLICATION NUMBER: US/10/372,481
CURRENT FILING DATE: 2003-02-21
PRIOR PELING DATE: 2003-02-21
PRIOR PELING DATE: 2003-02-21
PRIOR PILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-02-21
NUMBER: OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 15
LENGTH: 119
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Pred. No. 5.6e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93; DB 12; Length 11
Pred. No. 5.6e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/10371797
| Publication No. US20040001828A1
| GENERAL INFORMATION:
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
| APPLICANT: TUSCANO, JOSEPH
| APPLICANT: TEDDER, THOMBE
| TILLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
| TILLE OF INVENTION: ANTIBODIES
| FILE REFERENCE: 39754-0951
| FILE REFERENCE: 30754-0921
| FRIOR PELICATION NUMBER: US 60/420,472
| PRIOR PILING DATE: 2003-10-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2002-02-10
| PRIOR FILING DATE: 2002-02-10
| PRIOR FILING DATE: 2002-02-10
| PRIOR FILING DATE: 2002-10-21
| TYPE: FRICK APPLICATION NUMBER: US 60/359,419
| TYPE: FRICK APPLICATION NUMBER: US 60/359,419
| TYPE: PRIOR FILING DATE: 2002-02-10-21
| SOFTWARE: FRESEQ for Windows Version 4.0
| SEQ ID NO 15
| TYPE: PRI
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US-10-239-656-69
US-10-239-656-69

Sequence 69, Application US/10239656

Publication No. US20040038339A1

GENERAL INFORMATION:
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94.7%;
Publication No. US20030202975Al
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Best Local Similarity 94.7%;
Matches 18; Conservative
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APPLICANT: RIFTHMULLER, GERT
APPLICANT: LUTTERBUSE, RALF
APPLICANT: BORSCHERT, KATRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 94.7
18; Conservative
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; ORGANISM: Homo sapiens
US-10-372-481-15
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US-10-371-797-15
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GENERAL INFORTATION:
GENERAL INFORTATION:
APPLICANT: RUFER, RERT
APPLICANT: RIFTHMULLER, RERT
APPLICANT: LUTTERBUEZ, RALF
APPLICANT: ACCHEL, ROMAN
APPLICANT: MAYER, MONIKA
APPLICANT: MAYER, 10 AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
FILE REFERENCE: 029976/0106
CURRENT APPLICATION NUMBER: US/10/239,656
CURRENT APPLICATION NUMBER: PCT/RE01/03414
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 77
LENGTH: 503
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Sequence 15, Application US/09564329A

Patent No. US20010055751A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFREENCE: 30435.544514

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT FILING DATE: 1990-02

PRIOR PLILING DATE: 1997-03-10

PRIOR PLILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR PLILING DATE: 1998-02-17

PRIOR PLILING DATE: 1998-02-17

PRIOR PLILING DATE: 1998-02-17

PRIOR PLILING DATE: 1998-02-17

PRIOR PLILING DATE: 1998-03-16

PRIOR PLILING DATE: 1998-03-16

PRIOR PLILING DATE: 1998-03-10

PRIOR PLILING DATE: 1998-03-10

PRIOR PLILING DATE: 1998-03-10

PRIOR PLILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10xP5-
OTHER INFORMATION: 2 bispecific single chain FV
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APPLICATION NUMBER: 09/203,939
FILING DATE: 1998-12-02
APPLICATION NUMBER: 09/251,835
FILING DATE: 1999-02-17
Sequence 77, Application US/10239656
Publication No. US20040038339A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserv
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GENERAL INFORMATION:
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US-09-883-758-4
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Sequence 26, Appl
Sequence 5, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 45, Appli
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Sequence 45, Appli
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Sequence 4, Appli
Sequence 4, Appli
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                                                                          5 ; Search time 32.2034 Seconds (without alignments) 30.459 Million cell updates/sec
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Sequence 1,
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Sequence 4,
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Sequence
Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-881-758-4

US-09-883-758-2

US-08-868-1

US-08-466-2721-1

US-08-478-857-1

US-08-478-857-1

US-08-478-28

US-08-478-28

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US-08-481-771-1

US-08-481-771-1

US-08-481-749-1

US-08-192-102-5

US-08-192-102-5

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US-08-192-102-5

US-08-192-103-119-5

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                                                                                                                                                                                                                               389414 seqs, 51625971 residues
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                                                                               September 30, 2004, 06:00:45
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Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                US-09-674-716B-11
98
1 EIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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Match Length
           Copyright
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Maximum DB seq
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  JOHNBACH INFORMATION:
JOHNBACH INFORMATION:
JAPPLICANT: Shabat, Doron
JAPPLICANT: Rader, Christoph
JAPPLICANT: Rader, Christoph
JAPPLICANT: Rader, Christoph
JAPPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
JULIE REFERENCE: PLFOOLIS
CURRENT APPLICATION WUMBER: US/09/318,661
CURRENT PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09883758;
APPLICANT: Barbar II, Carlos F.
APPLICANT: Later Deron
APPLICANT: List, Benjamin
TITLE OF INVARVINON PRORUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLOO11S
CURRENT APPLICATION NUMBER: US/09/883,758
CURRENT FILING DATE: 2001-06-18
PRIOR FILING DATE: 1999-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Nucleotide OTHER INFORMATION: residue sequence of catalytic fragment
              Sequence
Sequence
Sequence
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US-09-246-258-21
US-09-53-106-21
US-08-767-128-24
US-08-767-128-36
US-07-977-6966-78
US-08-129-930B-78
US-08-129-930B-78
US-08-129-930B-78
US-08-976-288A-13
US-08-976-288A-13
US-08-809-739-20
US-09-809-739-21
US-08-809-739-21
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Patent No. 6268488
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 19; Conservative
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      2228888888888888844444
8004284597
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Query Match
Best Local Similarity
Matches 18; Conserv
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US-08-466-272A-1
                        US-09-883-758-2
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Fatent NO. 6268488
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Barbas III, Carlos F.
APPLICANT: Barbat, Doron
APPLICANT: Benjamin
APPLICANT: List, Benjamin
APPLICANT: Li
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| Patent No. 6677435
| Patent No. 6774435
| Patent No.
) NUMBER OF SEQ ID NOS: 6

) SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 285

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: residue sequence of catalytic fragment
US-09-883-758-4
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96.9%; Score 95; DB 3; Length 298;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels
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100.0%; Score 98; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 19; Conservative 0; Mismatches 0;
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; ORGANISM: Mus musculus
US-09-318-661-2
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US-09-318-661-2
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US-09-883-758-2
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APPLICANT: Boselet, Klaus
APPLICANT: Boselet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Princegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITT' Meahington
STATE: D.C.
COUNTRY: USA
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Query Match

96.9%; Score 95; DB 4; Length 298;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,661
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION WHERE: US 07/957,827
FILING DATE: 08-OCT-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: FORMATION NUMBER: 35,694
REGISTRATION NUMBER: 35,694
REGISTRATION NUMBER: 35,694
RECOMMULCATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 1
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US-008-661-1
Sequence 1, Application US/08468661
Patent No. 5639621
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                                                                                                                                                         205 EIRLRSDNYATHYAESVKG 223
                                                                                                       1 BIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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; MOLECULE TYPE: peptide
US-08-468-661-1
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RESULT 8
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                                                   APPLICANT: Sermin, Gerhard

TITLE OF INVENTION: Monoclonal Antibodies Against

TITLE OF INVENTION: Theorem Associated Antigens, Processes for the Preparation
TITLE OF INVENTION: Thereof and the Use Thereof
CORRESPONDENCE: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Mashington
STREET: ADDRESSEE: Dinner ADDRESSEE: Dinner ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: Dinner ADDRESSEE: 
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Patent No. 569578
GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Beeman, Gerhard
TITLE OF INVENTION: Tumor-Associated Antibodies Against
TITLE OF INVENTION: Thereof and the Use Thereof
NUMBER OF SEQUENCES:
ADDRESSES: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSES: Pinnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.9%; Score 93; DB 1; Length 115; Best Local Similarity 94.7%; Pred. No. 8.7e-08; Matches 18; Conservative 1; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,272A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 06-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BUGGISSKY, Lawrence B.
REGISSTRATION NUMBER: 35,066
REFERENCE/DOCKET NUMBER: 02481-1227-00000
TELEPHONE: 202-408-4000
STELEPHONE: 202-408-4400
STELEPHONE: 202-408-4400
STELEPHONE: AND APPLICATION: TELEPHONE: AND APPLICATION: TELEPHONE: AND APPLICATION: AND APPLICATION APPLICATION: AND APPLICATIO
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STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Bosslet, Klaus
Pfleiderer, Peter
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-466-272A-1
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TILLING DATE: 08-07-132

ATTOMNEY/MARIES 18/08/478,1227-00000

TEREPREVALUED MACHINES 18/08/478,1227-00000

TEREPREVALUED MACHINES 18/08/4000

TOTTER WARNES 18/08/4000

TOTTER WARNES 18/08/4000

AS TRANSING MACHINES PROBLES 18/08/4000

TITLE OF INVESTION FROM 18/08/401/701

TOTTER MACHINES 18/08/401/701

TOTTER MAC
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94.9%; Score 93; DB 3; Length 115;
Best Local Similarity 94.7%; Pred. No. 8.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FORMAN, DAVIG S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 0555;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                           1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                          46 EIRLKSNNYATHYAESVKG 64
TELEFAX: 202-408-4400

| INFORMATION FOR SEQ ID NO: 1:
| SEQUENCE CHARACTERISTICS: |
| LENGTH: 115 amino acids |
| TYPE: amino acid |
| TOPOLOGY: linear |
| MOLECULE TYPE: peptide |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-130-783-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                RESULT 9
US-09-130-783-1
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Gaps
Sequence 28, Application US/08767128

Sequence 28, Application US/08767128

Patent No. 6111079

BENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: MORRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLECTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis

STRIE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION 1926
PRIOR APPLICATION 1996
PRIOR APPLICATION 1996
PRIOR APPLICATION 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/41,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 55402
ZIP: 55402
COMPUTER READABLE FORM:
MBJIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTENG Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFRENCE/DOCKET NUMBER: 8648
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/331-9081
TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 EIRLKSNNYATHYAESVKG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 120 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: 1

ORIGINAL SOURCE:
US-08-767-128-28
                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                  US-08-767-128-28
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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us-09-674-716b-11.open.rai

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WESULT 13
US-08-483-749A-10
US-08-483-749A-10

Sequence 10, Application US/08483749A
Patent No. 6054561

Patent No. 6054561

STREAT INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION:
MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES:
ADDRESSEE: CHIRON CORPORATION
STREET: USA
COUNTY: USA
COUNTY: USA
ZIP: 94662-905

COMPUTER: READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: INP PC Compatible
COMPUTER: INP PC Compatible
COMPUTER: INP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
PILING DATE: O7-UNL-1995
CLASSIFICATION NUMBER: 36,914
REGIENTATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Best Local Similarity 84.2%; Pred. No. 1.7e-06;
Matches 16; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

92.9%; Score 91; DB 4; Length 151;
Best Local Similarity 89.5%; Pred. No. 2.5e-07;
Matches 17; Conservative 2; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DAFE: 1999-03-16
PRIOR PLING DAFE: 1999-03-16
PRIOR PLING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-12-02
PRIOR PLING DATE: 1998-12-02
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR PLING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATONIN VET: 2.0
SEQ ID NO 15
LENGRIH: 151
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15
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Sequence 15, Application US/09564329A

Patent No. 6541212

GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-310

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21
                                                    Sequence 2, Application US/08483749A

Sequence 2, Application US/08483749A

Patent No. 6054561

SAPPLICANT: RING, DAVID B.

APPLICANT: RING, DAVID B.

TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS TITLE OF EXCUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.9%; Score 93; DB 3; Length 122; 94.7%; Pred. No. 9.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,749A

FILING DATE: 07-UN-1995

CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: SAVERBIDE, PAUL B.
REGISTATION NUMBER: 36,914
REFERENCE/DOCKET WUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2885
TELEPHONE: (510) 601-2885
TELEPHONE: (510) 601-2885
TELEPHONE: (510) 601-2885
TELEFECCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 122 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.7<sup>3</sup>
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-483-749A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-564-329A-15
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50 EIKLKSNNYPTHYAESVKG 68

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APPLICANT: MINGTO, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-THE ANTIBODIES AND ASSAYS EMPLOYING
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYEE: Flopped is k
COMPUTER READABLE FORM:
MEDIUM TYEE: Flopped is k
COMPUTER READABLE FORM:
MEDIUM TYEE: Flopped is k
COMPUTER ES Flopped is k
COMPUTER ES Flopped is k
COMPUTER ES Flopped is k
SOFTWARE: TEMPORATION FOR SOFTWARE: BEALON DATA:
APPLICATION NUMBER: US/08/192,102
FLING DATE: 04-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,413
FLING DATE: 02-FEB-1993
FLING DATE: 10-FEB-1993
FROR APPLICATION NUMBER: US 08/010,406
FLING DATE: 10-FEB-1993
FROR APPLICATION NUMBER: US 07/943,852
FLING DATE: 11-SEP-1992
FRING DATE: US 07/670,827
FILING DATE: US 07/670,827
                                                                                                                                                                                                                                                                                                                                                                                                                    Hamilton, Brook, Smith & Reynolds, P.C
US-08-192-102-5
, Sequence 5. Application US/08192102
, Patent No. 565672
, GENERAL INFORMATION:
                                                                                                                         Le, Junming
Vilcek, Jan
Daddona, Peter B.
Ghrayeb, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: NY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brook, David E. REGISTRATION NUMBER: ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Militia I
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-192-102-5
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%; Score 80.5; DB 3; Length 119; 89.5%; Pred. No. 9.4e-06; ive 1; Mismatches 0; Indels
                                                                                                                                  GENERAL INFORMATION:

APPLICANT: WYLIE, DWANE E.

APPLICANT: LOPEZ, OSVALDO

APPLICANT: MYRAY, PETER JOSEPH

APPLICANT: GOEBEL, PETER

TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND

TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION OF 424
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION 1926
PRIOR APPLICATION 04-DEC-1996
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/U896/09258
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
ANALOSSIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEN VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8648.49USF1
                  RESULT 14
US-08-767-128-26

Sequence 26, Application US/08767128

Patent No. 6111079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/312-5078
TELEPHONE: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                          75.5%; Score 74; DB 1; Length 119; 84.2%; Pred. No. 0.00011; ive 0; Mismatches 3; Indels
                                                                                                                                                            1 EIRLFSDNYATHYAESVKG 19
                                                                                                                                                                                     50 EIRSKSINSATHYAESVKG 68
119 amino acids
amino acid
                                                                                                                           16; Conservative
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22,592 3R: NYU93-01M3

Search completed: September 30, 2004, 06:38:20

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Gaps

Job time : 34.2034 secs

Dank Sheat

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

serich time 3.25424 Seconds (without alignments) 88.677 Million cell updates/sec September 30, 2004, 05:55:56 Run on:

US-09-674-716B-13 16 1 FID 3 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\* 2: pir1:\* 3: pir2:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	DNA topoisomerase	PEB1 5'-region hyp	pyrrologuinoline g	hypothetical prote	lipocortin I - pig	nitrobenzene nitro	hypothetical prote	급	RNA-directed RNA p	hypothetical prote	hypothetical prote	hypothetical prote	protein-tyrosine-p	protein-tyrosine-p	hypothetical prote	hypothetical prote	rar	chai	proline-rich phosp	hypothetical prote	trar	larvicidal toxin -	gene 55.4 protein	hypothetical prote	calmodulin-related	cal p	al	cal 4	ical pro
SUMMARIES	QI	843834	4851	0	8406	518	68	H82818	PQ0413	PQ0416	A95119	H82096	533646	PS0363	PS0364	D87544	C70186	G95919	833402	B19803	D82085	A96026	A23098	ZDBPT9	B97505	C34669	H83816	8246	PC4133	9206
	DB	71	7	Н	(1	N	(7)	Ŋ	ď	~	~	~	~	0	~	7	7	7	7	7	~	~	7	-	0	N	(7	~	7	7
	Length	18	21	23	25	30	30	31	32	33	33	33	33	35	35	36	37	37	38	38	39	39	40	43	43	45	45	46	47	48
	- A	0		0.						0.		0.												0.						
æ	Query Match	100	0	100	0	0	0	100	0	O	100	0	0	0	0	O	0	O	0	0	О	100	0	100	0	0	100	100	100	100
	Score	16	16	16	16	16	16	16	16	. 16	16	16	16	16	16	16	16	16	16	, 16	16	16	16	16	16	16	16	16	16	16
	Result No.		Ν,	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

hypothetical prote hypothetical prote hypothetical prote	hypothetical prote cell division cycl hypothetical prote hypothetical prote	hypothetical prote hypothetical prote hypothetical prote	sex-determining pr SOX-11 protein - A Sry-related sequen	Sry-related sequen Sry-related sequen Sry-related sequen
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48 50 51	0 0 0 0 0 0 0 0	9999	ር የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ	5 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
0000	1000.0	0.00	100.0 100.0 100.0	100.0
16 16	9 1 1 1 1	110	76 76	9 1 1 1 1 1 1
30 31 32	23 23 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25	9 8 9 7 6 9 8 4 6	4 4 4 0 1 2	4.4.4. 5.4.7.

## ALIGNMENTS

DNA topoisomerase (EC 5.99.1.2) - Klebsiella sp. (ATCC 15380) (fragment) C;Species: Klebsiella sp. A;Variety: ATCC 15380 A;Variety: ATCC 15380 C;Accession: 843834 B;tynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J. Biochem. J. 299, 129-136, 1994 B;tyle: Characterization of the CysB protein of Klebsiella aerogenes: direct evidence the A;Reference number: 843834; Wullb:9422019; PMID:8166630	) (fragment) nge 07-Mav-1999
C;Species: Klebsiella sp. A;Variety: ATCC 15380 C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_cha C;Accession: S43834 R;Lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wil Biochem. J. 299, 129-136, 1994 A;Title: Characterization of the CysB protein of Klebsiella A;Reference number: S43834; MUID:94220019; PMID:8166630	nge 07-Mav-1999
As Variety: ATCC 15:80 C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_cha C;Accession: S4834 R;Lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wil Biochem. J. 299, 129-136, 1994 A;Title: Characterization of the CysB protein of Klebsiella A;Reference number: S43834; MUID:9422019; PMID:8166630	nge 07-Mav-1999
C;Accession: S43834 R;Lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wil Blochem. J. 299, 129-136, 1994 A;Title: Characterization of the CysB protein of Klebsiella A;Reference number: S43834; WIID:94220019; PMID:8166630	1111
Ribynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wil Blochem. J. 299, 129-136, 1994 A;Title: Characterization of the CysB protein of Klebsiella A;Reference number: 849834; WIID:94220019; PMID:8166630	•
Blocknem. J. 299, 129-136, 1294 A;Title: Characterization of the CysB protein of Klebsiella A:Reference number: 849834; MUID:94220019; PMID:8166630	kinson, A.J.
A;Title: characterization or the cyss procein of Klebsiella A:Reference number: S43834; MUID:94220019; PMID:8166630	100000000000000000000000000000000000000
	derogenes: direct evidence
A:Accession: S43834	
A;Status: preliminary; not compared with conceptual translation	ion
A; Molecule type: DNA	
A; Residues: 1-18 < LYN>	
A;Experimental source: ATCC 15380	
C; Genetics:	
A;Gene: topI	
C; Function:	
A; Description: catalyzes ATP-independent transient breakage	of DNA phosphodiester bonds
rejoining; this reaction will lead to the conversion of one	topological isomer of DNA t
C; Superfamily: bacterial type I DNA topoisomerase	
C; Keywords: DNA binding; DNA replication; isomerase; zinc finger	nger
Query Match 100.0%; Score 16; DB 2; Length 18;	18;
best botal Similairly 100.0%; Fleu. NO. 2.35708; Matches 3; Conservative 0; Mismatches 0; Indel	s 0; Gaps 0;
Qy 1 FID 3	
Db 8 FID 10	

PEBLS. - region hypothetical protein A - Campylobacter jejuni (fragment)
C;8pecies: Campylobacter jejuni
C;8pecies: Campylobacter jejuni
C;8pecies: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 19-May-1995
C;Accession: D48518
A;Attle: PEBL; the major cell-binding factor of Campylobacter jejuni, is a homolog of the A;Reference number: A48518; MUID:93366784; PMID:8360165
A;Accession: D48518
A;Status: pretliminary
A;Nolecule type: DNA
A;Residues: 1-21 cPEI>
A;Cross-references: GB:L13662

Gaps ; 0 Query Match 100.0%; Score 16; DB 2; Length 21; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 3; Conservative 0; Mismatches 0; Indels

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1 FID 3

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Hazella hypothetical protein XF0341 [imported] - Xylella fastidiosa (strain 9a5c)
CiSpecies: Xylella fastidiosa
Nature: Xilelis in X
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C,Species: Pseudomonas pseudoalcaligenes
C,Acte: 28-Fbb-1995 #sequence_revision 03-Mar-1995 #text_change 21-Mar-1996
C,Accession: A44682
R,Somerville, C.C.
submitted to the Protein Sequence Database, February 1995
A,Description: Purification and characterization of nitrobenzene nitroreductase from Pseu A,Beference number: A44682
A,Accession: A44682
A,Accession: A44682
A,Accession: A4682
A,Status: preliminary
A,Wolecule type: protein
A,Status: preliminary
A,Wolecule type: protein
A,Status: scon>
A,Esperimental source: strain JS455
C,Keywords: oxidoreductase
                                          C'Accession: A26188
The, B.K., Miscono, K.S.; Lukaa, T.J.; Mroczkowski, B.; Cohen, S.
The, B.K.; Miscono, K.S.; Lukaa, T.J.; Mroczkowski, B.; Cohen, S.
Tible. A calcium-dependent 35-kilodalton substrate for epidermal growth factor receptor A; Refearence number: A26188; MUID:87008618; PMID:3020049
A; Molecule type: protein
A; Mesiduces: 1-30 v.DEB
C; Superfamily: annexin ; annexin repeat homology
C; Keywords: phosphoprotein
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Feb-1997
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100.0%; Pred. No. 4.9e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                           pyrroloquinoline quinone precursor pqqA - Klebsiella pneumoniae
C;Specias: Klebsiella pneumoniae
C;Specias: Klebsiella pneumoniae
C;Specias: Klebsiella pneumoniae
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: S20453; S21838
R;Meulenberg, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.
Mol. Gen. Genet: 232, 284-294, 1992
A;Title: Nucleotide sequence and structure of the Klebsiella pneumoniae pqq operon.
A;Reference number: S20452; MUID:92212293; PMID:1313537
A;Molecule type: DNA
A;Residues: 1-23 <MEU>
A;Residues: 1-23 <MEU
A;Residues: 1-23 <MID:95394815; PMID:7665488
A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein BH334 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F84066
R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Reternce number: A83650; MUD:20512582; PMID:11058132
A;Residues: 1-25 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07053.1; GSPDB:GNOG A;Geneeits:
A;Accession: BH3334
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S,Superfamily: pyrroloquinoline quinone precursor pqqA
C,Keywords: quinoprotein
F,15,19/Product: pyrroloquinoline quinone #status predicted <MAT>
F,15,19/Product: pyrroloquinoline quinone (Glu, Tyr) #status predicted
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0; Mismatches

3; Conservative

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Query Match Best Local Similarity

0; Mismatches

Conservative

FID 15

Best\_Local Similarity Matches 3; Conserv

Query Match

A26188 lipocortin I - pig (fragment) Ç;Species: Sus scrofa domestica (domestic pig)

RESULT 5

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hypothetical protein SP1031 [imported] - Streptococcus pneumoniae (strain TIGR4) c; Species: Streptococcus pneumoniae c; Species: Streptococcus pneumoniae c; Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 #sequence_revision 03-Aug-2001 #tokey, E.s.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I snoon, T.; Hickey, E.K.; Holt, I.E.
Schence 293, 498-506, 2001
A,Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A,Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A,Reference number: A95000; MuID:21357209; PMID:11463916
A,Residues: preliminary
A,Nolecule type: DNA
A,Residues: 1-33 < KUR>
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C'Species: Vibrio cholerae
C'Species: Vibrio cholerae
C'Species: Vibrio cholerae
C'Species: Vibrio cholerae
C'Spacession: H82096
R,Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
C'Arcassion: H82096
R,Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
C'Arcassion: H8.Z.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A,Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A,Reference number: A82035; MulD:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005672; PIDN:AAK75146.1; PID:g14972505; GSPDB:GN00164; TIGR:SP46
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1031
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100.0%; Score 16; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0;
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A,Molecule type: DNA
A,Residues: 1-33 <HEI>
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C.Species: influenza A virus
C.Species: 30-68p-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C.Accession: PQ0416
R.Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom A.; Gerence number: PQ0408; MUD: 92300326; PMID: 1607856
A.; Accession: PQ0416
A.; Accession: Accession: PQ0416
A.; Accession: PQ0416
A.; Accession: Accession: PQ0416
A.; Accession: Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonstructural protein NS1 - influenza A virus (strain A/Hebei/24/89 [HIN2]) (fragment) C; Species: influenza A virus (strain A/Hebei/24/89 [HIN2]) (fragment) C; Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 R; Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom J. Gen. Virol. 73, 1320-1337, 1992 A; Richard and evolutionary characteristics of antigenic reassortant influenza A (H. A; Reference number: PQ0408; MuID:92300326; PMID:1607856
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A;Reference number: A59328
A;Contents annotation
C;Genetics:
A;Genetics:
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100.0%; Pred. No. 5e+02;
ative 0; Mismatches 0; Indels
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100.0%; Score 16; DB 2; Length 33
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: nonstructural protein
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Matches 3; Conservative
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Best Local Similarity
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Gaps

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Length 33,

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A; Cross-references: GB: AE004299; GB: AE003852; NID: 99656835; PIDN: AAF95428.1; GSPDB: GN001; A; Experimental source: serogroup 01; strain N16961; biotype Bl Tor C; Genetics: A; Gene. VC2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 2 - pin mould (Absidia glauca) plasmid PSSP15 (fragment)
C;Species: Absidia glauca
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
C;Date: 31-Dec-1993 #sequence_revision 31466
B;Haemfler, J; Woestemeyer, J; Weigel, C.T.
submitted to the EMBL Data Library, June 1992
A;Description: Complete nucleotide sequence of the pApD9 extrachromosomal DNA element of A;Reference number: 833645
A;Reference number: 833646
A;Molecule type: DNA
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10 RESULT

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Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A;Title: Differential expression of a novel murine non-receptor protein tyrosine phospha A;Reference number: JH0609; MUID:92272714; PMID:1590786
A;Accession: PS0363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: mRNA
A;Residues: 1-35 <DEN>
C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repetyrosine-phosphatase homology
C;Reywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PS0364
R;den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
Biochem. Biophys: Res. Commun. 184, 1241-1249, 1992
A;Title: Differential expression of a novel murine non-receptor protein tyrosine phospha
A;Title: Differential expression of a novel murine non-receptor protein tyrosine phospha
A;Accession: PS0364
A;Ac
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;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 20-Mar-1998
;Accession: PS0363
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D87544
hypothetical protein CC2381 [imported] - Caulobacter crescentus
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Pred. No. 5.4e+02;
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100.0%; Pred. No. ...
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A;Residues: 1-33 <HAE>
A;Cross-references: EMBL:M94861
C;Genetics:
A;Genome: plasmid
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87544
C;Accession: D87544
B; is peldblyum, T.U.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.! B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.H.; Kolons, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A,Residues: 1.36 <5TO>
A,Croser references: GB:AE005673; NID:g13423914; PIDN:AAK24352.1; GSPDB:GN00148
C;Genetics:
A,Gene: CC2381
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rickettsia ricketsia rhodobacter bacteriopha streptococc archaeoglob vaccinia vi

0092104 P12308 b P13308 b P49986 E 0029171 E P20566 v P11256 v

helicobacte homo sapien spiroplasma

Q48271 | Q9nrt5 | P15901

guillardia yersinia ps lymantria d

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Blomback B., Blomback M., Grondahl N.J.;
Blomback B. Dibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggregation.

-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

(ALPHA, BETA AND GAWA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

-!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinogenides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

Blood coagulation; Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
TOPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alebsiella aerogenes.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
NCBI_TAXID=28451;
[1]
                                                                                                                                                                                                                                                                                                                         oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-CT-2003 (Rel. 4), Last annotation update)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment)
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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COPP HELPY
SM64 HUMAN
VG10 SPV1R
YO23 RICCN
ACP RHOSH
YO6G BPT4
RECA STRGC
XA94 ARCFU
YVGB VACCU
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RS19 YERPS
YPO4 NPVLD
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                                                                                        6; Search time 1.83051 Seconds (without alignments) 85.337 Million cell updates/sec
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             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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length: 200000000
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Match 1
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1 FID 3
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                                                                                                                                                                                                                                                                                                                                               POOA KLEPN
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                          DNA, followed by passage and rejoining.

-!-SUBNIT: Monomer (By similarity)
-!- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
backbone bond, it simultaneously forms a protein-DNA link, in
which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
at one end of the enzyme-severed DNA strand.
-!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
            STRAIN=NCTC 418 / ATCC 15380; MEDIATE-94220019; PubMed-8166630; MEDIATE-94220019; PubMed-8166630; MEDIATE-94220019; PubMed-8166630; Characterization of the CysB protein of Klebsiella aerogenes: direct evidence that N-acetylserine rather than O-acetylserine serves as the linducer of the Cysteine regulon."; Biochem. J. 299:129-136 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim C.H., Han S.H., Kim K.Y., Cho B.H., Kim Y.H., Gu B.S., Kim Y.C.; Kim C.H., Han S.H., Kim K.Y., Cho B.H., Kim Y.H., Gu B.S., Kim Y.C.; Cloning and expression of pyrroloquinoline (PQQ) genes from a phosphate-solubilizing bacterium Enterobacter intermedium."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ) biosynthesis. Probably provides the giutamate and tyrosine residues that are cross-linked and modified to form the coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                              -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the conversion of one topological isomer of DNA to another.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coenzyme PQC synthesis protein A (Pyrroloquinoline quinone
biosynthesis protein A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 16; DB 1; Length 18; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
-!- SIMILARITY: Belongs to the pqqA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 AA; 2043 MW; 8C1C81238FF0EFA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000380; DNA tpisomrase.
PROSITE; PS00396; TOPOISOMERASE I PROK; PARTIAL.
Isomerase; Topoisomerase; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X78729; -; NOT_ANNOTATED_CDS. HSSP; P06612; 1YUA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
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Best Local Similarity
Matches 3; Conserva
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ID PQQA ENTIT
AC P59726;
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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J. Bacteriol. 177:5088-5098(1995).
--- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
biosynthemis. Probably provides the glutamate and tyrosine
residues that are cross-linked and modified to form the coenzyme.
---- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
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PREDINES=2512293; PubMed=1313537;
Meulenberg J.J.M., Sellink B., Riegman N.H., Postma P.W.;
"Nucleotide sequence and structure of the Klebsiella pneumoniae pqq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Synthesis of pyrrologuinoline guinone in vivo and in vitro and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Coenzyme PQO synthesis protein A (Pyrroloquinoline quinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                           764 mm, ...
100.0%; Score 16; DB 1; Lengtn 2.,
100.0%; Pred. No. 2.46+02;
                                                                                                                                                                                                                                                                                                                                                                                               ACCB321460871C5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                        (Probable)
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Gen. Genet. 232:284-294(1992)
                                                                                                                                                                                                                                                 EMBL; AY216683; AAP34378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 3; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                    23 AA; 2764 MW;
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                                                                                                                                                                                                                                                        EMBL; ALLANAP; MF_00656; -; 1.
PQQ biosynthesis; PQQ.
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PQQ biosynthesis; PQQ.
CROSSLNK 15 19
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SEQUENCE
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Matches
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MEDLINE=96382736; PubMed=8790600;
MEDLINE=96382736; PubMed=8790600;
Mertz A.K.H., Daser A., Skurnik M., Wiesmuller K., Braun J., Appel H.,
Batsford S., Wu P., Distler A., Sieper J.;
"The evolutionarily conserved ribosomal protein L23 and the cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukāryota; Metazoa; Brachiopoda; Linguliformea; Lingulata; Lingulida;
Linguloidea; Lingulidae; Lingula.
NCBI_TaxID=7575;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                100.0%; Score 16; DB 1; Length 23; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels
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PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
PROSITE; PS00550; Hemerythrins; Partial.
AETAL 24 124 IRON 1 (BY SIMILARITY).
(Probable).
23 AA; 2764 MW; ACCB321460871C5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 24 AA; 2825 MW; 28675F455462C44BB CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
36-FBB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein 519 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hemerythrin alpha chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91369922; PubMed=1892823;
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                                                                                                                                                 3; Conservative
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                                                                                Query Match
Best Local Similarity
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Q56847;
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                                  SEQUENCE
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HEWT LINRE
AC 223543;
DT 01-NOV-1)
DT 01-NOV-1)
DT 15-UU-1)
DE Hemeryth,
DE Lingula,
OC Eukaryot,
OC
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RES19 YEREN
AC Q56847;
DT 30-MAY-
DT 28-FEB-
DE 30S ril
GN REPS.
GN YERSIN:
OC Bacter:
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imbatus venom.";
Jimbatus venom.";
J. Biol. Chem. 273:2639-2644(1998).
-!- FUNCTION: Potent selective inhibitor of Kv1 voltage-gated
potassium channels (By similarity).
-!- STORELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium channel inhibitor subfamily.
PROSITE; PSOILIS; COORP SHORT_TOXIN; 1.
Toxin; Neurotoxin; Ionic channel inhibitor.
Potassium channel inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation)
10-OCT-2003 (Rel. 42, Last annot
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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 AA; 3659 MW; E534F701330F0338 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U11251; AAC43514.1; -.
HAMAP; MF_00531; -; 1.
InterPro; IPR002222; Ribosomal S19.
Pram; PR00203; Ribosomal_S19; 1.
Probom; PD001012; Ribosomal_S19; 1.
PROSITE; PS00323; RIBOSOMAL_S19; DARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
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Best Local Similarity
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                                                                                                                                                                                          STRAINSATCG 35210 / B31;
STRAINSATCG 35210 / B31;
STRAINSATCG 35210 / B31;
STRAINSATCG 35210 / B31;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palner N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                      Borrella burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrella.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses, dsDNA viruses, no RNA stage, Caudovirales, Myoviridae,
T4-like viruses.
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01-APR-1988 (Rel. 07, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Hypothetical 5.1 kDa protein in Gp55-nrdG intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

100.0%; Score 16; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al protein; Complete proteome.
37 AA; 4589 MW; SFAIF9470EDB51E2 CRC64;
                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypochetical protein BB0692.
   37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87203398; PubMed=3575111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001170; AAC67054.1; -. PIR; C70186; C70186.
TIGR; BB0692; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomaschewski J., Rueger W.;
                                                                                                                                                                                                                                                                                                                                                                                                                  burgdorferi.";
Nature 390:580-586(1997),
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage T4.
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SEQUENCE 37
Y692 BORBU
O51635;
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P07080;
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"Nucleotide sequence and primary structures of gene products coded for by the T4 genome between map positions 48.266 kb and 39.166 kb."; Nucleic Acids Res. 15:3632-3633(1987).
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                                                                          SEQUENCE FROM N.A.
MEDLINE=22514363; PubMed=12626685;
Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90245666; PubMed=2336394;
Neumann H., Zillig W.;
"Nucleotide seguence of the viral protein TPX of the TTV1 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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Similarity 100.0%; Score 16; DB 1; Length 52;
3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoproteus tenax virus 1 (strain KRA1) (TTV1). Viruses; dsDNA viruses, no RNA stage; Lipothrixvirus. Lipothrixvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X14855; CAA33003.1; -.
EMBL; X14717; CAA32839.1; -.
PIR; S15922; S15922.
Hypothetical protein.
SEQUENCE 52 AA; 5903 MW; 6293C63C4CCEDE2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       43 AA; 5146 MW; 9549CB24D73F8D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Hypothetical 5.9 kDa protein.
                                                                                                                                  "Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:2171-2171(1990).
                                                                                                                                                                                                                                                                                                                                                               EMBL, AF158101, AAD42495.1; -. PIR, C30292, ZDBPP9.
Hypothetical protein. SEQUENCE 43 AA, 5146 MM; 99
                                                                                                                                                                                                                                                                                                                                            EMBL; Y00122; CAA68317.1; -.
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Best Local Similarity 100.0
....has 3; Conservative
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Best Local Similarity
Matches 3; Conservi
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Coriat A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;

Coriat A.M., Muller U., Harry J.L., Uwanogho D., Sharpe P.T.;

Coriat A.M., Mullication of SYX-related gene sequences reveals evolutionary conservation of the SRY-box motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93184703; Pubmed=8443573;

Coriat A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;

Coriat A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;

Coriat A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;

Conservation of SRY-box motif.";

PGR Methods Appl. 2.218-222(1933).

-! SUBCELLULAR LOCATION: Nuclear (Potential).
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01-FEB-1995 (Rel. 31, Last sequence update)
10-DCT-2003 (Rel. 42, Last annotation update)
SRY-related protein AMA3 (Fragment).
Alligator mississippiensis (American alligator).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Crocodylidae; Alligatorinae; Alligator.
                                                                                                                                                                                                                                                                                                                 SRY-related protein AvA2 (Fragment).

SRI-related protein AvA2 (Fragment).

Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Crocodylidae; Alligatorinae; Alligator.
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                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                        54 AA.
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PIR; I50028; I50028.
HSSP, Q65066; IHRY.
InterPro; IFR000910; HMG_12_box.
Pfam; PF00505; HMG box; I.
SWART; SM00398; HMG; 1.
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DNA-binding; Nuclear protein.
NON TER 1 1 HMG
NON TER <1 51 HMG
NON_TER 54 54
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Best Local Similarity luv...
3, Conservative
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                                                                                        STANDARD;
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                                                                                        AMA2 ALLMI
P40642;
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DT 01-FEB

DT 01-FEB

DT 01-FEB

DC 02-FEB

OC ALLIGA

OC ALCHOSY

OC ALCHOSY

OC ALCHOSY

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RN 1119A

RN NEDLIN

RR SEQUEN

RX MEDLIN

RY MEDLIN

RY OCTAE

RY OCT
AMAZ_ALLIMI

ID MAAZ A ALLIMI

ID MAAZ A A A C P40642

DT 01-PEB

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DT 01-PEB

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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDINE-93184703; PubMed-8443573;

MEDINE-93184703; PubMed-8443573;

Medine U., Harry J.L., Uwanogho D., Sharpe P.T.;

"PCR amplification of SRY-related gene sequences reveals evolutionary conservation of the SRY-box motif.";

PCR Methods Appl. 2:218-222(1993).

-i. SUBCELLULAR LOCATION: Nuclear (Potential).

-i. SIMILARITY: Contains 1 HWG box domain.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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54 AA; 6535 MW; 1677E5076E959564 CRC64;
PCR Methods Appl. 2:218-222(1993).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Contains 1 HMG box domain.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
12-OCT-2014 (Rel. 42, Last annotation update)
Gallus gallus (Chicken).
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PIR; ISO029; ISO029.
HSSP, OSO666; HRN.
Pfam; PP00505; HMG box; I.
PROSITE; PS50118; HMG il.
DNA-binding; Nuclear protein.
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SEQÜENCE 54 AA; 6535 MW; 1677E
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PIR; ISO190; ISO190.
HSSP, Q05066; 1HRY.
INTERPO; IPR000910; HWG 12_box.
Emm; FR00505; HWG, box; 1.
SWART; SW00398; HWG, 1.
PROSITE; PS50118; HWG_BOX_2; 1.
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Matches 3; Conservative
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NCBI_TaxID=9031;
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CH01_CHICK
ID CH01_CHICK
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
SRY-related protein CH2 (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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54 54 54 MW; ASB915076E95957D CRC64;
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PTR, 150191; 150191.
HSSP, Q05066; 1HTV.
InterPro; IPR000910; HMG 12_box.
Pfam; PR05059; HMG box; 1.
PROSITE; PS50118; HMG BOX 2; 1.
DNA-binding; Nuclear Protein.
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   DNA-binding; Nuclear protein.
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Matches 3; Conservative
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CH02 CHICK
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54 AA.

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RESULT 15 CH03\_CHICK ID \_CH03\_CHICK AC P40667;

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DT 101-EE-1995 (Rel 131, Created)
DT 101-EE-1995 (Rel 131, Created)
DT 102-CC-2003 (Rel 124, Last annotation update)
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September 30, 2004, 05:55:56; Search time 9.81356 Seconds (without alignments) 96.454 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

	Description	Q9kiv5 anabaena sp	Q9r4k0 nocardia. n	Q85485 avian leuko	Q9z630 streptococc	Q9r2r0 streptococc	Oscame musculu	Q9k7m7 bacillus ha	Q8ks87 escherichia	Q8clj9 yersinia pe	Q87117 vibrio para	Q9nrc5 homo sapien	Q81ng6 bacillus an	Q9s0e6 borrelia bu	Q9pggl xylella fas	Q8kgf6 chlorobium	Q8eiw8 shewanella
	ID	Q9KIV5	Q9R4K0	085485	092630	Q9R2R0	68CGW9	Q9K7M7	Q8KS87	Q8CLJ9	Q87L17		Q81NQ6		Q9PGG1	Q8KGF6	QBEIWB
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o)(e	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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## ALIGNMENTS

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J. Bacteriol. 181:3599-3605(1999).
BMBL; AF106134; AAD17995-11; --
EMBL; AF106132; AAD17975-11; --
EMBL; AF106133; AAD17977-11; --
             MEDLINE=99287847; PubMed=10348877;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99287847; PubMed=10348877;
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                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae
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Binda O., Branton P.E.;
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MEDLINE-88230605; PubMed=2897475;
Raines M.A., Maihle N.J., Moscovici C., Crittenden L., Kung H.-J.;
Raines M.A., Maihle N.J., Moscovici C., Crittenden L., Kung H.-J.;
Raines M.A., Maihle N.J., Moscovici C., Crittenden L., Kung H.-J.;
Mechanism of c-erbB transduction: Newly released transducing viruees
retain poly(A) tracts of erbB transcripts and encode C-terminally
intact erbB proteins.";
J. Virol. 62:2437-2443 (1988).
EMBL, M19970; AAA42586.1;
Interpro; IPR009030; Grow_fac_recep.
                                                                           Chen Y., Rosazza J.P.; "Purification and characterization of nitric oxide synthase (NOSNoc) from a Nocardia species."; J. Bacteriol. 177:5122-5128(1995).
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            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae.
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                                                                                                                                                                      Length 15;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBL_TaxID=1313;
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NON TER 15 15
SEQUENCE 15 AA; 1818 MW; 2BD5B859DE288B77 CRC64;
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20 AA; 2167 MW; 2A4EFD2E3A709011 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gag-erbB fusion protein (Fragment).
Avian leukosis virus.
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                                                      SEQUENCE.
MEDLINE=95394819; PubMed=7545152;
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Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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                                NCBI_TaxID=1817;
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Q9Z630;
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Q85485
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Morona J.K., Morona R., Paton J.C.;
"Analysis of the 5' portion of the type 19A capsule locus identifies
two classes of cpsC, cpsD, and cpsE genes in Streptococcus
pneumoniae.";
J. Bacteriol. 181:3599-3605(1999).
EMBL; AF106135; AAD17981.1; -.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Capsular polysaccharide B (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Retinoblastoma-binding protein 1 (Fragment).
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EMBL; AF520223; AAM53254.1; -.
NON TER 28 28
SEQUENCE 28 AA; 3185 MW; A2F42416487ED57B CRC64;
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Q87L17
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STRAINS=ECCH-9;
MEDLINE=ECOS-3;
Sandt C.H., Hopper J.E., Hill C.W.;
Sandt C.H., Hopper J.E., Hill C.W.;
"Activation of Prophage eib Genes for Immunoglobulin-Binding Proteins
"Activation of Prophage eib Genesic Island of Escherichia coli ECOR-9.";
J. Bacteriol. 184:3640-3648(2002).
                                                                                                                                                                                                                  Gaps
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EMBL; AP001518; BAB07053.1; -.

PIR; F84066, F84066, F84066.

SEQUENCE 25 AA; 2986 MW; OC21EA93BE976875 CRC64;
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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STRAIN=C-125./ JCM 9153;
MEDLINE-20512582; Pubmed=11058132;
MEDLINE-20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.,
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                                                                                                                                                               , Match 100.0%; Score 16; DB 11; Length 24; Local Similarity 100.0%; Pred. No. 1.7e+03; les 3; Conservative 0; Mismatches 0; Indels
  "Mus musculus 129X1/SvJ Partial RBBP1 Genomic Sequence."; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX163235; AAN184616.1; -. NON-TER
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NCBI_TaxID=86665,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative oxidoreductase Fe-S subunit (Fragment).
B1589.
                                                                                                                        24 AA; 2685 MW; BF6991AC3D52BC4E CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein BH3334.
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SEQUENCE
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MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
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STRAIN=RIMD 2210633 / Serotype O3:K6;

MEDLINE=22508454; PubMed=1260739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(2003).
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaeae, Yersinia.
NCBI_TaxID=632;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=670;
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Query Match
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels
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29 AA; 3489 MW; A300F9DE2223524E CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                       Q8CLJ9;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R Palmer N., Haft D., Rosa P., Stevenson B.,

"A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrella burgdorferi.",

Mol. Microbiol. 0.0-0(1999).

EMBL; AR001577; AAR07528.1; -

GO: 00046821; C:extrachromosomal DNA; IEA.
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorri E.D., Bordin S., Bove J.M., Britones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H. Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costan-Neto C.M. Cocta M.C.R., Costan-Neto C.M. Cottan P.C. Blanco L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.F., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
Plasmid cp32-4.
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
NCBL_TaxID=139;
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Xanthomonadaceae; Xylella.
NCEI_TaxID=2371;
                                                                                                                    Length 30;
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     TIGR; BA3122; -. Hypothetical proteome. SEQUENCE 30 AA; 3565 MW; 8614AD8904A34084 CRC64;
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SEQUENCE 3: AA; 3761 MW; E9DF7AlF04A6FF3B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 2.1e+03;
iive 0; Mismatches 0;
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Matches 3; Conservative
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Matches
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MEDLINE=22608414; PubMed=12721629;
MEDLINE=22608414; PubMed=12721629;
Melson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBOY R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The genome sequence of Bacillus anthracis Ames and comparison to
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                                                                                                        100.0%; Score 16; DB 16; Length 29; 100.0%; Pred. No. 2.1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 16; DB 4; Length 30; 100.0%; Pred. No. 2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Wu Z.Y., Wang N., Murong S.X.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF234621; AAF89169.1; -.
NON TER 30 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
EMBL, AP005082, BAC61063.1; -. Hypothetical protein, Complete proteome. SEQUENCE 29 AA; 3534 MW; B1263708FB2189DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 AA; 3451 MW; 90ED003AF2D173FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       closely related bacteria.";
Nature 423:81-86(2003).
EMBL; AE017033; AAP26932.1;
                                                                                                                                                                 3; Conservative
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                                                                                                                                  Local Similarity
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Best Local Similarity
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                                                                                                              Query Match
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Q9NRC5
ID Q9NRC5
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NRC5;
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Matches
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Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

R Krieger J.E., Kuramae B.E., Laigret F., Lambais M.E., Kitajima J.P.,

Krieger J.E., Kuramae B.E., Laigret F., Lambais M.R., Leite L.C.C.,

Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,

Rachado M.A., Marcins E.A.L., Martins E.M., Marino C.L.,

Marques M.V., Martins E.A.L., Martins E.A.L., Martino C.L.,

Manches M.V., Martins E.A.L., Martins E.A.L., Martino C.L.,

A Monor D.H., Nagai M.A., Nascimento A.L.T.O., Netro L.E.S.,

Noon D.H., Nagai M.A., Nascimento A.L.T.O., Netro L.E.S.,

Noon D.H., Nagai M.A., Nascimento A.L.T.O., Netro L.E.S.,

Rooliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

Resoa V.E., Ur., de Sa R.G., Santelli R.V., Sawasaki H.E.,

A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA a Silvaira J.F., Silvaetri M.F., Silvaetri M.A., Tsuhako M.H.,

RA Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA Sago M.A., Zatz M., Meddanis J., Setubal J.C.,

REMBL, AE003886, AAP83151.1;

REMBL, AE003886, AAP83151.1;

PIR, HB2818, HB2818, HB2818, Complete proteome.

SEQUENCE 31 AA, 3827 MW, E895F867670E7382 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%; Score 16; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 16; DB 16; Length 31; 100.0%; Pred. No. 2.2e+03; ive 0; Mismatches 0; Indels
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Bacteria, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein, Complete proteome. SEQUENCE 31 AA; 3608 MW; 353F136B1A882EDF CRC64;
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Last annotation update)
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Best Local Similarity 100.
Matches 3; Conservative
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08KGF
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12 FID 14
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Search completed: September 30, 2004, 05:59:39 Job time : 12.9802 secs

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	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	
M protein - pro	M protein - protein search, using sw model	
kun on:	September 30, 2004, 05:55:56; Search time 14.6441 Seconds (without alignments) 57.883 Million cell updates/sec	
litle: Perfect score: Seguence:	US-09-674-716B-13 16 1 FID 3	
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	1586107 segs, 282547505 residues	
Total number of	rotal number of hits satisfying chosen parameters: 1586107	
O . Tanget Jenseth. O	ט יאונעס	

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2001s:\*

6: geneseqp2003s:\*

7: geneseqp2003as:\*

8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay32259 Light cha	4	Aaw55773 Immunisat	Aau86974 Estradiol	Abb84336 Human MBP	Aar29321 Endotheli	w	<u>ი</u>	4	Aab06594 Claudin-3	Aab06656 Claudin-4	3 Humar	'n	7 Claud	_	6	282	ý	Abg73046 Cryptococ	н	708 Plant	93	99 Vit	Aaw13609 HLA-A2.1	Aabo6662 Claudin-4
SUMMARIES	ID	AAY32259	AAP94794	AAW55773	AAU86974	ABB84336	AAR29321	AAR69115	AAW31469	AAB06774	AAB06594	AAB06656	ABU96533	ABU96535	AAB06597	AAB06777	AAB06659	AAU25282	AAU15626	ABG73046	ABP46831	ABG65708	ABG65705	AAR48299	AAW13609	AAB06662
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d	Query Match	100.0	0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0	100.0	100.0	100.0	8	100.0
	Score	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
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Aab06780 Claudin-6	Clai	Aab75620 HLA class	Aab75667 HLA class	Aab67398 Modified	Aab67397 Modified	Aab67395 Tobacco m	Aam49930 Human D40	Aau95252 Human nov		Abm66263 Propionib	Abj60588 184P1E2-r		Abj60811 184P1E2-r	Abj61554 184P1E2-r	7	ч	П	Abj60235 184P1E2-r	Abj60506 184P1E2-r	
3 AAB06780	3 AAB06600	4 AAB75620	4 AAB75667	4 AAB67398	4 AAB67397	4 AAB67395	5 AAM49930	5 AAU95252	5 AAU94879	6 ABM66263	6 ABJ60588	6 ABJ65630	6 ABJ60811		6 ABJ62172		6 ABJ57105	6 ABJ60235	6 ABJ60506	
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## ALIGNMENTS

cDD3; FCERII; IGE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroidtis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; psoriasis; unflammatory bowel disease; ulcerative colitis; Crohn's disease; sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy. Light chain CDR H3 of mouse anti-CD23 MAb C11. AAY32259 standard; peptide; 3 AA. (first entry) 15-FEB-2000 AAY32259; RESULT 1 AAY32259 

Mus musculus. WO9958679-A1. 18-NOV-1999.

98GB-00009839. 99WO-GB001434. 07-MAY-1999; 09-MAY-1998; Ellis JH, Rapson NT, Bonnefoy JMP, Crowe SJ,

(GLAX ) GLAXO GROUP LTD

Shearin J;

WPI; 2000-053101/04. N-PSDB; AAZ34744. Cell.receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 1; Page 40; 81pp; English.

This sequence represents complementarity determinating region 3 (CDR H3) of the heavy chain of murine anti-CD23 (FCBRII) monoclonal antibody Cl1 (See also AAN32253). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain CDRs (see AAN32254-59) to

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FID
                                                                                                         25-MAR-2003
08-JUL-1998
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                                                                                    AAW55773;
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                                       RESULT 3
AAW55773
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haematopoietic cells. The antibodies are used to block soluble CD23 commation for treatment of arthitis, lupus eryhematosus. Hashimoto's thyroiditis, multiple sclerosis, diabetes, uvaitis, dermatitis, inthematosus, mabhimoto's pscriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Siogran's syndrome, allergies, allergic asthma, intrinsic asthma acute asthmatic exacerbation, rhinlis, eczema, graft-versus-host disease, (OpD, insulitis, bronchitis, particularly chronic bronchitis) or diabetes are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences will normally be part of 9 to 15 AA sequence, excluded as motifs for immunisation but useful in tolerisation. . (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PA field.) (Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligopeptide and polypeptide compsns. - based on the amino acid sequence of an immunogen and used for modulating the immune system.
                                                                                                                                                                                                                                                                                                                                                                                        Periferal nervous system myelin protein, proteolipid protein, a PNS CNS myelin component and acetyl choline receptor epitope associated motif.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Autoantigen, MBP, myelin basic protein, transplantation antigen, myasthenia gravis, myasthenics; Transplantation antigen.
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0
                                                                                                                                                                              Length 3;
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                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                         AAP94794 standard; protein; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88EP-00307608
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.0
Matches 3; Conservative
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Best Local Similarity
3, Conserve
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                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                               RESULT 2
AAP94794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wherein said immunogen is restricted by a transplantation antigen of said host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                     Myelin basic protein, immunity, immune response, neurological; T-cell, human; immunogen; B-cell; transplantation antigen; immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide comprising human myelin basic protein fragment - useful as immuno modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 16; DB 2; L. larity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0;
                                                                                                                                                                   Immunisation motif associated with AChR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRD ) UNIV LELAND STANFORD JUNIOR.
AAW55773 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fage 8; 8pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU86974 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Estradiol mimotope peptide #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                97EP-00106788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-00086694
88EP-00307608
                                                                                                                         (first entry)
                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamvil S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-034664/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1987;
17-AUG-1988;
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Estradiol; mimotope; estrone-3-glucuronide; steroid detection;

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Peptide mimotope capable of binding specifically to antibody specific to estradiol, useful for assaying presence and/or amount of estradiol, especially estrone-3-glucuronide in sample.
immunoassay; phage display; immunogen.
                                                                                                             Berry MJ, Williams SC;
                                                                                                                                                                      Claim 3; Page 22; 57pp; English.
                                                       26-JUL-2001; 2001WO-EP008705
                                                                    03-AUG-2000; 2000EP-00306613
                                                                                 (UNIL ) UNILEVER PLC.
(UNIL ) UNILEVER NV.
(UNIL ) HINDUSTAN LEVER LTD.
                                                                                                                            WPI; 2002-241729/29
                            WO200212270-A1
                                          14-FEB-2002
                                                                                                              Badley RA,
               Synthetic
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The invention relates to a purified peptide mimotope capable of binding specifically to an antibody specific to estradiol. Also included are a solid support having immobilised (releasably) or non-releasably) peptide mimotopes, an immunoassay test device for the detection of estradiol in the sample, comprising the mimotopes and an antibody capable of binding specifically to the mimotopes to generate a detectable signal and an isolated nucleic acid encoding the peptide mimotopes. The mimotope is useful for assaying the presence and/or amount of estradiol preferably estrone-3-glucuronide in a sample which is unine or sarum sample to be tested and is also utilised and immunoassay test device, and further can be used as immunogens. The mimotope be used to construct new, or improve the performance of old, immunoassay test formats and devices. They can, for example, be utilised essentially to tune the signal in conventional displacement assays for the detection of estradiol. The mimotope can be bound directly to certain assay surfaces which are conventional displacement assays for the detection of estradiol. The mimotope can be bound directly to certain assay surfaces which are convention to the surface by complexing with another - often proteinaceus contection of estradiol, in the presence of excess quantities of other undesired materials, and tightly enough affinity) that when used in an immunoassay, it provides a togething the antion and in the present sequence is a peptide mimotopes of the

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100.0%; Score 16; DB 5; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels Length 5; Local Similarity 100. Les 3; Conservative 1 FID 3 FID 5 Query Match ઠ

Sequence 5 AA;

AAR29321 standard; peptide; 6 AA

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Gaps . 0

> ABB84336 standard; peptide; 5 AA ABB84336; RESULT S ABB84336

Human MBP protein derived peptide SEQ ID 36.

17-OCT-2002

Hypertension; myocardial infarction; congestive heart failure; endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias; acute renal failure; preeclampsia; diabetes; metabolic; endocrinological; neurological; disorders.

Endothelin antagonist peptide.

(revised)
(first entry)

25-MAR-2003 13-APR-1993

AAR29321;

Location/Qualifiers 1

Key Misc-difference

Synthetic

MBP; myelin basic protein; human; tolerance; immune system; multiple sclerosis; autoimmune response; autoimmune disease;

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This invention describes a novel method for modulating or tolerizing the immune system, and for treating multiple sclerosis comprising definities the speptide derived from hMBP (human myelin basic protein). The peptide induces an autoimmune response (T cell) to a self-antigen (or part of it), and binds to an MHC (major histocompatibility complex) antigen of a host susceptible to autoimmune diseases, i.e. competes with binding to MBP and inhibit proliferation of MBP-reactive cells. The peptide has immunosuppressive and neuroprotective activity. This sequence represents a peptide derived from the human MBP protein which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating or tolerizing the immune system, useful for treating multiple sclerosis, by administering a peptide derived from human myelin binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 15; 21pp; English
immunosuppressive; neuroprotective.
                                                                                                                                                                                                                                                                                   87US-00086694.
89US-00379500.
90US-00517245.
91WO-US002991.
93US-00066325.
93US-00125407.
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Best Local Similarity
-hes 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STEI/) STEINMAN L. (ZAMV/) ZAMVIL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-598709/64
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                                                                                                                  JS2002076412-A1.
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                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991;
30-APR-1992;
21-MAY-1993;
                                                                                                                                                                                                                                                                                         17-AUG-1987;
12-JUL-1989;
01-MAY-1990;
                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1993;
                                                                                                                                                                                                                                 17-JUN-1995;
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                                                                                                                                                                         20-JUN-2002
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Novel antagonists of endothelin are claimed which are C-terminal hexapeptides and analogs of ET-1. The first (N-terminal) amino acid of the new peptides has D-configuration. The peptides are claimed generically. The present peptide is a specifically claimed example of the generic compounds. The peptides are useful for treating hypertension, metabolic and endocrine disorders, congestive heart failure, myocardial infarction, endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute and chronic renal failure, preeclampsia, diabetes, neurological disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel disease, gastric mucosal damage, Raynaud's disease, restenosis, percutanseous transluminal coronary angioplasty, angina and cancer. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076 are fragments used in an assay to determine novel transcriptional activators.
                                                     New hexa:peptide derivs. inhibiting endothelin - for treatment of e.g. renal failure, hypertension, asthma, restenosis, angina, cancer etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activating sequence; Gal4; transcriptional activator; RNA polymerase; Protein-protein interaction; gene therapy; therapeutic; holoenzyme; Gal11; DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transcriptional activator containing DNA binding domain bound to peptide - useful for controlling gene expression, especially in gene therapy, and in protein-protein interaction assays, does not inhibit other transcription activators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 16; DB 2; L. 100.0%; Pred. No. 1.4e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcriptional activator peptide fragment LS132.
                                                                                                               Claim 5; Page 112; 146pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW31469 standard; protein; 6 AA.
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97US-00017016.
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Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-018502/02.
N-PSDB; AAV02567.
                  WPI; 1994-234617/28.
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6 AA;
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01-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW31469;
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                                                                                                                                                                                                                                                                                                                             New peptide(s) used as endothelin antagonists - for treating hypertension, metabolic and endocrine disorders, heart failure, diabetes, asthma, neurological disorders, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                          The peptide is an endothelin antagonist useful in controlling hypertension, myocardial infarction, congestive heart failure, endotoxishock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal failure, preeclampsia, diabetes and metabolic, endocrinological and neurological disorders. Administration is oral parenteral or by inhalathion in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endothelin C-terminal peptide analog, useful as antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h Similarity 100.0%; Score 16; DB 2; L Similarity 100.0%; Pred. No. 1.4e+06; 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                   Taylor MD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endothelin; ET-1; receptor; antagonist.
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/note= "Ac-D-Phe"
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 86; 116pp; English.
                                                                                                                                                                                                                                                     Doherty AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Depue P, Doherty AM,
                                                                                                               92WO-US003408.
                                                                                                                                                  91US-00701274
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                                                                                                                                                                                                           (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WARN ) WARNER LAMBERT CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                     WO9220706-A1
                                                                                                               24-APR-1992;
                                                                                                                                                  16-MAY-1991;
18-DEC-1991;
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05-MAR-1995
                                                                          26-NOV-1992
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healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic conformation

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100.0%; Score 16; DB 3; L 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;

Similarity 100. 3; Conservative

Query Match Best Local S: Matches 3

Sequence 7 AA;

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The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein protein interactions are identified in the assay by fusing a DNA-binding domain interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Ga14 which interacts with GallP into a cell containing a region of Ga14 which interacts with GallP into a cell containing a region of Ga14 which interacts with constructs are used to activate transcription in a cell, e.g. for controlling gene activity, particularly in gene therapy (e.g. recognizing a site close to a selected hrapeutic gene). Transcription can be activated without blocking other transcriptional activators. They probably act by interacting with a component of the RNA polymerase II holoenzyme, Galli, the strongest known yeast activator, which provides a more sensitive assay allowing detection of even weak protein-protein interactions. Such activators do not create toxicity problems even when
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin.
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99US-00282029.
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30-MAR-1999;
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AAB06774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin.
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                                                                                                                                       Claudin-3 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.
                                                                                                              Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                   BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 55; Page 99; 121pp; English.
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                          AAB06594 standard; peptide; 7 AA.
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99US-00282029.
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                                                                                   (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin.
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                                                                                                                                                                                            Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 174.
                                                                                                                                                                                                                                               Claudin-4 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 61; Page 101; 121pp; English.
AAB06656 standard; peptide; 7 AA.
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99US-00282029.
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30-MAR-1999;
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                                                                                                                           28-SEP-2000
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                                                             AAB06656;
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                                                                                                                                                                                                                             New polymorphic variants of the gene encoding Cytochrome P450 polypeptide 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g. arachidonic acid metabolism, cancer or cardiovascular diseases.
                                                                                                                                                                                                                                                                                                                          The invention describes a new polynucleotide comprises a polynucleotide: (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined in the specification; (b) encoding any of seven polypeptides having 7 amino acids, or a polypeptide with 3 amino acids; (c) capable of hybridising to a Cytochrome P450 polypeptide 2CB. (CYP2CB) gene; (d) encoding a molecular CYP2CB variant polypeptide or its fragment. The polynucleotide, gene, vector, polypeptide or antibody is useful for diagnosing or treating a disease, for preparing a diagnostic composition for treating a disease, or for preparing a pharmaceutical composition for treating a disease. This diseases includes arachidonic acid metabolism, cancer or cardiovascular diseases. This is the amino acid sequence of a human cytochrome P450 polypetide 2CB (CYP2CB) wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism; cancer; cardiovascular; gene therapy.
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                                                                                                                                                                Brinkmann U;
                                                                                                                               (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
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                                                                                                                                                                                                                                                                                                Disclosure; Page 58; 178pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU96535 standard; peptide; 7 AA.
                                                                31-MAY-2002; 2002WO-EP006000
                                                                                                01-JUN-2001; 2001EP-00112899
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                                                                                                                                                                Penger A, Sprenger R,
                                                                                                                                                                                              WPI; 2003-167344/16.
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Best Local Similarity
Matches 3; Conserv
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                               12-DEC-2002
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ABU96535
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WPI; 2003-167344/16

New polymorphic variants of the gene encoding Cytochrome P450 polypeptide 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g. arachidonic acid metabolism, cancer or cardiovascular diseases.

Disclosure; Page 58; 178pp; English

The invention describes a new polynuclectide comprises a polynucleotide:

(a) having any of 101 nucleic acid sequences with 18-19 bp fully defined in the specification; (b) encoding any of seven polypeptides having 7 amino acids, or a polypeptide with 3 amino acids; (c) capable of hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d) encoding a molecular CYP2C8 variant polypeptide or its fragment. The polynucleotide, gene, vector, polypeptide or antibody is useful for diagnosing or treating a disease, for preparing a diagnostic composition for treating a disease. This disease includes arachidonic acid metabolism, cancer or cardiovascular diseases. This is the amino acid sequence of a human cytochrome P450 polypetide 2C8 (CYP2C8) wild type peptide

Sequence 7 AA;

Query Match
100.0%; Score 16; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; 1 FID 3 3 FID 5 q ਨੇ

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Gaps

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6; Length 7; 0; Indels

AAB06597 standard; peptide; 8 AA. AAB06597;

(first entry) 28-SEP-2000

Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 230.

Claudin-3 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.

Mammalia

WO200026360-A1.

11-MAY-2000

99WO-CA001029 3-NOV-1999;

99US-00282029 98US-00185908 33-NOV-1998; 30-MAR-1999; (ADHE-) ADHEREX TECHNOLOGIES INC

slaschuck OW, Symonds JM,

Gour BJ;

Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin. WPI; 2000-365610/31.

Claim 55; Page 99; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-3 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides 

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can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin.
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                         Length
                                                                                                                                    Query Match

100.0%; Score 16; DB 3; I

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                         1 FID 3
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                                                                                                                                                                                                                                        6. FID 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1998;
30-MAR-1999;
                                                                                                         Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2000,
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                                                                                                                                                                                                                                                                                                                                                              AAB06777;
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Search completed: September 30, 2004, 06:06:24 Job time : 16.6441 secs

OM protein - protein search, using sw model  Run on: September 30, 2004, 06:01:30; Search time 50.339 Seconds  Title:  US-09-674-716B-13  19.178 Million cell updates/sec  1 PID 3  Scoring table: BLOSUM62  Gapop 10.0, Gapext 0.5  Searched: 1351062 seqs, 321799191 residues  Total number of hits satisfying chosen parameters: 1351062  Minimum DB seq length: 0  Maximum Match 100*  Maximum Match 100*  Listing first 45 summaries  Database: Published Applications AA:*  1 / CGD2 = 6/ptodata/1/pubpaa/PCT NEW PUB. pep:*  2 / CGD2 = 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*  3 / CGD2 = 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*  3 / CGD2 = 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*  4 / CGD2 = 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*  5 / CGD2 = 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*  4 / CGD2 = 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*
on: September 30, 2004, 06:01:3 ect 5001:3 ing table: 16 1910 3 ing table: BLOSUM62 Gapop 10.0, Gapext 0.5 ched: 1351062 segs, 321799191 res ind mumber of hits satisfying chosen para mum DB seq length: 0 mum DB seq length: 0 mum DB seq length: 200000000 processing: Minimum Match 0% Maximum Match 100% Maximum Actor 100% Maximum Match 100% Maximum Actor 100% Maximum Match 100% Maximum Actor 100% Maximum Match 100% Maximum Maximum Match 100% Maxi
t score: 16 ce: 1 FID 3 g table: BLOSUM62 g table: BLOSUM62 dapop 10.0 , Gapext 0. ed: 1351062 seqs, 32179919 number of hits satisfying chosen m DB seq length: 0 im DB seq length: 0 im DB seq length: 2000000000 vrocessing: Minimum Match 100% Listing first 45 summ Listing first 45 summ Listing first 45 summ 2: /cgn2_6/ptodata/1/ 2: /cgn2_6/ptodata/1/ 3: /cgn2_6/ptodata/1/ 4: /cgn2_6/ptodata/1/ 4: /cgn2_6/ptodata/1/ 4: /cgn2_6/ptodata/1/
BLOSUM62 Gapop 10.0 , Gapext 0. 1351062 seqs, 32179919 of hits satisfying chosen eq length: 0 eq length: 200000000 haximum Match 10% Maximum Match 10% Listing first 45 summ Published Application Published Application 1: /cgn2_6/ptodata/1/ 2: /cgn2_6/ptodata/1/ 4: /cqn2_6/ptodata/1/ 4: /cqn2_6/ptodata/1/ 4: /cqn2_6/ptodata/1/
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0% 100% 45 summ licatior odata/1/ odata/1/
Published Application  1: /cgn2 6/ptodata/1/ 2: /cgn2 6/ptodata/1/ 3: /cgn2 6/ptodata/1/ 4: /cqn2 6/ptodata/1/
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:* 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:* 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:* 8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:* 9: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:* 10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:* 11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:* 12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:* 13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:* 14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 36, Appl	Sequence 25, Appl	Sequence 130, App	Sequence 174, App	Sequence 227, App	Sequence 567, App			Sequence 177, App	Sequence 230, App	-	Seguence 2842, Ap	Seguence 92, Appl	Sequence 108, App	Sequence 511, App	
COMPARTED	ΩI	US-08-484-409-36	US-09-920-306-25	US-09-943-944E-130	US-09-185-908-174	US-09-185-908-227	US-10-190-082-567	US-09-946-678-8	US-09-791-378-511	US-09-185-908-177	US-09-185-908-230	US-09-880-748-2842	US-10-293-418-2842	US-10-601-100-92	US-10-601-100-108	US-09-791-377-511	
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	% Query Match	100.00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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Sequence 1152, App Sequence 1152, App Sequence 213, App Sequence 213, App Sequence 2125, App Sequence 45, Appl Sequence 45, Appl Sequence 45, Appl Sequence 2015, App Sequence 2015, App Sequence 2015, App Sequence 1153, App Sequence 3883, App Sequence 583, App Sequence 583, App Sequence 583, App Sequence 693, App Sequence 693, App Sequence 693, Appl Sequence 675, Appl Sequence 675, Appl Sequence 560, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 136, Appl Sequence 136, Appl
US-10-190-082-501 US-09-1185-098-1180 US-09-1185-098-1180 US-09-1185-098-1180 US-09-1185-082-1180 US-09-1185-082-082-082-082-082-082-082-082-082-082
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#### ALIGNMENTS

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RESULT 1

US-06-484-409-36

is Sequence 36, Application US/08484409

is Publication No. US202020076412A1

GENERAL INFORMATION:

APPLICANT: Steinman, Lawrence
APPLICANT: Pack of the Applicant Compatible
COMPUTER: Pack of the APPLICATION DATA:
COMPUTER: Pathory disk
APPLICATION NUMBER: US/08/484,409
FILING DATE: 07-1074-1995
CLASSIFICANTON NUMBER: 07-0606.409C1
FELECOMMUNICATION INFORMATION:
APME: Maki, David J.
RESTRANCE/DOCKET NUMBER: 60006.409C1
TELEFONE (206) 622-6031
TELEFONE (206) 62
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Sequence 174, Application US/09185908A
Publication No. US20020193294A1
GENERAL INFORMATION
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
TITLE OF INVENTION: FUNCTIONS
FILE REFERENCE: 100086.409
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SSCTWARE: Patentin Ver. 2.0
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 227, Application US/09185908A
Publication No. US20020193294A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED FILE REFERENCE: 100086,409
CURRENT APPLICATION NUMBER: US/09/185,908A
CURRENT APPLICATION NUMBER: US/09/185,908A
SOFTWARE: PATENTING DATE: 1998-11-03
SOFTWARE: PATENTING US OF C. 2.0
SEQ ID NO 227
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Product of OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R OTHER INFORMATION: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 16; DB 9; D
100.0%; Pred. No. 1.2e+06;
vative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100...
3, Conservative
       1 FID 3
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US-09-185-908-227
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Sequence 130. Application US/09943944E
Publication No. US20040014036A1
GENERAL INFORMATION:
The Publication No. US20040014036A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TOTAL OF INVENTION:
TOTAL OF INVENTION:
NUMBER OF SEQ ID NOS: 238
SOFTWARE: ParentIn Ver: 2.1
SEQ ID NO 130
LENGTH: 6
                                                                                                                                                                                                                                                                        NS-09-920-306-25

Sequence 25, Application US/09920306

Publication No. US20040029808A1

Sequence 25, Application US/09920306

Publication No. US20040029808A1

APPLICANT: Unilever PLC

APPLICANT: Unilever NV

TITLE OF INVENTION: Peptide Sequence of Functioning as Mimotopes for TITLE OF INVENTION: Hormonal Analytes

FILE REFERENCE: Peptide Mimotopes

CURRENT PAPLICATION NUMBER: US/09/920,306

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: EP00306613.1

PRIOR PILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

FEASO ID NO 25
                                                                                                  Gaps
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OTHER INFORMATION: Description of Artificial Sequence:Random peptide
OTHER INFORMATION: sequences.
US-09-943-944E-130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5;
                                             100.0%; Score 16; DB 8; Length 5; 100.0%; Pred. No. 1.2e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 3; Conservative
                                                                                               Conservative
                 Query Match
Best Local Similarity
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US-08-484-409-36
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Gaps

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Indels

Length 7;

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OTHER INFORMATION: Description of Artificial Sequence: Product of OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
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100.0%; Score 16; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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RESULT 6

В

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Gaps

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| Sequence 230, Application US/09185908A |
| Sequence 230, Application US/09185908A |
| Publication No. US20020193294A1 |
| GENERAL INFORMATION: |
| APPLICANT: Blaschuk, Orest W. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED |
| TITLE OF INVENTION: EUNCHIONS |
| CURRENT FILING DATE: 1998-11-03 |
| NUMBER OF SEQ ID NOS: 269 |
| SEQ ID NO 230 |
| LENGTH: 8 |
| LENGTH: 8 |
| LENGTH: 8 |
| LENGTH: 8 |
| LENGTH: 9 |
| LENGTH: 8 |
| LEN
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: FUNCTIONS
TITLE REFERENCE: 100086.409
CURRENT PALLIAND NUMBER: US/09/185,908A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SEQ ID NO 177
LENGTH: 8
TYPE: PRT
CURRENT ARLIFICIAL Sequence
FRATURE:
FRATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.20+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 177, Application US/09185908A, Publication No. US20020193294A1, GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: Patentin version 3.0
SEQ ID NO 511
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Cyclic Peptide US-09-185-908-177
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                        , TYPE: PRT
, ORGANISM: Homo sapiens
US-09-791-378-511
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APPLICANT: TO, Kotaro
APPLICANT: UMISUKI, Genryou
APPLICANT: WINSUKI, Genryou
APPLICANT: WINSUKI, Genryou
APPLICANT: WORAMA, Yasui,
TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
FILE REFERENCE: 0283-0158P
CURRENT APPLICATION NUMBER: US/09/946,678
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: UP 2000-270371
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 8
LENGTH: 8
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Patent No. US20020142303A1

GENERAL INFORMATION:

APPLICANT: Parekh, Rajesh

TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: SCHIZOPHRENIA

FILE REFERENCE: 9195-061-999

CURRENT APPLICATION NUMBER: US/09/791,378

CURRENT FILING DATE: 2001-02-23
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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                          Sequence 567, Application US/10190082
PUblication No. US20030148264A1
GENERAL INFORMATION
APPLICANT: Lawrence A.
APPLICANT: Sidhu, Sachdev S.
APPLICANT: Held, Heike A.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOWAIN LIGANDS
FILE REPERBNCE: P1905R1
CURRENT FLIAN NUMBER: US/10/190,082
CURRENT FLIAN DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/303,634
PRIOR APPLICATION NUMBER: US 60/303,634
NUMBER OF SEQ ID NOS: 683
SEQ ID NO 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09946678; Patent No. US20020106782A1; GENERAL INFORMATION:
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US-09-946-678-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-10-190-082-567
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          US-10-190-082-567
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US-09-791-378-511
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US-09-946-678-8
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0; Mismatches
         PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 3, Conservative
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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CRGANISM: homc sapiens
US-10-601-100-92
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US-10-601-100-108
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Sequence 2842, Application US/09880748

Publication No. US20030059937A1

SEQUENCE INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERBNES: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTI VET. 2.00
OTHER INFORMATION: Description of Artificial Sequence: Product of OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences FEATURE:
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| Publication No. US20030223996A1 |
| Publication No. US20030223996A1 |
| GENERAL INFORMATION: |
| APPLICATE INFORMATION: |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| FILE REPRESENCE: PF523P2 |
| CURRENT APPLICATION NUMBER: US/10/293,418 |
| CURRENT PILING DATE: 2001-11-27 |
| PRIOR APPLICATION NUMBER: 60/331,469 |
| PRIOR PILING DATE: 2001-11-16 |
| PRIOR PILING DATE: 2001-12-19 |
| PRIOR PILING DATE: 2001-12-19 |
| PRIOR PILING DATE: 2001-60-15 |
| PRIOR PILING DATE: 2001-06-15 |
| PRIOR APPLICATION NUMBER: 60/293,499 |
| PRIOR PILING DATE: 2001-05-25 |
| PRIOR PILING DATE: 2001-05-25 |
| PRIOR PILING DATE: 2001-03-21 |
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                       100.0%; Score 16; DB 9; Length 8; 100.0%; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                 0; Mismatches
                                                                                          ; OTHER INFORMATION: Cyclic Peptide US-09-185-908-230
                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-880-748-2842
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Sequence 92, Application US/10601100

Publication NO. US20040072261A1

GENERAL INFORMATION:

APPLICANT: INNOGRNETICS N.V.

TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of TITLE OF INVENTION: Method for the Diagnosis of FILE REFERENCE: 11362.0038.NPUSOI.

FILE REFERENCE: 1362.0038.NPUSOI.

CURRENT APPLICATION NUMBER: US/10/601,100

CURRENT FILING DATE: 2002-6-20

PRIOR FILING DATE: 2002-6-21

PRIOR FILING DATE: 2002-6-17

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin version 3.2

LENGTH: 8
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Publication No. US20040072561A1
GENERAL INFORMATION:
APPLICANT: INNOSENBETICS N V.
TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
TITLE OF INVENTION: Neurological Diseases
TITLE OF INVENTION: Neurological Diseases
FILE REFERENCE: 11362.0038.NPUSO1
CURRENT APPLICATION NUMBER: US/10/601,100
FRIOR PELING DATE: 2003-06-20
FRIOR PELING DATE: 2002-06-21
FRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 113
SOFTWARE PATENTIN NUMBER: US 60/396,437
NUMBER OF SEQ ID NOS: 113
SOFTWARE PATENTIN Version 3.2
LENGTH: 8
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                      0; Indels
100.0%; Score 16; DB 12;
100.0%; Pred. No. 1.2e+06;
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RESULT 15

US-09-791-377-511

SCHOOL NO. US/09791377

PUBLICATION NO. US/040110938A1

GENERAL INFORMATION:

APPLICANT: PAREKh, Rajesh

TITLE OF INVENTION: SCHIZOPHRENIA

TITLE OF INVENTION: SCHIZOPHRENIA

TITLE OF INVENTION: SCHIZOPHRENIA

TITLE OF INVENTION NUMBER: US/09/791,377

CURRENT APPLICATION NUMBER: US/09/791,377

CURRENT APPLICATION NUMBER: US/09/790,395

PRIOR APPLICATION NUMBER: US/09/750,395

PRIOR APPLICATION NUMBER: 09/750,395

PRIOR APPLICATION NUMBER: 09/750,395

NUMBER OF SEQ ID NOS: 677

SOFTWARE PATENT IN VERSION 3.0

SEQ ID NO 5.1

LENGTH: 8

TYPE: PRT

CREAN: Homo sapiens

US-09-791-377-511
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100.0%; Score 16; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
                                                                     Query Match
100.0%; Score 16; DB 12; Length 8; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 3; Conservative 0; Mismatches 0; Indels
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; ORGANISM: homo sapiens US-10-601-100-108
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Ig kappa chain V-J-C region - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: 840357

R;Klein, R.; Jeanichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: 840312; MUID: 94080891; PMID: 8258341

A;Reference number: 840312; MUID: 94080891; PMID: 8258341

A;Accession: 840357

A;Actus: preliminary; translation not shown

A;Residues: 1-136 eKLES

A;Cross-references: EMBL: X72467

C;Superfamily: immunoglobulin v region; immunoglobulin homology

C;Keyvords: heteroterramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>
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Kappa chain V r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
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Matches:
Conservative:
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Indels:
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  KVMS16
K2HUFR
S40324
S23230
S40341
S40340
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93.10%
87.07%
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-MODEL=frame+ nZp.model - DEV=xlp
-MODEL=frame+ nZp.model - DEV=xlp
-MODEL=frame+ nZp.model - DEV=xlp
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-D=CgnZ 1/USF70 spool p/USO9674716/runat 30092004 070259 25882/app_query.fasta_1.3164
-D=CGNZ-100 - TRE START=1 - END=-1 - MATRIXE-blosum62 - TRANS-munan40.cdi -LIST-45
-UNTING=bits -STRAT=1 - END=-1 - MATRIXE-blosum62 - TRANS-munan40.cdi -LIST-45
-OGALIGN=200 - TRE SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-OTTRYT=ptc - NORM-ext - HEAPSIZE=500 - MINLEN=0 - MAXIEN=200000000
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-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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(c) 1993 - 2004 Compugen Ltd
                                                                                                                 - protein search, using frame plus n2p model
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C; Accession: S40356

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                              Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                     81 SerGlyValProAspArgPheSerGlySerGlySerGlySerGlyThrAspPheThrLeuLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 AsplieValMetThrGinSerProLeuSerLeuProValThrProGlyGluProAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp
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A; Cross-references: BMBL:X72452; NID:g441372; PID:g441373
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroteramer; immunoglobulin
F; 29-108/Domain: immunoglobulin homology <IYM>
                                                                                                                                                                        301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGGTGGCT
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83.68%
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C'Species: Homo sapiens (man)
C'Accession: A90370; A9764; A01888
R'Puttam, F.W.; Whitley Jt., B.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780; J973
A;Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloi A;Tothents: Bence Jones protein Tew
A;Reference number: A90370; MUID:74148480; PMID:4596149
A;Contents: Bence Jones protein Tew
A;Reference number: Bence Jones protein Tew
A;Accession: A90370
A;Molecule type: protein
A;Molecule type: protein was isolated from the urine of a patient with plasma cell dyscrasia
A;Note: the C region of this chain has the Inv (1,2) marker
A;Note: the C region of this chain has the Inv (1,2) marker
B;Terry, W.D.; Pagas, D.L.; Ximura, S; Isobe, T.; Osserman, E.F.; Glenner, G.G.
J. Cilin. Invest. 52, 1276-1281, 1973
A;Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with A;Reference number: A92764; MUID:73166638; PMID:4700495
A;Rocession: A92764
A;Ro
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Bur. J. Immunol. 23, 3248-3271, 1993

AyTitle: Expressed human immunoglobulin chi genes and their hypermutation. AyAccession: $40356

AyAccession: $40356

AyAccession: $40356

AyAccession: $40356

AyAccession: $40356

AyAccession: $40356

AyAccession: $125 < XLE>

AyAccession: $125 < XLE>

AyAccession: $125 < XLE>

AyAccession: $1134.1; PID:g441401

CySuperfamily: immunoglobulin v region; immunoglobulin homology

CyKeywords: heterotetramer; immunoglobulin homology <IMM>
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61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTG---TATAAGGATGGGAAGACATACTTGAAT 117
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840321
19 kappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840321
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Accession: 840321
A;Accession: 840321
A;Residues: 1-130 «KLE»
A;Residues: 1-130 «KLE»
A;Cross-references: EMBL:X72431
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotestramer; immunoglobulin
F;31-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                              121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA 180
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                                                                                                TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla
                                                                                                                                                                                                                                        61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuiysIle
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                               1 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer
                                                                              ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGGAATTGG
                                                                                                                                                                                                                   TCAGGGGTCCCTGACAGGTTCAGTGGCAGGGCACAGGATTTTACACTGAAAATC
          GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGGCCTCC
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Matches:
Conservative:
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Best Local Similarity:
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Pred. No.:
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SSS201

Glight chain V region anti-F(ab')2 - human (fragment)

C.Species: Homo saplens (man)

C.Species: Homo saplens (man)

C.Species: Ja-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000

C.Accession: SSS207

R. Parlschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library, July 1995

A.Description: Characterization of heavy and light chain immunoglobulin variable region

A.Reference number: SS207

A.Status: preliminary

A.Status: preliminary

A.Status: Preliminary

A.Status: EMBL: X89056; NID:9929642; PIDN:CAA61443.1; PID:9929643

C.Superfemily: immunoglobulin V region; immunoglobulin homology

C.Keywords: immunoglobulin homology <IMM>
C;Genetics:
A;Gene: GDB:13KV2
A;Gene: GDB:136265
A;Cross-references: GDB:136265
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Seywords: amyloid; heterotetramer; immunoglobulin
C;Keywords: amyloid; heterotetramer; immunoglobulin homology < INM>
F;16-95/Domain: immunoglobulin homology < INM>
F;23-93/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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504.00
92.86%
86.61%
81.42%
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92.04%
84.07%
81.74%
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Query Match:
DB:
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Pred. No.:
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96 IleSerArgValGluAlaGluAspValGlyLeuTyrTyrCysMetGlnArg1leGluPhe 115

238 ATCAGCAGAGGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTAT

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(1-112)

US-09-674-716B-17 (1-348) x S58207

Query Match: DB:

us-09-674-716b-17.rpr

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A, Residues: 1-121 «KLB»

A, Rorss-references: EMBL: X72481; NID:9441430; PIDN:CAA51149.1; PID:9441431
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroretramer; immunoglobulin
F; 13-92/Domain: immunoglobulin homology < IMM>
                                                                                                                                                   Alignment Scores:
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C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 12-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: 826882
R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A;Title: Megabase inversions in the human genome as physiological events.
A;Reference number: 826882; MUID:90370099; PMID:2118596
A;Reference number: 826882; MUID:90370099; PMID:2118596
A;Reference rumber: 826882; MUID:93770099; PMID:2118596
A;Reference rumber: 826882; MUID:93770099; PMID:2118596
A;Reference rumber: 826882; MUID:93770099; PMID:2118596
A;Reference rumber: 826882; MUID:937626; PIDN:CAA38149.1; PID:g1335367
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
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A.Cross-references: GDB:136265
A.Map position: 2p12-2p12
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapt C.Complex: An immunoglobulin heterotetramer subunit gaw, the subunits associate into lan disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:2-117/Product: Ig kappa chain V II region (GM607) #status predicted <MAT>
F:20-99/Domain: immunoglobulin homology <IMM>
F:27-97/Disulfide bonds: #status predicted
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C,Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C,Accession: A01889; B24452
R;Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A,Title: Contribution of human V-kappaII germ-line genes to light-chain dive
                                                                                                                                                                                                                                                     1 MetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSerIleSerCys
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A;Residues: 1-117 <KLO>
A;Note: the sequence was determined from the differentiated gene
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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Indels:
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  4.028-42
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494.00
91.15%
85.84%
79.81%
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Best Local Similarity:
Query Match:
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Query Match:

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 1.29e-41 492.00 90.18% 84.82% 79.48% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 178 62 298 Query Match: DB: Score: g õ g 셤  $\stackrel{\circ}{\sigma}$ ò à d ò Вb 셤 ò 유 ò ď ò  $\dot{\delta}$ EBSULT 10

KZHUCM

Ig kappa chain V-II region (Cum) - human
C; Species: Homo sapiens (man)
C; Date: 24-pr-1894 #sequence revision 02-Jul-1998 #text\_change 02-Jul-1998
C; Date: Description of Date of Dat C)Genetics:
Appendix of the control 61 AICTCCTGTCGAGTAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120 TACCTGCAGAAGCCAGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA 180 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGAGATCAGGCACAGATTTTACACTGAAAATC 240 AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300 44 64 84 9 24 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer GATATTGTGATGACTCAGTCTCCAGTCTCCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC GlnThrPheGlyGlnGlyThrLysValGluIleLysArg 117 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGT 339 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-674-716B-17 (1-348) x K2HUGM (1-117) A,Contents: annotation C,Comment: This is a Bence Jones protein. 07e-42 493.50 91.23% 84.21% 79.73% Score:
Percent Similarity;
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: 25 121 65 241 82 301 105 Ŋ 181 a g a 8 8 В ò ð δ g à ò

Usually the chain V region anti-F(ab')2 - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000
C; Accession: 58206
E; Welschoff, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, F.
S; Welschoff, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, F.
S; Rescription: Characterization of heavy and light chain immunoglobulin variable region S.
A; Reference number: 558206
A; Reference number: 558206
A; Returne: preliminary
A; Molecule type: mRNA
A; Mo 61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120 180 240 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300 61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAG---GATGGGAAGACATACTTGAAT 117 118 TGGTACCTGCAGAAGCCAGGCGCAGTCTCCCTGATCTATTTGATGTCCACCCCGG 177 GCATCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA 237 40 9 80 238 ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTAT 297 9 20 22 IleSerCysArgSerSerGlnSerLeuLeuAspSerGlyAspGlyAsnThrTyrLeuAsn 41 9 21 42 IrpIyrleuGlnIysAlaGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 61 1 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrPheAspTrp 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeulleTyrLeuGlySerAsnArgAla 121 TACCTGCAGAAGCCAGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCGGGCA 181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 2 AspileValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer GATATTGTGATGACTCACTCTCCCTGCCCGTCACCCCTGGAGCCGGCCTCC 339 112 95 6 11 0 CCATTCACGTTCGGCCCAAGGGACCAAGGTGGAGATCAAACGT Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-674-716B-17 (1-348) x S58206 (1-112)

US-09-674-716B-17 (1-348) x K2HUCM (1-115)

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RESULT 14
S40372
Ig kappa chain V-J region - human
C.Species: Homo sapiens (man)
R.Machain, R.; Zachau, H.G.
R.Malein, R.; Jaenichen, R.; Zachau, H.G.
R.Macession: S40372
A.Reference number: S40312; MUID:94080891; PMID:8258341
A.Residues: Freinminiary; translation not shown
A.Molecule type: mRNA
A.Residues: 1-131 < KLE.
A.Residues: 1-131 < KLE.
A.Residues: 1-131 < KLE.
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCICCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGln---Pro 114
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1-126 <KLEP
A;Cross-references: EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:g441367
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-110/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLys1le
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96
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Mismatches:
Indels:
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Matches:
Conservative:
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82.88%
78.19%
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489.50
92.86%
85.71%
79.08%
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Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGGCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGT 339
                                                                                                        LeuThrPheGlyGlyGlyThrLysValGluIleLys 112
                                                                         301 TICACGIICGGCCAAGGGACCAAGGIGGAGAICAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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490.00
90.27%
84.07%
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Best Local Similarity:
Query Match:
DB:
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                          81
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Oy 301 TTCACGTTCGGCCAAGGGACCAAGGTGAAA 336  Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112  Search completed: September 30, 2004, 08:57:03  Job time : 15.7964 secs		L. 70			
21 ASDIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAlaSer 40 61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGAAGACATACTTGAATTGG 120	AGCAGACTGAAGGTTTTATTATTATTATTATTATTATTATTATTATT	KVMS16 IG kappa chain V region (M167) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996 C;Accession: A01908 R;Rudikcff, S.; Potter. M. B;Accession: A01908 A;Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot A;Reference number: A01908; MUD:79000273; PMID:99160 A;Reference number: A01908; MUD:79000273; PMID:99160 A;Ression: A01908 A;Restance: 1-112 <rud> C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Rap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer F;16-95/Domain: immunoglobulin homology <imm> F;23-93/Disulfide bonds: #status predicted</imm></rud>	Alignment Scores: 1.04e-40 Length: 112 Pred. No.: 483.00 Matches: 94 Score: 94 Conservative: 7 Best Local Similarity: 93.93* Mismatches: 11 Query Match: 18.03* Indels: 0 DB: 1 Gaps: 0 US-09-674-716B-17 (1-348) x KVMS16 (1-112)	1 GATATTGTGATGATCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 60	PheleudInArgProdlyGlnSerProGlnLeuLeuLleSerLeuMetSerThrArgAla TCAGGGGTCCTGACACAGTTCAGTGGATCAGGCACAGATTTTACACTGAAAATC

Dawl Shed

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 30, 2004, 06:00:45; Search time 5.08475 Seconds (without alignments) 30.459 Million cell updates/sec 389414 389414 segs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-674-716B-13 16 1 FID 3 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Ŋ	25,	25,	S	ထဲ	equence 2,	equence 5,	equence 7,	equence 2,	63	equence 1,	ı,	equence 1,	ų	'n	ednence e	15	15	ij	72	equence 27	Sequence 136, App	equence 70	equence 84,	e 55,	501	Sequence 15, Appl
ei ei	-08-197-792-2	US-08-459-850-25	-08-459-214-2	-071-	-09-94	-09-359-304	59-304B-	9-30	US-09-000-217-2	-09-341-982-	-08-277-00	-08-485-181-	-08-964-3	-08-975-917-	-09-817-310	I-US92-01433A	US-08-434-255-15	7-1	ᅻ	-871-1	US-09-517-439-27	US-09-428-082B-136	PCT-US91-02942-70	US-09-690-454-84	5	US-09-834-759-501	US-07-620-426B-15
DB	-	Н	н	m	4	4	4	4	4	4	Н	н	7	ო	4	ហ	Н	ч	Н	Н	4	4	Ŋ	4	4	4	Н
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ery	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	0	0	100.0
Score	16	16	16	16	16	16	16		16		16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
Result No.		7	m	4	Ŋ	9	7	60	O	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

4	Sednence 15, Appl	Sequence 16, Appi	Sequence 15, Appl	Sequence 16, Appl	7, A	Sequence 18, Appl	Sequence 15, Appl	4	INFORMATION FOR	8	Sequence 7, Appli	10,	1, Ap	Sequence 88, Appl	Sequence 52, Appl	Sequence 10, Appl	Seguence 52, Appl
US-07-620-426B-16	US-07-662-007B-15	US-07-662-007B-16	US-07-824-247-15	US-07-824-247-16	US-08-695-412B-7	US-08-574-959A-18	US-08-470-204A-15	US-08-470-204A-16	US/08/622	US-09-357-014-18	US-09-165-922A-7	US-08-325-553-10	US-08-527-113-1	US-08-432-871C-88	US-08-934-222-52	US-08-394-152A-10	US-08-933-402-52
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
28	29	30	31	32	33	34	35	36	37	38	6.6	40	41	42	4.3	4	4.5

#### ALIGNMENTS

RESULT 1	
; Sequence 25, Application US/08197792 ; Patent No. 5525488	
WENTION: Nucleic Acid Encoding the Alpha or Beta Chains of	s of Inhibin and N
, NUMBER OF SEQUENCES: 44	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Generated, inc.	
CIII: COUCH CAN FRANCESCO	
COUNTRY: USA	
; ZIP: 94080	
R READABI	
, MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk	
U	
; OPERATING SYSTEM: PC-DOS/MS-DOS	
; SOFTWARE: patin (Genentech)	
; CURRENT APPLICATION DATA:	
, APPLICATION NUMBER: US/08/197,792	
; CLASSIFICATION: 435	
-	
, APPLICATION NUMBER: 07/958414	
FILING DATE: 08-OCT-1992	
; APPLICATION NUMBER: 07/744207	
; FILING DATE: 12-AUG-1991	
, APPLICATION NUMBER: 07/215466	
FILING DATE: 05-JUL-1988	
; PRIOR APPLICATION DAIA:	
≓	-
; FILING DATE: 31-DEC-1986	
, APPLICATION NUMBER: 06/827710	
; FILING DATE: 07-FEB-1986	
; PRIOR APPLICATION DATA:	
_	
; FILING DATE: 03-OCT-1985	
/AGENT	
; REFERENCE/DOCKET NUMBER: 297P2D4	
5	
; TELEPHONE 415/225-1896	
; TELEFAX: 415/952-9881	

```
Sequence 25, Application US/08459214

APPLICANT: Peter H. Seebur Anthony J. Mason

APPLICANT: Peter H. Seebur Anthony J. Mason

TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or

TITLE OF INVENTION: Using such Nucleic Acid

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                         100.0%; Score 16; DB 1; Length 7; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPBEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,214
FILING DATE: 02-UTN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 297P2D6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-UN1 1995
CLASSIFICATION 0435
PRIOR APPLICATION DATA: 08/197792
RILING DATE: 17-FEB-1994
RILING DATE: 17-FEB-1994
RILING DATE: 17-FEB-1994
RILING DATE: 08-OCT-1992
RILING DATE: 08-OCT-1992
RILING DATE: 12-AUG-1991
RAPPLICATION NUMBER: 07/144207
FILING DATE: 12-AUG-1991
RAPPLICATION NUMBER: 07/115466
FILING DATE: 05-UUL-1988
RILING DATE: 05-UUL-1988
RILING DATE: 05-UUL-1988
RILING DATE: 06-006729
FILING DATE: 07-EB-1986
PRICATION NUMBER: 06/906729
FILING DATE: 07-FEB-1986
PRICATION NUMBER: 06/906729
FILING DATE: 07-FEB-1986
RILING DATE: 03-OCT-1985
ATTONNEY/GABER IRONAMINER: 06/18310
REGISTRATION NUMBER: 28,616
                                                ; TYPE: amino acid; ; TOPLOGY: Innear US-08-459-850-25
          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anthony J. Mason
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
TITLE OF INVENTION: Using such Nucleic Acid
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                              100.0%; Score 16; DB 1; Length 7; 100.0%; Pred. No. 3e+05; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 1BM PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,850
FILING DATE: 02-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/197792
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
FILING DATE: 05-JUL-1988
FILING DATE: 31-DEC-196
FILING DATE: 06/90129
FILING DATE: 06/90129
FILING DATE: 07-FEB-1966
FROR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1966
FROR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1965
FILING DATE: 03-O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08459850; Patent No. 5665568; GENERAL INFORMATION:
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                1 FID 3
                                                                                                                                                                                                US-08-197-792-25
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US-08-459~850-25
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TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same; FILE REFERENCE: 0283-0158P; CURRENT APPLICATION NUMBER: US/09/946,678; CURRENT FILING DATE: 2001-09-06; PRIOR APPLICATION NUMBER: JP 2000-270371; PRIOR FILING DATE: 2000-09-06; NUMBER OF SEQ ID NOS: 27; SOFTWARE: Patentin version 3.1
SEQ ID NOS: 27; SEPTIME OF SEQ ID NOS: 27; SEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 16; DB 4; Length 8; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Cryptococcus nodaensis
US-09-946-678-8
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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US-09-359-304B-5
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SOFTWARE: F
SEQ ID NO 2
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Patent No. 6294372
GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSES. SEED and BERY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
CONNTRY: USA
ZIP: 98104
COMPUTER: EALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,071
FILLING DATE: 13-MAR.1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 3;
Pred. No. 3e+05;
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NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 660081.407
TELECOMMUICATION INFORMATION:
TELEPHONE: (206) 682-490
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09946678; Patent No. 6541236; GENERAL INFORMATION: APPLICANT: ITO, Kotaro APPLICANT: UMITSUKI, Genryou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 100.0%;

Matches 3; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                              SEQUENCE CHARACTERISTICS LENGTH: 7 amino acids
                                                                                                                                                                                                               ; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-214-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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US-09-042-071-52
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US-09-946-678-8
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Sequence 5, Application US/09359304B
; Sequence 5, Application US/09359304B
; Patent No. 6468745
; GENERAL INFORMATION:
; APPLICANT: EITZMAURICE, Wayne P.
; APPLICANT: LINDBO, John A.
; APPLICANT: POGUE, Gregory P.
; TITLE OF INVENTION: MICHELC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
; TITLE OF INVENTION: NUMBER: US/09/359,304B
; CURRENT APPLICATION NUMBER: US/09/359,304B
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
                                                                                                                                                                                                                                                                                      GENERAL INCRAMINE.

GENERAL INCRAMINE.

APPLICANT: EINDBO, John A.

APPLICANT: PADGETT, Hall S.

APPLICANT: POGUE, Gregory P.

TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
FILLE REPERENCE: 008010137US02

CURRENT APPLICATION NUMBER: US/09/359,304B

CURRENT PILING DATE: 1999-07-21

NUMBER OF SEQ ID NOS: 37
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     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NOS: 37
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                               Sequence 2, Application US/09359304B Patent No. 6468745
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; ORGANISM: Tobacco mosaic virus
US-09-359-304B-2
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GENERAL INFORMATION:
APPLICANT: SINGLUFF, Craig L.
APPLICANT: BUINGLUFF, Craig L.
APPLICANT: BURELHARD, Victor H.
APPLICANT: ENGELHARD, Victor H.
APPLICANT: MITTLESEN, David
TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
TITLE OF INVENTION: CYSTEINE LUS/09/341,982
CURRENT APPLICATION NUMBER: US/09/341,982
CURRENT FILING DATE: 1999-09-20
EARLIER APPLICATION NUMBER: PCT/US98/01592
BARLIER FILING DATE: 1998-01-29
BARLIER FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
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APPLICANT: NISHINGTO, Tomoyuki
APPLICANT: NISHINGTO, Tomoyuki
APPLICANT: GUGIMOTO, Toshiyuki
APPLICANT: GUGIMOTO, Toshiyuki
APPLICANT: MIXAEK, Toshio
TITLE OF INVENTION: MALTOSE-TREHALOSE CONVERTING ENZYME, AND
TITLE OF INVENTION: PREPARATION AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: ROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
STATE: D.C.
STATE: D.C.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Fragment of OTHER INFORMATION: human protein
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100.0%; Score 16; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FPC Compatible
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,007
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
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APPLICATION NUMBER: JP 199971/1993
FILING DATE: 20-JUL-1993
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APPLICATION NUMBER: JP 144092/1994
FILING DATE: 03-JUN-1994
                                             Sequence 67, Application US/09341982
Patent No. 6558671
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Patent No. 5538E83
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ORGANISM: Artificial Sequence
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  RESULT 10
US-09-341-982-67
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US-08-277-007-1
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APPLICANT: LINDBO, JOHN A.
APPLICANT: PADETT; Hal S.
APPLICANT: POGUE, Gregory P.
APPLICANT: POGUE, Gregory P.
TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
FILE REFERENCE: 008010137U302
CURRENT APPLICATION NUMBER: US/09/359,304B
CURRENT APPLICATION NUMBER: US/09/359,304B
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                       100.0%; Score 16; DB 4; Length 9; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
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PREENT NO. 6521598
PREENT DOORMATION:
APPLICANT: GOULMY, IIS A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The H-Y Antigen
FILE REFERENCE: Sequence ID No. 6521598. 1-9 for 294-43
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CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09359304B Patent No. 6468745 GENERAL INFORMATION:
; ORGANISM: Tobacco mosaic virus US-09-359-304B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Tobacco mosaic virus
                                                                     Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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US-09-359-304B-7
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Sequence No. 596411
| Patent No. 596411
| GENERAL INFORMATION:
| APPLICANT: NISHINGTO, TOMOYUKI |
| APPLICANT: GUGIMOTO, TOSHIYUKI |
| APPLICANT: MIYAKE, TOSHION |
| APPLICANT: MIYAKE, TOSHION |
| TITLE OF INVENTION: MALTOSE-TREHALOSE CONVERTING ENZYME, AND TITLE OF INVENTION: PREPARATION AND USES THEREOF |
| NUMBER OF SEQUENCES: S |
| ADDERSSED: BROWDY AND NEIMARK
                                                                                                                                                                                                                                             100.0%; Score 16; DB 1; Length 10; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARDERSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: BLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN RELEASE #1.0, Version #1.30
SUGRENT APPLICATION DATE.
APPLICATION NUMBER: US/08/964,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 16; DB 2; I Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 3; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/277,007
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 0F 144092/1994
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NEINARK, Sheridan
REGISTRATION NUMBER: 20,520
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                         single
                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-181-1
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amino acid
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                                         STRANDEDNESS:
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| Sequence 1, Application US/08485181
| Patent No. 5736380
| GENERAL INFORMATION:
| APPLICANT: NISHIMOTO, Tomoyuki
| APPLICANT: SUGIMOTO, Toshiyuki
| APPLICANT: MIYAKE, TOShiO
| TITLE OF INVENTION: MATTOSE-TREBALOSE CONVERTING ENZYME, AND TITLE OF INVENTION: PREPARATION AND USES THEREOF
| NUMBER OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 16; DB 1; Length 10; 100.0%; Pred. No. 2.8e+02;
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ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
CONFURE: PatentIN Balesis #1.0, Version #1.30

CURRENT APPLICATION DATA:
FILING DATE: 07-70N-1995

RICK APPLICATION NUMBER: US 08/277,007

PRING APPLICATION NUMBER: US 08/277,007

PRING DATE: 19-70L-1994

APPLICATION NUMBER: UP 199371/1993

PRILING DATE: 20-70L-1993

PRILING DATE: 03-70N-1994

ATTORNEY AGENT INFORMATION:
NAME: NEILNG AGENT INFORMATION:
NAME: NEILNG AGENT INFORMATION:
NAME: NEILNG WATER: OF PATORNEY AGENT INFORMATION:
NAME: NEILNG WA
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REGISTRATION NUMBER: 20,520
REPERENCE/DOCKET NUMBER: NISHIMOTO=2
TELECOMUNICATION INFORMATION:
TELEPHOME: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                       NISHIMOTO=2
                                         NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFRENCE/DOCKET NUMBER: NISHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELERX: 202-628-5197
TELERX: 203-137-3528
TELEX: 24863
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 3; Conservative
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MOLECULE TYPE: peptide
US-08-277-007-1
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US-08-485-181-1
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                                                               Sequence 1, Application US/08975917
Fatent No. 6090792
GENERAL INFORMATION:
FAPLICANT: MISHIMOTO, Tomoyuki
APPLICANT: CHAEN, Hiroto
APPLICANT: GYGIMOTO, Toshiyuki
APPLICANT: GYGIMOTO, Tomoyuki
APPLICANT: GYGIMOTO, Tomoyuki
APPLICANT: GYGIMOTO, Tomoyuki
APPLICANT: GYGIMOTO, Tomoyuki
APPLICANT: Washington
CITY: Washington
CITY: Washington
CONUTRY: USA
ZIP: ZOOG
CONUTRY: GYGIMOTO
CONUTRY: GYGIMOTO
COMPUTER: TEN PC COMPATION
COMPAT
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100.0%; Score 16; DB 3; Length 10
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels
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Patent No. 6534311
GENERAL INFORMATION:
APPLICANT: Stewart, Mary
APPLICANT: Thomas, George
TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,917
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CLASSIFICATION NUMBER: US/U8/975,91,
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/277,007
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: UP 199971/1993
FILING DATE: 20-JUL-1993
FILING DATE: 20-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 144092/1994
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 anino acads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-975-917-1
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 FID 10
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RESULT 14
US-08-975-917-1
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US-09-817-310-5
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us-09-674-716b-1/.rsp
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GenCore version 5.1.6	200	378	61.1	129 1	KV3L HUMAN	77
Copyright (c) 1993 - 2004 Compugen Ltd.	. 22		60.1 59.9	109	L KV3B_HUMAN	z m
	23		59.8	109	L KV3E_HUMAN	<b>7</b> .
OM micleic - protein search, using frame blus n2b model	24		59.5	109	L KV4D_HUMA	<del></del>
	25		59.1	109	L KV3F_HUMAL	7.
Run on. Sentember 30, 2004, 08:20:22 : Search time 7.5503 Seconds	26		59.0	111	KV30 MOUS	Gc)
100000000000000000000000000000000000000	27		59.0	108	L KV3A_HUMAL	7
4799.922 Million cell updates/sec	- 28		58.5	109	1 KV3G_HUMAL	z
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	3		58.3	129	1 KV3H_HUMA	z
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	3		56.0	108	1 KV1M HUMA	z
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Post-processing: Minimum Match 0%					ALT GNMENTS	ENTS

P18135 homo sapien
P18136 homo sapien
P01650 homo sapien
P01663 homo sapien
P01623 homo sapien
P01624 homo sapien
P01654 homo sapien
P01657 homo sapien
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Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Cercl=1/USFPC spool \_p/USC09674716/runat\_30092004\_070257\_25855/app\_query.fasta\_1.3164
-De\_Cencl=1/USFPC spool \_p/USC09674716/runat\_30092004\_070257\_25855/app\_query.fasta\_1.3164
-DEVALISPC -GPWT=fastan -SUFFIX=sp -MINNATCH=0.1 -TOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -MATRIX=500 -MINNEN0 -MAXLEN=200000000
-USER=US09674716 @CGN 1 1 82 @runat\_30092004\_070257\_25855 -NCPU=6 -ICFU=3
-NO MAAP -LARGEQUERY -NGG\_CGORES=0 -MAIT -DSPBLOCK=100 -LONGING
-DEV\_TIMEOUT=120 -MARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPOX=0 -DELOP=6 -DELEXT=7

Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	DB ID Description	1 KV2D HUMAN P01617 homo sapien	50E30G	1 KV2A HUMAN P01614 homo sapien		P01626		P06310 homo			1 KV2G MOUSE P01631 mus musculu	P01630 r		P01629				P06313 homo	
	Query Match Length DB	113	117	115	113	112	113	133	112	120	113	113	113	112	108	134	114	133	
de	Query	81.7	79.8	79.7	79.2	78.0	77.7	76.4	74.9	73.5	71.7	71.6	70.9	69.8	67.3	67.1	65.2	62 7	
	Score	506	494	493.5	490	483	481	473	463.5	455	444	443	439	432	416.5	415.5	403.5	aac	ה ה
	Result No.		(1)	m	4	'n	9	7	00	o	10	디디	12	13	14	15	16	-	

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Pred. No.:

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241 AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGGTGGTAGAGTATCCA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 TyrLeuGlnLysProGlnGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLySIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
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P01614;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-II region Cum.
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12664 MW; 92C57DC719E558B1 CRC64;
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Mismatches:
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Matches:
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                               EMBL, Z00009, -, NOT ANNOTATED_CDS.
PIR, A01899; KTHUGM.
HSSP, P80362, 1WTL.
GO, GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006952; F:antigen binding; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR0073596; IG-V.
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   or send an email to license@isb-sib.ch)
                                                                                                                                                                         PEAM; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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SIGNAL <1
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91.15%
85.84%
79.81%
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Query Match:
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Pred. No.:
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-AUD-1999 (Rel. 38, Last annotation update)
19-Appa chain VII region GM607 precursor (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84191566, PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                            COMPLEMENTARITY-DETERMINING-1.
                                                                               COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                     COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                        12316 MW; OC3C38F81F1843CA CRC64;
              .mmunoglobulin V region; Bence-Jones protein; Amyloid.
                                                                                                                                                                                                                                               101 IleThrPheGlyGlnGlyThrArgLeuGlulleLysArg 113
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Matches:
Conservative:
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113 PA;
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PS50835;
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KV2E HUMAN

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P01626;
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ID KV2A MC
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DT 21-JUL
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"Welcular basis of antibody formation.";

"Molecular 
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                                                                Hilschmann N , , "The complete amino acid sequence of Bence Jones protein Cum (kappa-"The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCATTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGT 339
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115 AA; 12676 MW; S9E9F90A379569EC CRC64;
                                                                                                                    Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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MEDLINE=70063440; PubMed=4188189;
                                                  MEDLINE=68242259; PubMed=5586923;
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NCBI_TaxID=9606;
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                                                                                                                                                                                            Appella E.;
"Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein.";
Mol. Immunol. 17:711-718 (1980).
-i. MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.
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Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                           SEQUENCE.
MEDLINE=81052016; PubMed=6776396;
                                                                                                                                                                                                                                                                                                                                                                PIR, 100910; KVMSS1.

INCEPPO, 1WTL.

INTERPO, 1PR007110; Ig-like.

INTERPO, 1PR007110; Ig-like.

Pfam; PP00047; ig; 1.

PROSITE; PS50835; Ig V.

PROSITE; PS50835; Ig Like.

Immunoglobulin V region.

PROMAIN

24 54 FR2

DOMAIN

55 61 COM

DOMAIN

62 93 FR2

DOMAIN

62 93 FR2

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62 93 FR2

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63 94 FR2

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66 93 FR3

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67 94 FR2

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Alignment Scores:
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                                                                                             Biochemistry 17:2703-2707 (1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY PIR; A01908; KWASI6.
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                                                                                                                                                                                                                                                                                                                                                                                           61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
                                                           MEDLINE=79000273; Pubmed=99160;
Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                     A58EDFD6404B9726 CRC64;
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110
110
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                    SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        US-09-674-716B-17 (1-348) x KV2A_MOUSE (1-112)
                                                                                                                                                                                                        FRAMEWORK-1
                                                                                                                                                                                                                                                           FRAMEWORK-4
                                                                                                                                                                                                                                                                                                                                                           Gaps:
chain V-II region MOPC 167
                                                                                                                                       HSSP, P80362, 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PR00047; ig, I.
SWART; SM00406; IGv; I.
Imwunglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                      12349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV2B HUMAN STANDARD;
AC PO1615;
DT 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                             4.54e-46
483.00
90.18%
83.93%
78.03%
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39
61
61
93
          Mus musculus (Mouse)
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94
103
23
112
                                 NCBI_TaxID=10090;
                                                                                       myeloma protein."
                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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Ig kappa
                                                                                                                                                                                                                                                                 DISULFID
NON TER
SEQUENCE
                                                   SEQUENCE
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61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 TyrLeuGlnLysProGlyGlnSerProGluLeulleTyrLeuSerSerTyrArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 11eGlnCysArgSerSerGlnSerLeuValTyrArg***Gly***ThrTyrLeu***Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SerGlyValProAspArgPheSerAspSerGlySerGlyThrAspPheThrLeuLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
                                                                                                                                                                                                                                     chain from a Waldenstroms IgM
                                                              Homo sapiens (Human).
Stararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCHI_TaxID=9606;
                                                                                                                                                                                                          Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms with specificity for phosphorylcholine.";
Biochemistry 15:382-3833(1976).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCODA39E46DB96BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 TyrThrPheGlyGlnGlyThrLysLeu***IleLysArg 113
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Matches:
Conservative:
Mismatches:
Indels:
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region FR.
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BY SIMILARITY
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HSSP, P01607, IREI.

GO, GO:0005576, C:extracellular; NAS.

GO:0003823; F:antigen binding; NAS.

GO:0000855; P:immune response; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR00710; Ig-11ke.

Ffam; PF00047; ig; I.

SMART; SM00406; IGV; I.

Immunoglobulin V region.

PROMIN V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                  SEQUENCE.
MEDLINE=76253627; Pubmed=821524;
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12660 MW;
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481.00
89.38%
77.88%
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40
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103
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113 AA;
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Best Local Similarity:
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RESULT 7

113 AA

PRT;

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61 ATCTCCTGTCGGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                            AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
                                                                                                   101 SerargvalglualagluaspvalglyvalTyrTyrCysMetGlnGlyThrHisTrpSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 TyrLeu***LysProGly***SerPro***LeuLeulleTyrLeuGlySerAsnArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGGTCACCCCTGGAGAGCCGGCCTCC
        181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.

Dreyer W.C., Gray W.R., Hood L.E.,

Dreyer W.C., molecular, and cellular basis of antibody formation:

some facts and a unifying hypothesis.";

cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E5B22E2FA7ABE481 CRC64;
                                                                                                                                       TTCACGTTCGGCCAAGGACCAAGGTGGAGATCAAACGT 339
                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                 21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
15-Exppa chain V-II region MIL.
Homo Sapiens (Human)
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Matches:
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SMART, SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
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HSSP; P80362; LWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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463.50
89.38%
76.11%
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53
60
60
101
111
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112
12055 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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SEQUENCE
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KV2C HUMAN
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                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATCTCCTGTCGCTCGAGTAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-II REGION RPMI 6410.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=86641852, PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
Hig., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 2
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Matches:
Conservative:
Mismatches:
Indels:
                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
115-AUL-1999 (Rel. 38, Last annotation update)
115-Augpa chain V-II region RPMI 6410 precursor.
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HSSP; B01825; 1WTL.
GO; GO:0005576; Cextracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006895; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                              Nucleic Acids Res. 13:6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00047; ig, 1.
SMART; SM0406; IGV: 1.
PROSTTE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z00020; CAA77315.1; -.
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473.00
88.50%
79.65%
76.41%
                 STANDARD;
                                                                                                              Homo sapiens (Human).
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Best Local Similarity:
                                                                                                                                                          NCBI_TaxiD=9606;
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KV2F HUMAN
ID KV2F HUMAN
AC P06310;
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SEQUENCE
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21 AspileValileThrdlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
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                                                   300
           TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
                               79
                                                            SerGlyValProAsnArgPheSerGlySerGlySerGlyThr***PheThrLeuLysIle
                                                 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTTATTACTGTCAACAGCTGGTAGAGTATCCA
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAPPA CHAIN V-II REGION VKAPPA167.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDILIBE-82025223; FubMed=6791832; MEDILIBE-820025223; FubMed=6791832; Selaing E., Scorb U.; Normation of immunoglobulin light-chain variable-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEMORN-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN V-II REGION VKA
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2.
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63BB571F0E4DE3E8 CRC64;
                                                                                          301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGT 339
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5
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-II region VKappa167 precursor.
Mus musculus (Mouse).
                                                                                                                                                        120 AA.
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, J00562; AAA39032.1; -.
EMBL; KO2415; AAA39051.1; -.
FIR, A01909; KVMS67.
HSSP, P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam, PF00047; igj 1.
FRAM; SM00406; Igy 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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13280 MW;
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88.00%
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KV2B_MOUSE
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ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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STRAIN=A/J;

MOVOTUY J., Margolies M.N.;

MI-idigoxin hybridoma antibody.";

Biochemistry 22:1153-1156(1983).

LISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA CONTRINGED THAT BINDS DIGOXIN.

PROFIET THAT BINDS DIGOXIN.

PROFIET THAT BINDS DIGOXIN.

PROFIET THAT BINDS DIGOXIN.

PROFIET THAT BINDS DIGOXIN.

RESP, P80362; IMTL.

RESP, P80362; IMTL.

RESP, P800467; ig.1.

REPROFIET PS0047; ig.1.

REPROFIET PS0047; ig.1.

REPROFIET PS0047; ig.1.

REPROFIET PS0045; IG.1.

REPROF
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                                                                                                                                                                                                                                                                                                                                81 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle
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15-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-II region 26-10.
18 kappa chain V-II region 26-10.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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Matches:
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113 AA;
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US-09-674-716B-17 (1-348) x KV2B\_MOUSE (1-120)

Percent Similarity: Best Local Similarity:

Query Match:

Indels: Gaps:

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ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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Acherbold R., Herbel H., Grutter T., Chang J.Y., Braun D.G.;
The state of 
                                         21 IleSerCysArgSerSerDerLeuLeuHisSerAsnGlyAsnThrTyrLeuTyrTrp
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTGGAGAGCCGGCCTCC
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23-OCT-1986 (Rel. 02, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
15-ULL-1999 (Rel. 38, Last annotation update)
16 kappa chain V.II region 17829.1.
18 was musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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Matches:
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Mismatches:
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BY SIMILARITY
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MEDLINE-85128968; PubMed-6441768;
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KV2E MOUSE
P03976;
                                                                                                                                                                                                                                                                                                                                                                        181
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REQUENCE.

XX CADDINE=83256427; PubMed=6409088;

RA Chang J.-Y., Herbbert H., Aebersold R., Braun D.G.;

Chang J.-Y., Herbbert H., Aebersold R., Braun D.G.;

RA chains from a mouse hybridoma-derived anti-(streptococcal group RT 1ight chains from a mouse hybridoma-derived anti-(streptococcal group RT 1 ight chains from a mouse hybridoma-derived anti-(streptococcal group RT Application of the dimethylaminoazobenzene isothlocyanate technique for the isolation of peptides.";

RI Application of peptides.";

RI ELOCHEM. V. 211:173-180(1983).

CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

DR PIR, A01913; KWASS.

DR HSSP; P80362; IWTL.

DR HSSP; P80362; IWTL.

DR HSSP; P80362; IWTL.

DR HSSP; PRO077110; Ig-like.

DR HTGPPTO; IPRO03596; Ig_V.
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               ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Repa chain V-II region 7634.1.

Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.

VCBI_TaxID=10090;
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv: 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
FRAMEWORK-1.
23 COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2
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"The amino acid sequence of the light chain variable region of a
caninne myeloma immunoglobulin: evidence that the VK subgroups
predated mammalian speciation.";
Immunochemistry 15:303-305(1978).
-!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
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PIR; A01907; K2DGGM.
HSSP; P01607; IREI.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V region GOM.
Canis familiaris (Dog).
Canis familiaris (Dog).
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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SMART; SM00406; igy; 1.
PROSITE; PS50835; ig, LiKE; 1.
Immunoglobulin V region.
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InterPro, IPR003596; Ig-v.
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MEDLINE=83055101; PubMed=7141411;

Merber H., Charg J.Y., Aebersold R., Braun D.G.;

Herber H., Charg J.Y., Aebersold R., Braun D.G.;

"Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for the group A streptococcal polyyaccharide.";

Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).

HOPPE-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).

- I. MISCELLANDOOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

RANTIBODY AD1011; KVMSS1.

RIGHT PROFIGO, IPRO0110; Ig-like.

RIGHT PROFIO; IPRO01596; Ig-v.

R Pfam, PF00047; ig; 1.

R PROSITE; SM00406; IGv; 1.

R PROSITE; PSES0835; IG_LIKE; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
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FRAMEWORK-4.
BY SIMILARITY.
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COMPLEXENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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21-JJL-1986 (Rel. 01, Last sequence update)
15-JJL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-II region 281.3.
Mus musculus (Mouse).
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US-09-674-716B-17 (1-348) x KV2E_MOUSE (1-113)
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                                                                                                            GATATIGIGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGAGAGCCGGCCTCC
                                                                                                                            1 AspileValMetThrGlnThrProLeuSerLeuSerValSerProGlyGluProAlaSer
                                                                                                                                                                                                                         TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=86041854, PubMed=2997713,
Marsh P., Mills F., Gould H.,
"Detection of a unique human V kappa IV germline gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marsh P.;
Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGT 339
Matches:
Conservative:
Mismatches:
Indels:
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01-APR-1988 (Rel. 07, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
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                                                                                 US-09-674-716B-17 (1-348) x KV1 CANFA (1-108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scleic Acids Res. 13:6531-6544(1985)
416.50
82.30%
72.57%
67.29%
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           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTAT---AAGGATGGGAAGACATACTTGAAT 117
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                                              IG KAPPA CHAIN V-IV REGION B17. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                        FRAMEMORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEMORK-4.
BY SIMILARITY.
                                                                                                                     COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                            6413A22FD0738832 CRC64;
                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                      FRAMEWORK-2
 LIKE; 1.
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415.50
81.58%
72.81%
67.12%
ROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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Pred. No.:
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SEQUENCE
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Dank She

Run

us-09-674-716b-17.rspt

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QUISO, MESSAGE MESSAGE
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OSNEKO;

OSNEKO;

O1-OCT-2002 (TYENBLrel. 22, Last sequence update);

O1-OCT-2003 (TYENBLrel. 25, Last annotation update);

Hypothetical protein.

Hypothetical protein.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       Q8vc55 mus
Q9u180 homo
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QBTCD0
QBTCD0
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-MODEL-frame+ n2p.model -DEV=x1p
-Q=/Cog12_1/USPTC=prool_p/USO9674716/runat_30092004_070258_25867/app_query.fasta_1.3164
-Q=/Cog12_1/USPTC=prool_p/USO9674716/runat_30092004_070258_25867/app_query.fasta_1.3164
-DB=SPTENENEL_25_CFWT=fastan -SUFFTX=rspt -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UDGALIGN=200 -THR_SORE=per -THR_MAX=100 -TRANS=human40.cdi -LIST=45
-UDGALIGN=200 -THR_SORE=per -THR_MAX=100 -TAIGN=15 -MODE=LOCAL
-UOSFR-US09674716_@CGN 11_499_@runat_31092004_070258_28867 -NCPU=6 -ICPU=3
-NO_MARP -LARGEQUERY -NGS_SCOSES=0 -MAIT -DSPELOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOFEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                         US-09-674-716B-17
619
1 gatattgtgatgactcagtc.....agatcaaacgtacggtggct 348
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                nucleic - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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1. sp_archea:*
2: sp_tungi:*
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5: sp_invercebrate:*
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Xgapop 10.0 , Ygapext 0
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Fgapop 6.0 , Fgapext 7
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Maximum DB seq length: 200000000
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Alignment Scores:
Pred. No.:
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Pred. No.:
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                                                                                                           Query Match:
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hymosapiens (Human).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                        F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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Pfam; PF00047; ig; 2.
SMART; SM00407; IGG1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00395; IG_LIKE; 2.
PROSITE; PS00396; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26024 MW; F
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516.00
92.24%
86.21%
83.36%
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                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                Alignment Scores:
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240
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGGTGGCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SerThrPheGlyGlnGlyThrLysLeuGluIleLysArgThrValAla 136
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L Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, ROC1181, AAH21781.1; -.

R PIR, A33933, AAH21781.1; -.

R PDB, INCS; 24-UUL-02.

B GO, GO:0016570; F:toxin activity; IEA.

DR GO, GO:001670; F:toxin activity; IEA.

DR InterPro; IPR00110; Ig-1ike.

DR InterPro; IPR00110; Ig-1ike.

DR InterPro; IPR00110; Ig-1ike.

DR InterPro; IPR00110; Ig-1ike.

DR Pfam; PF00447; ig; 2.

DR Pfam; PF00447; ig; 2.

DR PRART; SM00406; IG-MHC; 1.

DR PROSITE; PS00239; IG-MHC; 1.

KW Hypothetical protein.

SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
239
113
0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08.055,
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                Gaps:
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  2.56e-47
478.00
88.79%
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458.00
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                                              Percent Similarity:
Best Local Similarity:
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Percent Similarity:
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238 AA
                                      US-09-674-716B-17 (1-348) x Q9UL80 (1-114)
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Submitted (JAN-2001) to the EME EMBL; BGC02035, AAH02035.1; -.
FIR; A31807; A31807.
FIR; A32248; A32248.
FIR; B32248; B32248.
FIR; C32248; B32248.
FIR; PH1042; PH1042.
FIR; PH1043; PH1042.
FIR; PH1043; PH1044.
FIR; S07455; S07455.
FIR; S16112; S16112.
FIR; S24500; S24500.
FIR; S24501; S24501.
FIR; S24501; FIR*O00006; IG_MHC.
INTERPRO; IPRRO03006; IG_MHC.
INTERPRO; IPRRO03006; IG_WHC.
FERNERS FROOWAT; IGY: 1.
FROOWATT; SMON406; IGY: 1.
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                                                                                                                                                                                                                                                                                                         21 AspvalvalLeuThrGlnThrProLeuSerLeuProValAsnIleGlyAspGlnAlaSer 40
                                                                                                                                                                        GATATTGTGATGACTCAGTCTCCAACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
WHO X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY 2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Matches:
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NON TER 114 114
SEQUENCE 114 AA; 12775 MW;
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121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCGGGGA 180
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1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
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(0.170N-2001 (TrEMBLrel. 17, Created)
(0.170N-2001 (TrEMBLrel. 17, Last sequence update)
(0.170N-2003 (TrEMBLrel. 25, Last annotation update)
(1.0CT-2003 (TrEMBLrel. 25, Last annotation update)
(1.0CT-2003 (TrEMBLrel. 25, Last annotation update)
(1.0CT-2003 (TrEMBLrel. 26, Last annotation update)
(1.0CT-2003 (TrEMBLrel.
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PIR; PH1010; PH1030.

PIR; PH1011; PH1031.

PIR; PH1024; PH1031.

PIR; PL0277; PL0257.

PIR; S07455; S07455.

PIR; S07455; S07455.

PIR; S07605; S07750.

PIR; S07605; S07750.

PIR; S07605; S07750.

PIR; S07605; S07750.

PIR; S07750; S07750.

PIR; S070606; S07750.

PROMOTOF; PR0003596; IG_V.

PROSITE; PS00047; ig_ LIKE; 2.

PROSITE; PS00047; ig_ LIKE; 2.

PROSITE; PS00047; ig_ LIKE; 2.

PROSITE; PS00040; ig_ MHC; 1.
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                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 238 AA; 2
                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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Q8K0F8;
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DB:
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                                                                                                                                                                                      20 AspvalvalMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                        301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGGTGGCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Colon;
A Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BENBL; BCO19760; AAH19760.1; -.
PIR; A32248; A32248.
R PIR; A33933; A33933.
R PIR; B30577.
R PIR; B31455; B37837.
R PIR; B31455; B31485.
R PIR; B31465; B31485.
R PIR; B31485; B31485.
R PIR; C32248; C32248.
R PIR; C32248; C32248.
R PIR; C32933; E2887.
R PIR; D27887; D27887.
R PIR; D27887; D27887.
R PIR; D27887; D27887.
R PIR; D27897; D27887.
R PIR; D27897; D27887.
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Q8VCI6,

Q1-MAR-2002 (TrEMBLrel. 20, Created)

Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein.

Mus musculus (Mouse)
                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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               ll protein.
238 AA; 26344 MW;
                                                          3.94e-44
451.00
86.21%
74.14%
 PROSITE; PS00290; IG_MHC; 1.
                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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              Hypothetical
SEQUENCE 23
                                                  Alignment Scores:
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PH0106;
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                                                                                                                                                                                                                                                                                         ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
                                                                                                                                                                                                                                                                                                                                                                            40 IleSerCysArgSerSerGInSerLeuValHisSerAsnGlyAsnThrTyrLeuHisTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 TyrLeuGlnLysProGlyGlnSerProLysLeulleuIleTyrLysValSerAsnArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLySIle
                                                                                                                                                                                                                                                                 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLOCT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Solurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-Breast tumor;
Straubberg R.;
Submitted (M. 2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031498; AAH31498.1; -.
PIR; A33933; A33933.
  35EC08E3DE5414AD CRC64;
                                                              238
864
100
000
                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                       Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
26224 MW;
                                                            8.89e-44
448.00
86.21%
74.14%
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79

9

us-09-674-716b-17.rspt

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Pfam; PF00047; ig; 1.
SMART; SM0409; ig; 1.
SMART; SM0406; iGv; 1.
PROSITE; PS50835; iG_LIKE; 1.
Hypothetical protein.
SEQUENCE 148 AA; 16345 MW; 1
                                                                                                                                                                                                                                                                                                                                           2.11e-40
419.00
84.078
71.688
67.698
    InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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201182
AC 091182;
DT 01-0CT--2
DT 01-0CT--2
DT 01-0CT--2
DE Anti-myC
DE MAMB musch
OC MAMB 
                                                                                                                                                                                                                                                                                                                                                                                                     Score:
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OBKI22;

OBKI22;

OL-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
HYCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGGTGGCT 348
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GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro; IPR00199; MDH short.

RINEERPO; IPR001359; IG_CI.

RINEERPO; IPR003599; IG_CI.

RINEERPO; IPR003006; IG_MHC.

RINEERPO; IPR003006; IG_MHC.

RINEERPO; IPR00409; IG; 2.

RINEERPO; IPR00409; IG; 2.

RINEERPO; IPR00409; IG; 2.

RINEERPO; IPR00409; IG; 2.

RINEERPO; IPR00409; IG_CI.

RINEERPO; IRROPO; IG_CI.

RINEERPO; IRROPO; IG_MHC; 1.

RINEERPO; IRROPO; IG_MHC; 1.

RINEERPO; IRROPO; IG_MHC; 1.
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TISSUBS-Salivary gland;
Strausberg M.A.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC028925, APH28925.1;
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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83
115
0
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Matches:
Conservative:
Mismatches:
Indels:
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433.00
84.48%
71.55%
69.95%
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Best Local Similarity:
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Pred. No.:
Score:
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08K122
1D 08K121
0C 08K1
01-0
0T 01-0
0T 01-0
0T 01-0
0X MANN
0C MANN
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TRAIN=BALB/C;

STRAIN=BALB/C;

Malkiel S., Liao L., Cunningham M.W., Diamond B.;

Trel-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive try with cardiac myoshin.;

Infect. Immun. 68: 5803-5808 (2000).

REMBL; APS06044; AAF69322.1;

REMBL; ARS06044; AAF69322.1;

REMPL; PROFOTILI, Ig-like.

InterPro: IPR007110; Ig-like.

Property: PR00356; Ig-v.

Pfam; PF0047; ig-1.

REMPL; PS0835; Ig-v.

Pfam; PROSITE; PS0835; IG-LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                     40 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrTyrLeuAsnTrp
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Was musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090182;
01-0CT-2000 (TrEMBLrel, 15, Created)
01-0CT-2000 (TrEMBLrel, 15, Last sequence update)
01-0CT-2003 (TrEMBLrel, 25, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
183920BBD9F3B521 CRC64;
                                                         148
81
14
17
0
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Matches:
Conservative:
Mismatches:
Indels:
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                             Percent Similarity:
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Q9UL83;
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DB:
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                                                                                                                                                                                                                                 CTCCTGTATAAGGATGGGAAGACATACTTGAATTGGTACCTGCAGAAGCCAGGGCAGTCT
                                                                                                                                                                                                                                                                                                                                                             CTCTCCCTGCCCGTCACCCCTGGAGAGAGCGGCCTCCATCTCCTGTCGCTCGAGTAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                          205 GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
                                                                                                                                                                                                                                                                                                                                            145 CCACAGCTCCTGATCTATTTGATGTCCACCCGGGCATCAGGGGTCCCTGACAGGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                 5DA8BBFD5F0AA1AE CRC64;
                                                                 104
113
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Matches:
Conservative:
Mismatches:
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                                                                                                                                              Gaps:
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 104
11360 MW;
                                                               9.93e-40
413.00
87.50%
75.00%
66.72%
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104 AA;
                                                                                                               Best Local Similarity:
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                                                                                              Percent Similarity:
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NON TER
SEQUENCE
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DB:
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61 AICICCIGICGCICGAGIAAGAGICICCIGIAIAAGGAIGGGAAGACAIACIIGAAIIIG 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;

"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";

fetus.";

Clin. Immunol. Immunopathol. 67:184-192(1998).

FIRE, BRO35031; AAD56267.1; -..

PIR; B30609; B30609.
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Matches:
Conservative:
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Indels:
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PIR; H30607, H30607.
PIR; H30608, H30608.
PIR; PH0963, H90963.
PIR; PH0965, PH0965.
PIR; S34096, S34096.
HSSP; P60622, 1WTL.
INTERPRO, IPR007110; Ig-like.
INTERPRO, IPR003596, Ig_v.
Pfam, PF00047; ig; 1.
SMART, SM00406, IGY; 1.
NOW TER 109 LIKE; 1.
NOW TER 109 SA, 11646 MW;
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375.00
79.65%
64.60%
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Alignment Scores
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Memo sapiens (Human).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu Lu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus ""
EACLS ""
EMBL: AF035028; AAD56264.1; -
PIR, B30607; B30607.
B10601; 130601.
HSSP; P80362; 1WTL.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
                                                                                                                                                                                                                      9F9C5A92EBA96EEA CRC64;
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Matches:
Conservative:
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PIR; C30609; C30609.
PIR; D30609; D30609.
PIR; S34098; S34099.
PIR; S34099; S34099.
PIR; S34099; C34099.
PIR; S40030; C34099.
INCEPPO; IPR007110; Ig-like.
INCEPPO; IPR007110; Ig-like.
INCEPPO; IPR007110; Ig-like.
PR071T; SM04406; Ig-v.
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108 AA; 11834 MW;
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362.50
77.88%
61.95%
58.56%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Q9UL86;
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AC 09118
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181 TCAGGGGTCCCTGACAGGTTCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307935; AAL09419.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Igy 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q920E9 PRELIMINARY; PRT; 111 AA. 0920E9; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2003 (TrEMBLrel. 25, Last annotation update) Pterin-mimicking anti-idiotope kappa chain variable region
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NON TER 111 111
SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;
                                                                                                                                                243325F72C7DAC83 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR007110; Ig-like.
InterPro; IPR00396; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 109 109
SEQUENCE 109 AA; 11928 MW; 2
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358.00
77.88%
62.83%
57.84%
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Thu Sep

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A Strausborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Sapleton M., Soares M.B., Bonaldo M.P., Gasavant T.L., Scheetz T.E.,
Repleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Rabas S.A., McKwan P.J., McKernan K.J., Marek J.A., Guntarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabes S., Worley K.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Cones S.J., Marra M.A.,
A. Mones S.J., Marra M.J.,
A. Mones S.J., Marra M.J.,
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Q72473, Q7243,
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein.
Hypothetical primates; Catarrhini; Hominidae; Homo.
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     Length:
Matches:
Conservative:
Mismatches:
Indels:
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TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
3.58e-33
357.50
75.00%
64.29%
57.75%
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TISSUE=Lung;
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64 ICCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGGTAC 123
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                                                                                                                                                                                                                                                                            22 IleArgMetThrGlnSerProSerSerPheSerAlaSerThrGlyAspArgValThrIle 41
                                                                                                                                                                                                                                                                                                                                    42 ThrCysArgAlaSerGlnSerIle------GlySerTyrLeuAlaTrpTyr 56
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                                                                                                                                                                                                                                                  77 GlyValProSerArgPheSerGlySerAlaSerGlyThrAspPheThrLeuSerIleSer
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDINDE-98277139; PubMed=9614934; MEDINDE-98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 ACGITCGGCCAAGGACCAAGGIGGAGAICAAACGIACGGIGGCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 ThrPheGlyGlnGlyThrLysValGluileLysArgThrValAla 131
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0562256; AAH56256.1; -.
Hypothetical protein:
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB5845F19724FB4E CRC64;
                                                                                                234
71
71
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EMBL, AF035035, AAD56271.1; -
PIR; S23689, S236.8.
HSSP, PO1607, IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR0073596; Ig_v.
Pfam; PF00047; ig].
SMART; SM00406; IGy! 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1 1.
                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                    4.25e-33
357.50
73.91%
61.74%
57.75%
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                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Alignment Scores:

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108 69 13 5 1		rcacccragaagag	:::  aserThrGlyAspA	ATGGGAAGACATACT		rctatttgatgtcca		GCACAGATTTTACAC	lythraspPhethri	STCAACAGCTGGTAG		3T 339	rg 108	
Length: Matches: Conservative: Mismatches: Indels: Gaps:	1-108)	GATATTGTGATGACTCAGTCTCCACTCTGCCGTCACCCTGGAGAGCGGCCTCC		ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG	 ly11e	TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCGGGCA	TyrglnglnLysProglyLysAlaProgluLeulleTyrAlaAlaSerThrLeugln	TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGGATCAGGCACAGATTTTACACTGAAAATC	SerGlyValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrl	AGCAGAGTGGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA		TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGT	96 ProThrPheGlyGlnGlyThrLysValGluIleLysArg	
4.1e-32 348.50 72.57% 61.06% 56.30%	(48) × Q9UL79 (3	GATGACTCAGTCTCC		TCGCTCGAGTAAGAC		GAAGCCAGGGCAGTCTC	nLysProGlyLysA	CCCTGACAGGTTCAC	lbroSerArgPhese	GTGGAGGCTGAGGATG		CGGCCAAGGGACCA	eGlyGlnGlyThrLy	
Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-09-674-716B-17 (1-348) x Q9UL79 (1-108)	1 GATATTGT	Aspileva	61 ATCTCCTG	21 IleSerCy	121 TACCTGCA	36 TyrGlnGl	181 TCAGGGGT	56 SerGlyVa	241 AGCAGAGT	76 SerCysLe	301 TICACGII	96 ProThrPh	
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Search completed: September 30, 2004, 08:53:40 Job time : 45.0663 secs

2 May Shel

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CD23; FCERII; IgB receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
Ady82611 Human PTH
Ade22469 Human ant
Adb72231 Humanised
Adb72231 Humanised
Adb72231 Humanised
Adb72233 Humanised
Adb72233 Human sed
Adv22251 Human ant
Ade28477 Human ant
Adv27544 Human ant
Adv27540 Consensus
Adv27560 Consensus
Adv27558 Light cha
Adv25586 Light cha
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Adv262437 Human ant
Adv22487 Human ant
Adv22481 Human ant
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Adv39172 Human ant
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Abr39792 Humanised
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    /note= "framework region 1"

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AAB72227
AAB72227
AAW22613
AAW276447
AAW27646
AAW27661
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/note= "CDR 1"
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     Homo sapiens.
Synthetic.
     AAY32262;
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AAX32862
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COUD
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          Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-VG=/CGT2 1/USFTC spool_p/US09674716/runat_30092004_070257_25848/app_query.fasta_1.3164
-DB=A_Geneseq_297an04_QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPECL=0.0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -ENN=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_NAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_OUTFWT=PROFENSEX -FREAPSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USER=LOCAL_OUTFWT=PROFENSEX -NGG_SCORES=0 -WAIT - DSPBLOCK=100 -LONGLOG
-USER=LOCAL_OUTFWT=PROFENSEX -NGG_SCORES=0 -WAIT - DSPBLOCK=100 -LONGLOG
-NO MMARP -LARGEQUERY -NGG_SCORES=0 -WAIT - DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ade28461 Human ant
Abp64972 Human pro
Aay828615 Human PTH
Ade28405 Human ant
Abb57576 HLM-DR-sp
Ade28465 Human ant
Aay22261 Mouse ant
Ade28397 Human ant
Ade28391 Human ant
Ade28421 Human ant
                                                                                                                                                                September 30, 2004, 08:19:42; Search time 41.458 Seconds (without alignments) 4743.430 Million cell updates/sec
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                                                                                                                                                                                                                                                               US-09-674-716B-17
619
1 gatattgtgatgactcagtc......agatcaaacgtacggtggct 348
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                   OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
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AABP64972
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AAY32261
ADE28465
ADE28465
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1. geneseqp1980s:*

2. geneseqp1990s:*

4. geneseqp2000s:*

5. geneseqp2001s:*

6. geneseqp2001s:*

7. geneseqp2003bs:*

8. geneseqp2003bs:*
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Match Length
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Database :

12645678901

Result No.

Minimum DB Maximum DB

Searched:

Run on:

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US-09-674-716B-17 (1-348) x ADE28461 (1-239)
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                                                                                                                                                                                                                                                                                                                                        This sequence represents the light chain variable region (VL) of humanised anti-CD23 (PCERII) monoclonal antibody Cl1, composed of a human framework (HSIGKVII) and the light chain complementarity determining regions (see AAV32254-56) of murine antibody Cl1. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimseric or humanised antibodies, which comprises sufficient of the amino decid sequences of the Cl1 light and heavy chain complementarity determining regions to render them capable of binding to the CD3 type II molecule expressed on haematopoietic cells: The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, inflammantory bowel disease, unciriar, nephrotic syndrome, glomentlonephritis, inflammantory bowel disease, uncerative collitis, Grohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graftversus-host disease, COPD, insullitis, bronchitis (particularly dispersed) and backli for studying interactions malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGGTTCAGGCACAGATTTTACACTGAAAATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
                                                                                                                                                                                                                                                                      ptor specific antibodies useful for treating e.g. arthritis, multiple sclerosis and psoriasis.
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Matches:
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region 3"
                                                   /note= "framework region
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                                                                                                                                                                                                              Ellis JH,
'note= "framework
            94. .102
/note= "CDR 3"
                                                                                                                                                                                                                                                                                                                   Claim 9; Fig 3; 81pp; English
                                                                                                                                 99WO-GB001434
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                                                                                                                                                                                                                                                    N-PSDB; AAZ34747.
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                                                                                                                                                                                                              Bonnefoy JMP,
                                                                                                                                                                                                                                                                               receptor
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                                                                                                                                 07-MAY-1999;
                                                                             WO9958679-A1
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CBOO. The anti-CDAO antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder souch as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD4O antibodies may also be useful for detecting CD4O in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD4O antibody variable region light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; variable region light chain; 23-28-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                              81 SerArgValGluAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrFro 100
241 AGCAGAGTGGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anti-CD40 antibody 23-28-1 variable region light chain protein.
                                                                                                                   301 ITCACGITCGGCCAAGGACCAAGGIGGAGAICAAACGIACGGIGGCT 348
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522.00
93.10%
86.21%
84.33%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PFIZ ) PFIZER PROD (ABGE-) ABGENIX INC.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                    ADE28461;
                                                                                                                                                                                                                                       RESULT 2
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us-09-674-716b-17.rag

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Human, expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; extiallergic; antiinfammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective.
                                                                                                        120
                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                      SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnValLeuGlnThrPro 120
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                                                                                                                                                                                                                       TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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                                AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer
                                                                                                                                            TCAGGGGTCCCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
                                                                                                              ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
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?, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheThrPheGlyProGlyThrLysValAspIleLysArgThrValAla 136
  GATATTGTGATGACTCAGTCTCCACTCTCCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP64972 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-NOV-2001; 2001WO-US042950
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N-PSDB; ABQ99558.
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ABB 649
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polymucleotides are useful in diagnostics as expressed sequence tags

(ESTs) for identifying expressed genes or for physical mapping of the

(human genome. The proteins may be used as molecular weight markers, or as

nutritional sources or supplements. The proteins may be used to maintain

and expand cell population in a totipotential or pluripotential state

(useful for re-engineering damaged or diseased tissues, transplantation,

manufacture of bio-parmaceuticals or the development of bio-sensors. The

polymucleotides and proteins are useful for preventing, treating or

ameliorating disorders involving aberrant protein expression or

biological activity, e.g., haematopoietic disorders, central/peripheral

nervous system diseases, mechanical and traumatic disorders, non-healing

voral, bacterial or fungal infection, autoimmune disorders, allergic

reactions and conditions, coaquiation disorders, allergic

polymucleotide sequences of the invention were assembled from ESTs

isolated mainly by sequencing by hybridisation, and in some cases,

sequences obtained from one or more public databases. Note: The sequence

data for this patent did not form part of the printed specification, but

was obtained in electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, parathyroid hormone related protein, PTHrP, monoclonal antibody, hypercalcaemia, rheumatoid arthritis, bone cancer, metastasis, pain, facture, cachexia, tooth disease, periodontal disease, gingiva; sepsis, systemic inflammatory response syndrome, SIRS, hypophosphataemia; antiarthritic, cytostatic, antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTCCTGTCGCTCGAGTAAGAGTCTCCTG---TATAAGGATGGGAAGACATACTTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 IleSerCysArgSerSerGinSerLeuLeuAspSerAspAspGlyAsmThrTyrLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpTyrLeuGlnLysProGlyGlnSerProGlnLeuleulleTyrThrLeuSerTyrArg
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101
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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519.50
93.16%
86.32%
83.93%
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Best Local Similarity:
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Pred. No.:
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Query Match:
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us-09-674-716b-17.rag

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anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV, hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; variable region light chain; 7-1-2.
                                                                                                                                                                                    Human anti-CD40 antibody 7-1-2 variable region light chain protein.
standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2002; 2002WO-US036107
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2001; 2001US-0348980P
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N-PSDB; ADE28404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infections.
                                                                                                                                                                                                                                                                                                                                     WO2003040170-A2.
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                                                                                                                                                                                                                                                                                                     Homo sapiens,
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                                                                                                                  ADE28405;
                   121
                                                                                    ADE28405
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DB:
                                                   RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or its fragments, following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of PTHrP (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metassessis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PTHrP monoclonal antibody clone protein sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA 180
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                                                                                                                                                                                                                                                                                                                                   A human monoclonal antibody to parathyroid hormone related protein. -useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
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Matches:
Conservative:
Mismatches:
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                                                                 /note= "possible Ala'
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 31; Page 45-46; 88pp; Japanese.
                            Location/Qualifiers
155
                                                                                                                                                                                                                                                                                                                                                                   including metastasis, and pain.
                                                                                                                                                                                                  98JP-00188196
98JP-00196729
                                                                                                                                                                    98JP-00304793
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519.00
92.24%
85.34%
83.84%
                                                                                                                                                                                                                                                  (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                   WPI; 2000-286723/25.
N-PSDB; AAA13925.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 239 AA;
                                                 Misc-difference
                                                                                                   JP2000080100-A
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 Homo sapiens
                                                                                                                                                                    12-OCT-1998;
                                                                                                                                                                                                                  26-JUN-1998;
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Query Match:
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The invention relates to a novel chimeric or human monoclonal antibody or lits antigen-binding portion that specifically binds to and activates human CB40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder souch as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region light chain protein of the invention.
                                                                                                                                               New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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Conservative:
Mismatches:
Indels:
Jia X,
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                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 12; 177pp; English.
Corvalan J,
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519.00
92.24%
87.07%
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180

80

240

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Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; and parteribility complex; antidiabetic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antignoriatic; immunosuppressive; dermatological; antidiabetic; nephrotropic; promimetic; hepatotropic; immune response suppressor; narcolepsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis; grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis; irritable bowel disease; Sjogren's syndrome.
                                                                                                      SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys11e 100
                                                                                                                                                          AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface.
IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnPheLeuAspTrp
                           TACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA
                                             TyrLeuGlnLysProGlyGlnSerProGlnLeulleUlleTyrLeuGlySerAsnArgAla
                                                                                  TCAGGGGTCCCTGACAGGTTCAGTGGCAGGATCAGGCACAGATTTTACACTGAAAATC
                                                                                                                                                                                                 HLA-DR-specific protein MS-GPC16 VL sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomassen-Wolf E;
                                                                                                                                                                                                                                                                                        ABB57576 standard; peptide; 114 AA
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06-OCT-2000; 2000US-0238762P.
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                                                                                                                                                                                                                                                                                                                                                 18-MAR-2002 (first entry)
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antidiabetic, antipsoriatic, immunosuppressive, dermatological, antityroid, nephrotropic, immunosuppressive, dermatological, antityroid, nephrotropic, ihyromimetic and hepatotropic activities, and suppressing activation of immune response. (I) is useful for suppressing activation or proliferation of a cell of the immune system, suppressing activation or proliferation of a cell of the immune system with another cell, timunosuppressing a patient and for killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on the surface of the cell, where neither cytocoxic entities on the killing. (I) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus crythineatosus, ankylosing spondyllitis, ransplant rejection, graft versus host disease, Hashimoto's disease, myasthenia gravis, pempiagus vulgaris, climulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary climulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary climulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary climulonephritis, thyroiditis, pancreatitis, sequence used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-CD40 monoclonal antibody, CD40; cytostatic, virucide, antibacterial, immunostimulant, anti-HIV, hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; light chain; 23-28-1.
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Matches:
Conservative:
Mismatches:
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518.00
92.11%
88.60%
83.68%
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Best Local Similarity:
Query Match:
DB:
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Homo sapiens

The present invention describes a composition (I), comprising a polypeptide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the surface of a cell, where treating cells expressing the antigen with the polypeptides leads to suppression of an immune response, and the ICSO for the suppression of immune response, and the ICSO for antirheumatic, antiathritic, neuroprotective, antihilammatory,

Example; Fig 15; 139pp; English.

9

AAY32261 standard; protein; 145 AA.

(first entry)

15-FEB-2000

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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibocterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiancy conditions including neutropenia or HIV in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
                                                                                                                                                                                                                                                          New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 lleSerCysArgSerSerGnSerLeuLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ArgfhrPheGlyGlnGlyfhrLysValGluileLysArgfhrValAla 136
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                                                                                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 72; 177pp; English.
                                                                                                                                                                              Corvalan J,
                                                              08-NOV-2002; 2002WO-US036107.
                                                                                               09-NOV-2001; 2001US-0348980P
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518.00
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N-PSDB; ADE28464.
                                                                                                                              PFIZER PROD
ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                            viral infections.
 WO2003040170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 239 AA;
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This sequence represents the light chain variable region (VL) of murine anti-OD23 (FCERII) monoclonal antibody C11. The invention provides anti-OD23 (FCERII) monoclonal antibody C11. The invention provides alteria antibodies, such as chimeric or humanised antibodies (see AAY32262 and AAY32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on hamanacopoietic calls. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple clerosis, diabetes, uveltis, dermatitis, psoriasis, urricaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative collitis, Crohn's disease, COPD, insulitis, bronchitis (particularly chronic versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                        CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lugus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; lugus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcreative colitis; Crohn's disease; slogren's syndrome; allergy, asthma; thintis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
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                                                                                                          Mouse anti-CD23 MAb C11 light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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--- "CDR L1"
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/note= "CDR L2"
125. .134
/note= "CDR L3"
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                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09958679-A1
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                                                                                                                                                                                                                                                                                                TACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCGGGCA
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                                                                                                                                                                                            ATCTCCTGTCGCTCGAGTAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
                                                                                                                                                                                                                 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
                                                                                                                                        Human anti-CD40 antibody 3-1-1 variable region light chain protein.
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Mismatches:
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                                                                          US-09-674-716B-17 (1-348) x AAY32261
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N-PSDB; ADE28396.
Local Similarity:
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                Query Match:
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cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region light chain protein of the invention.
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Matches:
Conservative:
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92.24%
85.34%
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                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CB40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibocterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder souch as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region light chain protein of the invention.
                                                                                                                                 that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                                                            or human monoclonal antibody or its antigen-binding
  Feng X;
Jia X,
                                                                                                                                                                                                                       Claim 1; SEQ ID NO 28; 177pp; English.
Corvalan J,
Gladue RP,
                                            WPI; 2003-441521/41.
                                                                  N-PSDB; ADE28420
                                                                                                            New chimeric
Bedian V,
                                                                                                                                                                            viral
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## Sequence 239 AA;

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       Length:
Matches:
Conservative:
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                                                                   US-09-674-716B-17 (1-348) x ADE28421 (1-239)
      2.78e-46
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                                21 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer
                                                                                                                      41 IleSerCysArgSerSerGInSerLeuLeuHisThrAsnGlyTyrAsnTyrPheAspTrp
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301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGGTGGCT 348
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AAY82611 standard; protein; 239 AA
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AAY82811
1D AAY82811
1D AAY82
XX AAY82
XX DT 02-AU
XX B Human
XX Human
XX Human
XX Human
XW Human
XW Human
XW Human
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Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.

Human; parathyroid hormone related protein; PTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;

301 TTCACGTTCGGCCAAGGACCAAGGTGGAGATCAAACGTACGGTGGCT 348

The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or lits fragments, following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of PTHrP his the following content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphateemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PTHrP monoclonal antibody clone protein sequence from the present human monoclonal antibody to parathyroid hormone related protein. - seful, for treating hypercalcemia, rheumatoid arthritis, cancer of bone systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory. Claim 31; Page 34-35; 88pp; Japanese. including metastasis, and pain. 98JP-00304793 98JP-00188196. 98JP-00196729. (NISB ) JAPAN TOBACCO INC. WPI; 2000-286723/25. N-PSDB; AAA13921. JP2000080100-A Homo sapiens. 17-JUN-1998; 26-JUN-1998; 12-OCT-1998; 21-MAR-2000 invention 

239 96 112 0 0 Length:
Matches:
Conservative:
Mismatches: Indels: 511.00 93.10% 82.76% 82.55% Similarity: Percent Similarity: Alignment Scores: Query Match:

Sequence 239 AA;

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41	
121	121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCGGGCA 180
61	:::
181	TCAGGGGTCCCTGACAGGTTCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
81	
241	241 AGCAGAGTGGAGGGTGGTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCGACGGGCA
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Homo sapiens.
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AAB72235
ID AAB72235
IXX
AXX
DT 10-MA
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DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
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PheThrPheGlyProGlyThrLysValAspIleLysArgThrValAla 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 76; 177pp; English.
                                                                                                                  ADE28469 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2002; 2002WO-US036107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-2001; 2001US-0348980P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-441521/41.
N-PSDB; ADE28468.
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This invention relates to a combination of an anti-Ep-CAM (cyclic adenosine monophosphate) antibody with a chemotherapeutic agent, that is chapable of arresting Ep-CAM antigen expressing cells in the synthesis ($) phase or the second growth phase ($M$) of cell enlargement ($G2\/DNA$ replication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in $S$ or in $G2/M$, is $C0-faractered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal cancer, breast cancer, gastric cancer, presents cancer or non-small-cell lung cancer. The present sequence represents the kappa light chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG2Cys) which can be used in the combination of the invention
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                                                                                                                                                                                                                                                                                            241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA
                                                                                                                    181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGGGACAGGCACAGATTTTACACTGAAAATC
                                                                                                                                                                   81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLySIle
61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis; chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised 323/A3 (IgG2cys) antibody kappa light chain amino acid.
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capable of arresting Ep-CAM antigen expressing cells in the synthesis (S) phase or the second growth phase (M) of cell enlargement (G2)/DNA treplication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is coadministered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal cancer, breast cancer, prostate cancer or non-small-cell lung cancer. The present sequence represents the kappa light chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used in the combination of the invention
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99WO-EP005271.

23-JUL-1999;

This invention relates to a combination of an anti-Ep-CAM (cyclic adenosine monophosphate) antibody with a chemotherapeutic agent, that is

Example 3; Fig 6; 103pp; English.

(GLAX ) GLAXO GROUP LTD

Thurmond LM; Knick VC, Stimmel JB,

WPI; 2001-182729/18. N-PSDB; AAF63373.

Combination for treating cancer (e.g. breast, gastric or prostate cancers), or in the manufacture of a medicament for anti-cancer therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody with a chemotherapeutic agent.

Disclosure, Fig 15; 103pp; English

This invention relates to a combination of an anti-Ep-CAM (cyclic adenosine monophosphate) antibody with a chemotherapeutic agent, that is peapable of arresting Ep-CAM antigen expressing cells in the synthesis (S) phase or the second growth phase (M) of cell enlargement (G2)/DNA replication. The antibody exhibits cycostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is coadministered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal cancer, breast cancer, prostate cancer on non-small-cell lung cancer. The present sequence represents the light chain of anti-Ep-CAM antibody known as humanised 323/A3 (19G1) which can be used in the combination of the invention 

Sequence 238 AA;

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Indels:
Gaps: 4.56e-46 510.00 90.52% 87.07% 82.39% Score:
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US-09-674-716B-17 (1-348) x AAB72227 (1-238)

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241 AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300 

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US-10-292-088-40
US-10-292-088-16
US-10-292-088-16
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US-10-292-088-13
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US-10-292-088-13
US-10-292-088-10
US-10-292-088-12
US-10-000-986-8
US-10-292-088-12
US-10-292-088-12
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Publication No. US20030211100A1
GENERAL INFORMATION

APPLICANT: BEDIAN, VAHE

APPLICANT: GLADUE, RONALD F.

APPLICANT: GLADUE, RONALD F.

APPLICANT: GONALAN, JOSE

APPLICANT: TON XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

TITLE OF INVENTION ANTIBODIES. US/10/292,088

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 60/348,980

FRIOR PRILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: Patentin Ver. 2.1

SERVICE 1399
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        TYPE: PRT;
CRGANISM: Homo sapiens
US-10-292-088-40
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-MODEL=frame+ .ngp. model -DEV=xlp
-MODEL=frame+ .ngp. model -DEV=xlp
-MODEL=frame+ .ngp. model -DEV=xlp
-DE-CGNZ 1/USFTO_spool p/USO9674716/runat 30092004 070302 26027/app_query.fasta_1.3164
-DB=Published Applications AA -QFMT=fasta_ .SUPFIX=rapb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -GFART=1 -EMD=-1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -FORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09674716 @CGN 1 1 496 @runat 30092004 070302 26027
-NCPUe.5 -ICPU=3 -NO MMAP -LARGEQUERY NEG $\overline{SCORES}=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5
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619
1 gatattgtgatgactcagtc......agatcaaacgtacggtggct 348
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| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.Pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.Pep:*
| cgn2_6/ptodata/1/pubpaa/DCT_NEW PUB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.Pep:*
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| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.Pep:*
| cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.Pep:*
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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0 4 1 0		TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: MS-GPC16 VL -10-275-046-83 ignment Scores: -10-275-046-83 indels: -10-275-046-83 indels: -10-275-046-83 ignment Scores: -10-275-046-83 ignment Scores	
H WE W	0y 121 TACCTGCAGGGCAGTCTCCACAGGTCCTATTGATGATGCCACCGGGCA	pplicatio US20030 ATION: US20030 DIAN: UADUE, RO ORVALAN, IA, XIAO- RIO, XIAO- NTION: RE: ABX-PF CATION NUMB ION NUMB DATE: 200 DATE: 20	mo sapiens : 7.81e-45 Length: 519.00 Matches: 21.04 Conservative: arity: 87.074 Mismatches: 12.848 Indels: 12.848 Gaps: 7 (1-348) x US-10-292-088-16 (1-239) TATTGTGATGACTCCCCCTCCTCCCCGCCGTCAFFILL

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Alignment Scores:
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| Publication No. US20040110933A1
| GENERAL INFORMATION:
| APPLICANT: Rondon, Isaac J.
| APPLICANT: Edge, Albert
| APPLICANT: Rent, Rachel Baribault
| TILE OF INVENTION: CD44 LIGANDS
| FILE REFERENCE: 10280-063001
| CURRENT APPLICATION NUMBER: US/10/663,244
| CURRENT APPLICATION NUMBER: US 60/410,758
                                                                                                                                           APPLICANT: BEDIAN, VAHE
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-HI
APPLICANT: FENG, XIAO-HI
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REPERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT PILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR PLING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 56
                                                                                  Sequence 56, Application US/10292088 Publication No. US20030211100A1 GENERAL INFORMATION:
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518.00
91.38%
87.07%
83.68%
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Best Local Similarity:
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US-10-663-244-149
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                                                                                                                                                                                                                  FEATURE:

CTHER INFORMATION: Synthetically generated peptide.

US-10-663-244-149
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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APPLICANT: Edge, Albert
APPLICANT: Edge, Albert
APPLICANT: Edge, Albert
APPLICANT: Edge, Albert
APPLICANT: Kent, Rachel Baribault
ITLE OF INVENTYON: CD4 LICANDS
FILE REFERENCE: 10280-063001
CURRENT APPLICATION NUMBER: US/10/663,244
CURRENT APPLICATION NUMBER: US 60/410,758
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 60/469,123
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 149
LENGTH: 236
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Sequence 145, Application US/10663244

; Publication No. US20040110933A1

; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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516.00
92.24%
86.21%
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Best Local Similarity:
Query Match:
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Alignment Scores:
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US-10-292-088-32
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10292088;
Publication No. US20030211100A1
GENERAL INPORMATION:
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: USPALAN, UGSE
APPLICANT: UTA, XIAO-CHI
APPLICANT: UTA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE REFERENCE: ABX.PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088;
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR PRIOR APPLICATION NUMBER: 03/348,980
PRIOR FILING DATE: 2001-11.09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 8
LENGTH: 239
TYPE: PRT
CREANISM: Homo sapiens
US-10-292-088-8
         3.25e-44
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92.24%
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Pred. No.:
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US-10-292-088-8
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61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120

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                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/10292088
| Sequence 32, Application US/10292088
| Publication No. US20030211100A1
| GENERAL INFORMATION:
| APPLICANT: BEDIAN, VAHE
| APPLICANT: GLADUE, RONALD P.
| APPLICANT: CORVALAN, JOSE
| APPLICANT: UIA, XIAO-CHI
| APPLICANT: CORVALAN, JOSE
| APPLICANT: UIA, XIAO-CHI
| APPLICANT: ABL-CHI ON WHERE: US/10/292, 088
| CURRENT APPLICATION NUMBER: 60/348, 980
| PRIOR FILING DATE: 2003-13-14
| PRIOR FILING DATE: 2001-11-09
| NUMBER: OF SEQ ID NOS: 147
| SEQ ID NO 32
| LENGARE: PatentIn Ver. 2.1
| SEQ ID NO 32
| LENGARE: PATENT: 239
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ORGANISM: Homo sapiens
US-10-292-088-32
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LOCATION: (156)

POTHER INFORMATION: Variable amino acid
US-10-292-088-64
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US-10-292-088-64
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121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGGTCCTGATCTATTTGATGTCCACGGGGCA 180
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Sequence 102, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION WUMBER: US/10/292,088
CURRENT PILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
TILE OF INVENITON: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US/
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT APPLICATION NUMBER: 00/348,980
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
FINGHH: 239
TYPE: PRI
TYPE: PRI
ORGANISM: HOMO Sapiens
US-10-292-088-80
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 102
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
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41 IleSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyrLeuTyrTrp
                                121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCGGGCA
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US-10-308-817-177
; Sequence 177, Application US/10308817
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US-10-453-698-177
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Sequence 12, Application US/10404724

Sequence 12, Application US/10404724

Publication No. US20030203447A1

GENERAL INFORMATION:

APPLICANT: HOTWIZ, Arnold H.

TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant

TITLE OF INVENTION: PolyPeptides

FILE REFERENCE: 13698US01

CURRENT APPLICATION NUMBER: US 10/10/404,724

CURRENT APPLICATION NUMBER: US 60/368,530

PRIOR APPLICATION NUMBER: US 60/368,530

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin version 3.2

LENGTH: 239

TYPE: PRT

COGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                      Gaps:
                                               6.64e-44
510.00
91.38%
86.21%
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510.00
90.52$
86.21$
82.39$
                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
JS-10-292-088-102
                                Alignment Scores:
Pred. No.:
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Pred. No.:
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TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; Publication No. US20040110933A1
; GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J.
APPLICANT: Rede, Albert
APPLICANT: Rede, Albert
APPLICANT: Rent, Rachel Baribault
TITLE OF INVENTION: CD44 LIGANDS
FILE REFRENCE: 10280-063001
CURRENT FILING DATE: 2003-09-13
FRIOR APPLICATION NUMBER: US 60/410,758
PRIOR PILING DATE: 2003-09-13
; PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
APPLICANT: Rother, Russell
APPLICANT: Rother, Russell
APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
TITLE DE INVENTION: HYBRID ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SEQ ID NO 177
LENGTH: 113
LENGTH: 113
TYPE: PRT
ORGANISM: human
US-10-308-817-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                      1.996-43
505.00
92.04%
86.73%
81.58%
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Percent Similarity:
Percent Similarity:
Query Match:
DB:
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US-10-663-244-148
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                                                                                                                       1 GATATIGIGACICAGICICCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: Synthetically generated peptide

; OTHER ALLONDON, US-10-663-244-148

Publication No. US20030219861A1 GENERAL INFORMATION:

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66, Appl
66, Appl
66, Appl
108, Appl
108, Appl
98, Appl
97, Appl
97, Appl
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112, Appl
112, Appl
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111, Appl
112, Appl
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115, Appl
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Sequence 5
Sequence 5
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Sequence 4
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APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: 973
CORRESPONDENCES: 373
CORRESPONDENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CONTY: New York
CONTY: New York
CONTY: USA
ZIP: 10021
COMPUTER: IBM PC compatible
OMPUTER: PLOPDY disk
COMPUTER: IBM PC compatible
OMPUTER: PLOPDY disk
COMPUTER: IBM PC compatible
OMPUTER: IB
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
        RESULT 1
US-09-025-769B-15
        Command line parameters:
-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-Ca-Conglar 1/0570-Gspool _PUS09674716/runat 30092004 070259 25901/app_query.fasta_1.3164
-DE-ISBUED PATENTS-FOCKEDOOL _PUS09674716/runat 30092004 070259 25901/app_query.fasta_1.3164
-DE-ISBUED PATENTS-FOCKED -OFFITE -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=A5 -DOCALIGN=200 -THR SCORE=PQC -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=pto -NORM=ext -HEAPS:IZE=500 -MINLEN=0 -NAXLEN=200000000
-USER=US09674716 @CGN 11 107 @runat 30092004 070259 25901 -NCPU=6 -ICPU=3
-NO MARAP -LARGEQUERY -NGG SCORES=0 -WAIT -BSPELOCK=100 -LONGICG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS:I -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    September 30, 2004, 08:41:28; Search time 8.5124 Seconds (without alignments) 4221.672 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                    1 gatattgtgatgactcagtc.......agatcaaacgtacggtggct 348
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                   protein search, using frame_plus_n2p model
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US-09-025-769B-29
US-09-025-769B-178
US-09-025-769B-178
US-08-053-171-16
US-08-264-093-10
US-08-44-093-88
US-08-476-349A-88
US-08-48-882-66
US-08-48-892-66
US-08-487-113D-66
US-08-487-113D-66
US-08-487-113D-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                               US-09-674-716B-17
619
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                   nucleic
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Run

Result No.

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61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 SerArgyalGluAlaGluAspValGjyValTyrTyrCysGlnGlnHisTyrThrThrPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45. Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Gr. Liming
APPLICANT: Gr. Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TICACGITCGGCCAAGGGACCAAGGIGGAGAICAAACGIACG 342
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Matches:
Conservative:
Mismatches:
Indels:
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                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                              TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      6.51e-55
507.00
91.23%
87.72%
81.91%
                                                                                                                                                                                                                                                        LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-025-7698-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
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Best Local Similarity:
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US-09-025-769B-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 1021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
TURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
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97
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APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckchun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TICACGITCGGCCAAGGGACCAAGGIGGAGAICAAACGT 339
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Matches:
Conservative:
Mismatches:
Indels:
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: (212)596-9000
: TELEFAX: (212)596-9090
: INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino
                                                                                                                                                                                                                                                           4.87e-55
508.00
92.92%
85.84%
                                                                                                 LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                , MOLECULE TYPE: protein
US-09-025-769B-15
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                                                                                                                                                                                                                                                                                    Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-025-769B-29
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DB:
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181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGGATCAGGCACAGATTTTACACTGAAAATC 240
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COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-ADG-1995
ATTORNEY/ACENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
RECISTRATION NUMBER: 27,794
RECISTRATION NUMBER: 27,794
RECISTRATION NUMBER: APORTALION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212)596-9900
INPORMATION POR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
TENTIFIE IL4 amino acids
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; Patent No. 630064
; GENERAL INFORMATION:
APPLICANT: Raappik, Achim
APPLICANT: Pack, Peter
; APPLICANT: Ilac, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
; APPLICANT: Plucekthun, Andreas
; TITLE OF INVENTION: Procein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
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Matches:
Conservative:
Mismatches:
Indels:
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507.00
91.23%
87.72%
81.91%
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amino acid
3Y: linear
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Best Local Similarity:
Query Match:
DB:
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COMPRESPONDED ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 100.21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PE-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-REB-1998
FILING DATE: 18-AUG-1995
ATTORNEY/ABGNT INFORMATION:
REGISTRATION NUMBER: Z7,794
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Mismatches:
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Matches:
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APPLICANT: Co, Loibner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
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507.00
91.23%
87.72%
81.91%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity:
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US-08-053-171-16
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CORRESPONDENCE ADDRESS:

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81 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnAlaPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA 237
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                                                                                                                                                                                RESULT 6
US-08-264-093-10
Sequence 10, Application US/08264093
Parent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
TITLE OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
98
11
11
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COUNTRY: Canada
ZIP: MSH 2J7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IEM FC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICALLO.

PILING DATE:
CLASSIPICATION: 536
CLASSIPICATION: 536
PRIOR APPLICATION DATA: NO. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMONICATION INFORMATION:
TELECHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
"""" LENGTH: 113 amino acids
"""" LENGTH: 113 amino acids
"""" LANGTH: 113 amino acids
"""" LANGTH: 113 amino acids
""" LANGTH: 113 amino acids
"""" LANGTH: 113 amino acids
"""" LANGTH: 113 amino acids
"""" LANGTH: 113 amino acids
                                                                                  301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 336
                                                                                                                101 IleThrPheGlyGlnGlyThrArgLeuGluIleLys 112
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not applicable TOPOLOGY: linear
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92.04%
86.73%
81.18%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "E.A. Kabat, et al.,
Sequences of Protein of Immunological Interest,
4th Ed. (1987), US Dept. of Health and Human Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGGATCAGGCACAGATTTTACACTGAAAATC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Sequence of Tew antibody
                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171 FLING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: Smith, Willaim M REGISTRATION NUMBER: 30,223
REFERENCE/COCKET NUMBER: 11823-54-1
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFRAX: (415) 326-2422
INPORMATION POR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acide
TYPE: Amino acide
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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505.00
91.96%
85.71%
81.58%
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                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1.112
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-08-053-171-16

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Patent No.

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US-09-674-716B-17 (1-348) x US-08-478-039-88 (1-112)
Best Local Similarity: 84.82%
Query Match: 80.78%
DB:
                                                                                                                                                    81 IleSerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnArglleGluPhe 100
                                                                                                                238 ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTAT 297
       61 AlaSerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLy9 80
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 88, Application US/08478039
Patent No. 5681722
GENERAL INPORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TILLE OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ...

STATE: VA

COUNTRY: USA

ZIP: 2313-1404

ZIP: 2313-1404

COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFFILIAN PARE: PATENTIN RElease #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039

FILING DATE: 07-UN-1995

CLASSIPTCATION DATA:
APPLICATION NUMBER: US 08/379,072

FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING APPLICATION NUMBER: 012/12-160

FILING APPLICATION NUMBER: 012/12-160

TELEPHONE: TOS-US-CO21

INPORMATION FOR SEQ ID NO: 88:
ENGURNE CHARACTERISTICS:
LEBETA: Amino acids

LTC. Amino acid

TELEPTON:
AMINO ACIDS

LTC. AMINO A
                                                                                                                                                                                                                                                      298 CCATTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 336
                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.85e-54
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Pred. No.:
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US-08-478-039-88
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Percent Similarity:

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Mismatches: Indels:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
FRICK APPLICATION DATA: US 07/894,061
FILING DATE: 05-UN-1992
FRILING DATE: 05-UN-1992
FRILING DATE: 05-UN-1992
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
FRILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773218ANG, Greta E.
REGISTATION NUMBER: US 07/827,689
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773218ANG, Greta E.
REGISTATION NUMBER: 35,3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/08483389
Patent No. 5811517
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32
TELECOMUNICATION: (312) 474-6300
TELEFRAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25.3856

INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 116 Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 116 amino acids
amino acid
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91.07%
84.82%
80.45%
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Best Local Similarity:
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US-08-483-389-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATTCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeulleTyrLysValSerAsnArgPhe 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazelux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods;
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 336
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-674-716B-17 (1-348) x US-08-476-349A-88 (1-112)
                                                                                                                                                                                  ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VK2 consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66, Application US/08482882
Patent No. 5773218
                                                                                               SS: not relevant
not relevant
      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
                                                             LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: not relevan
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           85e-54
                                                                                                                                                                                                                                                                                                                            500.00
91.96%
84.82%
80.78%
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Best Local Similarity:
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Pred. No.:
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181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
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                                                                                                                                                                                                                                                                                                              61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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                                                                                                                                                                                                                                                                                                                                          25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp
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Matches:
Conservative:
Mismatches:
Indels:
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181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
                                                                                                                 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
                                                                                                                                                        301 TICACGTICGGCCAAGGACCAAGGTGGAGATCAAA 336
301 TICACGTICGGCCAAGGACCAAGGTGGAGATCAAA 336
301 TICACGTICGGCAAGGACCAAGGTGGAGATCAAA 336
301 TICACGTICGGCAAGGACCAAGGTGGAGATCAAA 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, W. Michael
APPLICANT: Vacaux, Rosemay
TITLE OF INTENDICAL: Vacaux, Rosemay
TITLE OF INTENDICAL: 10 CAMPRILATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS: 118
CORRESPONDENCE ADDRESS: 118
CORRET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
CITY: United States of America
CITY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMMUTER: INP PC COMPACION:
MEDIUM TYER: Floppy disk
APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
MING APPLICATION NUMBER: US 07/894,061
FILING DATE: 27-MAY-1992
MING APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
MING APPLICATION NUMBER: US 07/894,061
FILING DATE: 27-MAY-1992
MING APPLICATION NUMBER: US 07/894,061
FILING DATE: 27-MAY-1992
MAME: SUMPRICATION NUMBER: US 07/894,061
FILING DATE: 27-MAY-1993
MAME: SUMPRICATION NUMBER: US 07/894,061
FILING DATE: 27-MAY-1993
MAME: SUMPRICATION NUMBER: US 07/894,061
FILING DATE: 27-MAY-1993
MAME: SUMPRICATION NUMBER
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Matches:
Conservative:
Mismatches:
Indels:
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84.82%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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rsvalgluileiys 116	ael ated Materials and Methods le, Gerstein, Murray & Borun 233 South Wacker Drive Bs-Dos #1.0, Version #1.25 487,113D 102,852 009,266 894,061 889,724 827,689
Db 105 TyrThrPheGlyGlnGlyThrLysValGluI	US-08-487-113D-66  US-08-487-113D-66  US-08-487-113D-66  US-08-487-113D-66  US-08-487-113D-66  US-08-487-113D  PATENT: OASEMY ROSEMAY  TITLE OF UNVENTION: ICAM-Related Mate NUMBER OF SEQUENCES: 120  CORRESPONDENCES: 120  CORRESPONDENCES: 120  CORRESPONDENCES: 120  CORRESPONDENCES: 120  CORRESPONDENCES: 120  CORRESPONDENCES: 120  STREET: 6300 Sears Tower, 233 South CITY: Chicago  STATE: 111inois  COUNTRY: United States of America 2 SOUTH STATE: 111inois  COUNTRY: DATE: 120-204/S-DOS  SOUTHARN: PPLICATION DATA: APPLICATION NUMBER: US 07/894,061  FILING DATE: 05-400-1993  RAPLICATION NUMBER: US 07/894,061  FILING DATE: 20-3040-1993  RAPLICATION NUMBER: US 07/899,724  FILING DATE: 20-3040-1993  RAPLICATION NUMBER: US 07/899,724  FILING DATE: 20-3040-1992  APPLICATION NUMBER: 35,302  RESERRENCE CHARACTERISTICS: LENGTH: 116 amino acide 170POLOGY: Innear MOLECULE TYPE: protein 105-00-007: 110-00-007: 110-00-007: 110-00-007: 110-00-007: 110-00-00-007: 110-00-007: 110-00-007: 110-00-007: 110-00-00-007: 110-00-00-007: 110-00-007: 110-00-00-007: 110-00-00-007: 110-00-007: 110-00-00-007: 110-00-00-007: 110-00-00-007: 110-00-00-00-007: 110-00-00-00-00-00-00-00-00-00-00-00-00-

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US-09-674-716B-17 (1-348) x US-08-473-503-66 (1-116)
                                       ALIGNMENT AND ALL TREMALLING.

NAME: No. 5669262and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32.78

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6448

TELEFA: 25-3856

INFORMATION FOR SEQ ID NO: 66: SEQUENCE PARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              498.00
91.07%
84.82%
80.45%
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-473-503-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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US-08-483-932-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104
                                                                                                                                                                                        1 GATATIGIGAGESCICAGICICCACTCICCCGICACCCCTGGAGGCCGGCCTCC 60
                                                                                                                                                                                                                     5 ASpIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
                                                                                                                                                                                                                                                                                                               25 IleSerCysArgSerSerGinSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
                                                                                                                                                                                                                                                                                                                                                                                                           45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeulleTyrLysValSerAsnArgPhe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66, Application US/08473503
Patent No. 5869262
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
COMMERCESPONDENCE ADDRESS:
ADDRESSEB: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZUE: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-UUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATE:
PRIOR APPLICATION NUMBER: 08/286,754
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  Matches:
Conservative:
Mismatches:
Indels:
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PRIOR DATE: 05-AUG-1994

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-AN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-UNN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
498.00
91.078
84.828
80.45$
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                        Percent Similarity:
Best Local Similarity:
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                                                                        Query Match:
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61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
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Fatent No. 5880268
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
ITILE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Geretein, Murray & Boru
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 336
Length:
Matches:
Conservative:
Mismatches:
Indels:
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241 AGCAGAGTGGAGGCTGAGGATGTTGGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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Matches:
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Mismatches:
Indels:
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              US/08/483,932
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US-08-720-420A-66
; Sequence 66, Application US/08720420A
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: ICAM-Related Materials and Methods
TITLE OF INVENTION: ICAM-Related Materials
GORGESPONDENCE: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: Gloso Sears Tower, 233 South Wacker Drive
CURY: Chicago
STRIE: Illinois
COMPUTER: PEDEPO disk
COMPUTER: PEDEPO disk
COMPUTER: PEDEPO disk
COMPUTER: O'S AUG. 1994
APPLICATION NUMBER: US 08/286,754
FILING DATE: 0'S AUG. 1993
FILING DATE: 0
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Mismatches:
Indels:
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
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91.07%
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amino acid
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Best Local Similarity:
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8.75e-54
498.00
91.07%
84.82%
                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-714-017-66
  amino acid
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Best Local Similarity:
                                                                                                        Alignment Scores:
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ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
                                                                                  121 TACCTGCAGAAGCCAGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA 180
                                                                                                                                                                  181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGAGGCACAGATTTTACACTGAAAATC 240
                                                                                                                                                                                                                                                     241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
                                                                                                                                                                                                                                                                              25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
                                                                                                               45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeulleTyrLysValSerAsnArgPhe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STRIE: Illinisis

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: C.C.

ZIP: 60606

ZIP: 60606

ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
FILING DATE:
APPLICATION NUMBER: US 08/266,754
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 25-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,689
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
APPRICATION NUMBER: 333307
                                                                                                                                                                                                                                                                                                                                                              105 TyrThrPheGlyGlnGlyThrLysValGlulleLys 116
                                                                                                                                                                                                                                                                                                                                        301 TTCACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-714-017-66
; Sequence 66, Application US/08714017
; Patent No. 6040176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
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101.01.001.-4.0-60-80

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

September 30, 2004, 08:29:27; Search time 52.926 Seconds (without alignments) 4852.647 Million cell updates/sec Run on:

US-09-674-716B-18 2405 1 gaggtgcagctggtggagtc......ccctgtctccgggtaaatga 1335 Title: Perfect score: Sequence:

BLOSUM62 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\* Database :

1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Ig gamma-1 chain C	Ig gamma-3 chain C	Ig gamma-3 chain C	Ig gamma-2 chain C	Ig gamma-4 chain C	monoclonal antibod	Ig heavy chain pre		Ig gamma-2a chain	Ig gamma-1 chain -	Ig gamma-2a chain		Ig gamma-2b chain	Ig gamma 2a chain
	QI	GHHU	A23511	A60764	G2HU	G4HU	PC4436	S22080	869339	S37483	S31459	840295	G2MS11	801321	147159
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	Query Match Length DB	330	377	377	326	327	444	470	374	469	472	446	474	475	328
dю	Query Match	73.0	67.3	67.3	6.99	65.7	65.0	60.3	59.5	59.0	58.9	58.2	9.99	56.2	52.3
	Score	1756	1619.5	1617.5	1608	1579.5	1563	1450.5	1430.5	1419	1415.5	1400.5	1361.5	1351	1259
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gamma 2b	g gamma-1 chain (	g gamma chain C	g gamma 1 chain	g gamma 3 chain	g gamma chain	g gamma-2 chain	g heavy ch	g gamma-1	g gamma-3	g gamma-1	g gamma-1 chai	g gamma-2k	g gamma-3	g gamma-3	g gamma-2a cha	c cha	g gamma-2a	g gamma-	g gamma-2a	g gamma-	g gamma-2k	g gamma 4 chain	g epsilon chai	g heavy chain pr	g heavy chain	g Y heavy c	g heavy	g gamma-1 heavy	g heavy chain (D	g heavy
	S31866	_	147158	147161	GHRB	GZGP	C30554	PS0017	G3HUWI	GIMS	GIMSM	PS0018	G3MSC	G3MSM	GZMSA	500847	PS0019	G2MSAB	GZMSAM	806611	GZMSBM	147162	388	S04845	693	B46529	A36040	4944	869131	682
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52.1	51.9	51.7	51.4	51.2	。	50.1	48.1	48.0		47.6		47.2	47.0		46.4	46.3	46.3	46.3	46.2	45.4	44.8		4.	Š	4	33.9	m	ά.	31.9	0
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## ALIGNMENTS

RESULT 1

Gramma-1 chain C region - human C; Species: Homo sapiens (man) Sapiens

A; Accession: A93433

A, Molecule type: DNA A, Molecule type: DNA A, Residues: 1-330 < ELL> A, Cross-references: EMBL: Z17370 A, Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, 2 A, Note: Lys-330 is removed after translation B, Harris, L.J. Submitted to the EMBL Data Library, October 1992 A, A, Reference number: S33904 A, A, Residues: 2-330 < HAR> A, Residues: 2-330 < HAR> A, Residues: 2-330 < HAR> A, Residues: 2-350 < HAR> A, Residues: 2-350 < HAR> A, Residues: 2-350 < HAR> A, Reference number: S33087; MUID: B3001943; PMID: 6811139

A;Accession: S33887
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Ross-references: BMBL:Z17370
B;Cumingham, B.A; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C
B;Cumingham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C
B;Cumingham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C
B;Cumingham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C
B;Cohemistry 9, 3161-3170, 1970
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Recession: B90563

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region gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGluGluTyrAsn 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 100
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          21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer
                                                                                                                                                     41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
                                                                                                                                                                                                                                                     523 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACC
                                                                                                                                                                                                                                                                                            61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 AAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCGCGGGGGCA
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Ajreference number: A91668; MUID: 77070269; PMID:826475

A/Accession: B91608

A/Accession: A91723

A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Ac
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C;Genetics:
A;Contents: annotation; disulfide bonds
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A;Accession: A23511
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A;Roseldues: 1-377 <HUC>
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A;Crose-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics: references: GB:119339; OMIM:147120
A;Crose-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
A;Introns: 98/3; Infla193
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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Mismatches:
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C;Accession: Acorda
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 255-257, 1889
A;Title: A human immunoglobulin 1889
A;Title: A human immunoglobulin 1890007613; PMID:2571587
A;Accession: Acorda
A;Reference number: Acorda
A;Residues: 1-377 cHCC
C;Superfamily: immunoglobulin C region; immunoglobulin homelogy
C;Keywords: immunoglobulin homelogy <IMM>
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GlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAla
                                                      261 ProlleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyrThr
                                                                                                                             281 LeuproProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys
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A) Composer references: GDB:119338, OMIM:147110
A) Composer references: GDB:119338, OMIM:147110
A) Map position: 1492.33-14923.33
A) Map position: 1492.33-14923.33
C) Complex: An immunoglobulin heteroterramer subunit consists of two identical light (kapp hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into land (S. Superfemily: immunoglobulin C region; immunoglobulin homology
C) Superfemily: immunoglobulin homology < MI>
F) 133-205/Domain: immunoglobulin homology < MI>
F) 133-205/Domain: immunoglobulin homology < MI>
F) 147/Disulfide bonds: interchain (to light chain) #status experimental
F) 72 - 83, 140-200, 245-304/Disulfide bonds: #status experimental
F) 102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F) 105/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                         Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a h
A;Areference number: A90752; MuID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
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A.Molecule type: protein

A.Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ', 175,'B', 177-193,'D', 195-196,'Q', 198-2

A.Note: this sequence been revised

R.Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A.Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gath A.Reference number: A93132; MUD:80114419; PMID:118920

A.Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Contents: annotation; myeloma protein Sa, disulfide bonds
A;Contents: annotation; myeloma protein Sa, disulfide bonds
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
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A; Residues: 1-19, Q', 21-57, Z', 59, 'A', 61-193, 'D', 195-325 <
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
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A; Residuce: 238-275 <4NOF>
R; Hdfmann, T; Parr, D.M.
submitted to the Atlas, March 1980
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A93906; A22809; A90752; A93132; A02148
R;Ellison, U: Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence and sequence homology of two human immunoglobulin gamma heavy chain A;Title: Linkage and sequence and sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 ProlleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyrThr 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LeumetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp
                                                                        101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               742 CICATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGACCACGAAGAC
                                                                                                                                                                                                                                                                                             ---GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                     682 GCACCTGAACTCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
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402	20	462
343 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCAAGAGCACCTCTGGG 402	1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20	403 GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 462
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gg .	21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40	A, Molecule type: DNA
δ i	TGGAACTCAGGGGCCCTGACCAGCGGCGTGCACATTCCCGGCTGTCCTACAGTCCTCA	A, Note: the sequence was R, Pink, J.R.L.; Buttery,
ДD	41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60	Blochem. J. 117, 33-47, 347, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 34-47, 3
y g	523 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCGTGGGCACCCAGCC 582	A;Reference number: A9024 A;Accession: A90249 A:Molecule type: protein
}	TACATCHICAACGTGAATCACAAGCCCAACACCAAGGAAGGTGGAAGGTGGACCC	A)Residues: 1-30;81-326 (C)Genetics:
Z qo		A, Gene: GDB:IGHG4 A, Cross-references: GDB:
ò	643 AAATCTTGTGACAAAACTCACACACCCACCGTGCCCAGCACCTGAACTCGGGGGGGCA 702	A,Map position: 14q32.33. A;Introns: 99/1; 111/1; ;
Db		C;Complex: An immunoglobi hain disulfide bonds. In
<i>λ</i> ο	703 CCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 762	C;Superiamily: immunogion; C;Keywords: duplication; F:20-85/Domain: immunogl
Db	117 ProSerValPheLeuPheProProLysProLysAspThrLeuMet11eSerArgThrPro 136	F.120-02/ Committee F.120-121/ Phinge F.134-203/ Domain immino
<i>λ</i> ο	GAGGTCACATGCGTGGTGGACGTGGACCACGAAGACCCTGAGGTCAAGTTCAACTGG	F;240-307/Domain: immunos F;14/Disulfide bonds: in
Dp	GluValThrCysValValValAspValSerHisGluAspProGluValGlnPheAsnTrp	F;27-83,141-201,247-305/1 F;106,109/Disulfide bond
δy.	TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCGGGGGAGGAGGAGGAGTGCAACAAC	F;177/Binding site: carbo
Db		Alignment Scores: Pred. No.:
oy B	883 AGCACGTACCGTGTGGTCAGCGTCCTCACCGCACCAGGACTGGCTGAATGGCAAG 942 	Score: Percent Similarity: Best Local Similarity:
ογ	943 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCC 1002	Query Match: DB:
Db		US-09-674-716B-18 (1-133
δ	1003 AAAGCCAAAAGGCACCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 1062	Oy 343 GCCTCCACCA
Db		Db 1 AlaSerThri
ζ	1063 CTGACCAAGAACCAGGTCAGCTTGACCTGGTCAAAAGCTTCTATCCCAGCGACATC 1122	Qy 403 GGCACAGCGG
Db	237 MetThriysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspile 256	Db 21 SerThrAlaA
ò	1123 GCCGTGGAGTGGGAAGAGCAATGGGCAGCGGGAGAACAACTACAAGACCACGCCTCCCGTG 1182	Qy 463 TGGAACTCAG
Db	257 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMet 276	Db 41 TrpAsnSerG
٥٧	1183 CTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 1242	Qy 523 GGACTCTACT
Db	277 LeudspSerAspGlySerPheFheLeuTyrSerLySLeuThrValdspLysSerArgTrp 296	Db 61 GlyLeuTyrs
%	1243 CAGCAGGGGAACGICTICTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAG 1302	Qy 583 TACATCTGCA
qq	297 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 316	Db 81 TyrnhrCysA
٥٨		
gg Gg	317 GlnLysSerLeuSerLeuSerProGlyLys 326	Db 101 Lys
RESULT 5 G4HU		
Iq qamma-4	-4 chain C region - human	Db 118 ProSerValP

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

2.21e-79 1579.50 93.94% 90.30% 65.68%

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GAGGICACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 822
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09-674-716B-18 (1-1335) x G4HU (1-327)
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ross-references: GDB:119340; OMIM:147130
lap position: 14q32.33-14q32.33
natrons: 99/1, 111/1; 221/1
natrons: 99/1, 111/1; 221/1
natrons: 99/1, 111/1; 221/1
n disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into lan uperfamilty: immunoglobulin C region; immunoglobulin homology
leywords: duplication; glycoprotein; hererotetramer; immunoglobulin
0-95/Domain: immunoglobulin homology <IMI> olecule type: DNA
estiduces: 1-32 FELL3
cesiduces: 1-32 FELL3
ces: the sequence was determined from the germline gene
ink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
chem, J. 117, 33-47, 1970
itle: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant re
eference number: A90249; MUID:70207560; PMID:4192699 34-203/Domain: immunoglobulin homology <IM2>
40-307/Domain: immunoglobulin homology <IM3>
40-307/Domain: immunoglobulin homology <IM3>
4/Disulfide bonds: interchain (to light chain) #status experimental
783,141-201,247-305/Disulfide bonds: #status predicted
66,109/Disulfide bonds: interchain (to heavy chain) #status experimental
77/Binding site: carbohydrate (Asn) (covalent) #status predicted olecule type: protein esidues: 1-30;81-326 <PIN> cession: A90249 ene: GDB:IGHG4

AAATCTTGTGACAAAACTCACACATGCCCACCTGCCCAGCACCTGAACTCGCGGGGGCA 702 TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGGCTGTCCTACAGTCCTCA 343 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGG 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 523 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACC TACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGAGGACAAGAAAGTGGAGCCC 703 CCGTCAGTCTTCCTCCTCCCCCAAAACCCCAAAGGACACCCTCATGATCTCCCGGACCCCT 103 GGCACAGCGGCCCTGGCTTGGTCAAGGACTACTTCCCCGGAACCGGTGACGGTGTCG

462

522

9

40

582

80

642

137

191 CATTATOCCGACTOTOTOMAGGGAAATCACCATOTOMGAGATCATOCATOTOMAGACTOTOMAGGGGAAATCACCATOTOMGAGATCATOTOMAGGGGAAATCACCATOTOMGAGGGAAATCACCATOTOMGAGGGAAATCACCATOMGAGGGAAATCACCATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGGAAATCACATOMGAGGAAAACCAGGAAAACCAGGAAAACCAGGAAAACCAGGAAAACCAGGAAAAACCAGGAAAAACCAGGAAAAACCAGGAAAAACCAGGAAAAAA	333
6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B	8 8 8 8 8 8
### AGACGTACCATGGTACCATCACCATCACCACCACCACCACCACCACACACCAC	Jabs:   Jabs:   Jabs:   Jabs:   Jabs:   Jagus:   Jagus:

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1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGTGGACAAGAGCAGGTGGCAGGAGGAACGTCTTCTCATGCTCGTGATGCATGAG 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 ValargThrileSerArgThriysGlyProAlaArgGluProGlnValTyrValLeuAla 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413
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        217 SerGly---GlnThrPheThrCysAsnValAlaHisProAlaSerSerThrLysValAsp
                                                                                                                                                                                                                                                                                                                                           AAGAAAGTGGAAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCAGCACCT
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                                                                                                                                                                                                                                                                              568 ITGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
                                                                             AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTTGGTCAAGGACTACTTCCCCGAA
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8220B1 7
8220B1 7
8220B2 19 heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
NiAlternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos Pirinigenius tauturus (cattle)
C:Date: 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; Ā31303
R;Sanders, P.G.
Sanders, P.G.
Sanders, P.G.
Sanders, P.G.
A;Recence number: S22080
A;Residues: 1-470 <-SAN
A;Residues:
1237 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1296
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                                                             TACACGCAGAAGAGCCTCTCCCTGTCCCGGGTAAA 1332
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Indels:
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60.31%
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Best Local Similarity:
Query Match:
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142	25 25 27 27 11 11 11 11	279 ProproserargoludluMetThriysAsnGlnValSerLeuThrCysLeuV 1105 TTCTATCCCAGCACACCGTGAGAGAGAGAGAGAGAGAGAG	Oy 1285 CTGCACACCACCACCACGAGAGAGCTCTCCCTGTCTCGGGTAAA 1332  Db 359 LeuhisAsnHisTyThrClnLysSerLeuSerProdlyLys 374  RESULT 9 S37483 IQ gamma-2a chain - mcuse C;Becies: Was musculus (house mcuse) C;Accesion: S37483 R;Ducancel, F:F.D. submitted to the EMBL Data Library, February 1993 A;Accession: 837483 A;Accession: 837483 A;Accession: 837483	A,Status: preliminary A,Status: preliminary A,Molecule type: mRNA A,Molecule: 1-469 < DUC> A,Molecule: 1-469 < DUC> A,Gtoss-references: BMBL:X70423, NID:g406252, PIDN:CAA49868.1; PID:g406253 C,Superfamily: immunoglobulin C region; immunoglobulin homology C,Keywords: immunoglobulin homology <imm> Alignment Scores: 1.3e-70 Length: 469 Pred. No.: 1419.00 Matches: 269 Bercent Similarity: 74.45% Conservative: 69 Best Local Similarity: 59.25% Mismatches: 102</imm>
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 C;Accession: S6339; S72664 R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M. Bur. J. Biochem. 229, 54-60, 1995 A;Tile: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MUID:95262687; PMID:7744049 A;Reference number: S69339; MUID:95262687; PMID:7744049 A;Redension: S69339 A;Redension: Preliminary A;Rocoss-references: EMBL:X81695 A;Redension: S72664 A;Reference number: S72664 A;Reference number: S72664 A;Resfeus: preliminary A;Molecule type: mRNA A;Residues: 1-140, CC,142-374 < XH2> A;Residues: 1-140, CC,142-374 < XH2> A;Residues: 1-140, CC,142-374 < XH2> A;Cross-references: EMBL:X81695 C;Superfamily: immunoglobulin C region; immunoglobulin homology	, E	Oy 1 GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Oy 235 TCTAGACTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGT 294 :::::::	142

	RESULT 10 \$31459 Ig gamma-1 chain - sheep (fragment) Ig gamma-1 chain - sheep (fragment) C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999 C;Accession: S31459 R;Patri, S.; Nau, F. submitted to the EMBi Data Library, December 1992 A;Reference number: S31459 A;Recession: S31459 A;Recession: S31459 A;Ression: S1459 A;Ression: S1459 A;Ression: S21459 C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Reywords: immunoglobulin F;277-346/Domain: immunoglobulin homology <imm></imm>	## Alignment Scores:    Alignment Scores
Query Match:         59.00\$         Indels:         14           DB:         2         Gaps:         6           US-09-674-716B-18         (1-1335) x 837483 (1-469)         0y         1 GAGGTGCAGCTGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC         60           COMMINICATION OF CONTRACT TO A CO	Oy  118 AlaMetGlyAlaThrAlaThrCaTAGACTGGGGCCAGGGAACACTAGTCACCGTC 336  118 AlaMetGlyAlaThrAlaThrLeuLeuAspTyrTrpGlyGlnGlyThrThrLeuThrVal 137  Oy  337 TCCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 396  138 SerSerAlaLySThrThrAlaProSerValTyrFroLeuAlaProValCysGlyAspThr 157  Oy  397 TCTGGGGGCACAGCGGCTGGGCTGCTCAAGACACTACTCCCCGAACCGGTGACG  158 ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr 177  Oy  457 GTGTGGTGGAACTCAGGCGCCTGACCAGCGCTGACCACTTCCCGGCTGTCCTACAG 516  178 LeuThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGln 197  Oy  517 TCCTCAGGACTCTAAGTCCCTCAGGGGGTGACCTTCCGAGCACTTGGGCACC 576	

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\$ A	RESULT 10 \$31459 Ig gamma-1 chain - sheep (fr C;Species: Ovis orientalis a C;Date: 13-Jan-1995 #sequenc C;Accession: \$3145 P:Detri G Nan F	R S C C C C C C C C C C C C C C C C C C	Ali Pre Sco Per Der DB:	US-09	ò	do o	상 음	ò	ΩD	8 8	ò	qq	8

RESULT 11 S40295 IG Gamma-2a chain (mAb735) - mouse C;Species: Mus musculus (house mouse) C;Date: O'-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999 C;Accession: 540295 R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bitt submittee to the EMBL Data Library, January 1993 A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against A;Accession: \$40295 A;Accession: \$40295 A;Molecule type: Protein A;Residues: 1-446 cKLE>	C;Genetics: A;Map position: 12 S;Superfamily: immunoglobulin C region; immunoglobulin homology C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid F;1-446/Product: 1g gamma-2a chain #status experimental <mat> F;1-446/Promain: V-D-J region <vnj> F;118-446/Domain: C region <chr> F;118-214/Domain: C region <chr> F;215-233/Region: hinge</chr></chr></vnj></mat>	F:341-446/Domain: Oz region <ch3> F:341-446/Domain: Oz region <ch3> F:360-427/Domain: Oz region <ch3> F:360-427/Domain: immunoglobulin homology <imm> F:31/Modified site: pyrrolldone earboxylic acid (Gln) #status experimental F:22-96.144-199.261-321,367-425/Disulfide bonds: #status predicted F:122/Disulfide bonds: interchain (to light chain) #status predicted F:224,227,229/Disulfide bonds: interchain #status predicted F:227/Binding site: carbohydrate (Asn) (covalent) #status experimental</imm></ch3></ch3></ch3>	Alignment Scores: 1.35e-69 Length: 446 Score: 1400.50 Matches: 267 Score: 1400.50 Matches: 267 Score: 3.38\$ Conservative: 67 Best Local Similarity: 59.07\$ Mismatches: 103 Query Match: 2 103 Best Local Similarity: 59.23\$ Indels: 6 US-09-674-716B-18 (1-1335) x \$40295 (1-446)	Oy 1 GAGGTGCAGCTGGAGACTCTGGGGGGGGGTCCCGGGGGGTCCCTTAGACTC 60 :::::	Oy 61 TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCGCCAGGCT 120	Qy 181 CATTATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  bb 59 LysfyrAsnGluLysPheLysGlyLysAlaThrLeuThrValAspThrSerSerThr 78  Qy 241 CTGTATCTGCAAATGAACAGCCTGAAAACGGGGACACAGCCGTGTTACTGTACA 297	298	Qy 340 TCAGCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCT 399	9y 400 GGGGGCACAGGGCCTCGGGCTGCTCAAGGACTACTTCCCGAACGGTGAGGG 459
S ValAspTyrAspSerSerHisAlaPheAlaTyrAlaSerTyrAspPheTrpGly 6 CAGGGAACACTAGTCACCGTCTCCACCAAGGGCCCATGGGTCTTCCCCCTG	496 ACCTTCCCGGCTGTCCTAAGTCCTCAGGACTCTACTCCCTCAGCAGGTGCTGACCGTG 555	233 ThriysValaspLysArgValGluProGlyCysProAspProCysLysHisCyl. 676 IGCCCAGCACCTCGCGGGGGGCCCTCACTCTCCTCCTCCCCCCAAACCCAAG 251 252 CysProProProGluLeuProGlyGlyProSerValPhellePheProProLysProLys 271 736 GACACCTCATGATCTCCCGGACCCTGAGGTCATGGTGGTGGTGGTGGTGGTCAC 795 11111   11111   111111   1111111   111111		916 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC 975 	976 CCAGCCCCATCGAGAAACCATCTCCAAAGGGAGCCGCGGAGACCACAGGTG 1035	1096 GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGGAGAGCAATGGGCAGCGG 1152  392 ValThrGlyPheTyrProAspTyrIleAlaValGluTrpGluLysAsnGlyGlnProGlu 411  1153GAGAACAACTACAAGACCACGCCTCCGTGCTGGACTCCGAGGCTCCTTCTTCCTC 1209  412 GarGluAntroCttClyThrThrAntroCorgon 1	o paccacacacacacacacacacacacacacacacacaca	1270 GTGATGCATGAGGCTCTGCACAACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1329	1330 AAA 1332 
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994 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 1053 1054 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTCAAAGGCTTCTATCCC 1113 1114 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCCAGCCGGAGAACAACTACAAGACCACG 1173 1174 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGCTCACCGTGGACAAG 1233 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 1293 GlubrovalLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuAsgValGlubys 414 177 Asp---LeuTyrThrLeuSerSerSerValThrValThrSerSerThrTrpProSerGln 195 LeuGlyGlyProSerValPhellePheProProLys1leLysAspValLeuMetlleSer 254 294 AspTyrAsnSerThrLeuArgValValSerAlaLeuProlleGlnHisGlnAspTrpMet 314 ThrileSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProPro 354 | GluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetPro 374 375 GluaspileTyrvalGluTrpThrasnasnGlyLysThrGluLeuAsnTyrLysAsnThr 394 LysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsn 434 639 215 693 234 753 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 813 TTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 873 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 933 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAAAAAGCCCTCCCAGCCCCATCGAGAAA 993 GlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrLeu 156 ::: SerileThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGlu CCCAAATCTTGTGACAAAACTCACACATGCCCACCG-----TGCCCAGCACCTGAACTC |||:: | ProArgGly---ProThrIleLysProCysProProCysLysCysProAlaProAsnLeu TCGTGGAACTCAGGGCCCTGACCAGCGGCGTGCACACTTCCCGGCTGTCCTACAGTCC 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGTGGAG 694 GCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1329 315 335 395 415 580 640 235 295 355 460 196 216 255 814 934 435 275 g g g g Пр à g ò g Š ò d ò g g δ g g . d ŏ ò ò ò ò ò ठे ò ò

RESULT 12 (22MS11)

GZMS11

GZMS11

GZMS12

GJMS12

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A, Molecule type: mRNA
A, Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A, Rolecule type: mRNA
A, Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A, Note: Lye-474 is probably removed posttranslationally
R, Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A, Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglot A, Reference number: A26232, MUID:80081502; PMID:117849
A, Accession: A26232
A, Molecule type: DNA
A, Residues: 138-172, 'P', 174-189, 'FP', 193-376,'T', 378-474 <TU2>
R, Ollo, R.; Rougeon, F.
R, Rougeon, P.
Nature 206, 761-763, 1982
A, Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm;
A, Reference number: A26233; MUID:82173203; PMID:6803173
A, Contents: b allele
A, Accession: A26233
A, Molecule type: DNA
A, Residues: 138-161, L', 163-189,'FP', 193-300,'R', 302-331,'A', 333-437,'DI', 440-474 <OLL>
A, Cross-references: GB:J00461
B, K: Masuda, R: Masuda, R: Masuda, C: Yamamoto, K:; Irimura, T:; Takahashi
B, Molecule Chem. 269, 12345-12350, 1994
A, Title: O-Glycosylation in hinge region of mouse immunoglobulin G2b.
A, Accession: A2632 the murine gamma2b heav A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1474 < FRZ
A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
B;Yamawaki-Katacka, Y.; Katacka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cl
A;Reference number: A02157; MUID:80120716; PMID:676534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161, L',163-189, FP',193-474 < YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Title: Structure of the constant and 3' untranslated regions of the murine
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Accession: A26235;
A;Accession: A26236;
A;Accession: A26236;
A;Accession: A26236;
A;Accession: A26236;
A Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.83e-67 1361.50 71.33% 56.67% 56.61% Percent Similarity: Best Local Similarity: A;Accession: A53598 A;Status: preliminary Query Match:

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gamma2b chain gene cloned from

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(1-474) $(1-1335) \times G2MS11$ 

specific

	GGGGGGCCCTTAGACTC 60 [GJALaSerVallysleu 39 TCCTGGGTCCGCCAGGCT 120 SerTrpVallysGlnArg 59 TCTGATAATTATGCAACA 180 [          :::    GATGATTCAAAATCTAGA 240
Db 378 LeuProProchagGacArgGycGacArgGycGacAcArgCysLeuValval Db 378 LeuProProchagGacArgCyGGGACArgCysLeuValval Db 398 GlyPheAsnProChyApileSerValGluTpThrSerArgGyBrandCysLeuValcul Db 398 GlyPheAsnProChyApileSerValGluTpThrSerAsnGlyHisThrGluGluAsn Oy 1162 TACAGACCACCTCCGGACGCACCACCCCCACACACCTC Db 418 TyrLySAspThrAlaProValLeuAspSerAspGlySerTyrPhelleTyrSerLysLeu Oy 1222 ACCGTGGACACACGCACGACGCACACACCTCCTCTCATCCTCTCTCT	1351.00   Matches: 260   1351.00   Conservative: 70   Matches: 10   100   Conservative: 70   Marches: 111   100   Marches: 110   100   Marches: 110   Marches: 110
Db 378 LeuProProProAl  Oy 1102 GGCTTCTATCCCAC  Oy 1162 TACAAGACCACGC  Oy 1162 TACAAGACCACGC  Oy 1222 ACCGTGGACAAGAC  OY 1222 ACCGTGGACAAGAC  OY 1282 GCTCTGCACAAGAC  OY 1282 ACCGTGACAAGAC  OY 1282 GCTCTGCACAAGAC  OY 1282 GCTCTGCACACAC  OY 1282 GCTCTGCACACACAC  OY 1282 GCTCTGCACACACAC  OY 1282 GCTCTGCACACACAC  OY 1282 GCTCTGCACACACACACACACACACACACACACACACACA	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Dusry Match: US-09-674-716B-18 (1- QY 1 GAGGGG QY 1 GAGGGG QY 61 TCCTGGG QY 61 TCCTGGG QY 121 CCAGGGA QY 241 CATTATG QY 241 CTTATG QY 241 CTTATG QY 298
GAGGTGCAGCTGGTGGAGGTGGGGGAGGCTTGGTAAAGCCCGGGGGGTCCTTAGACTC GIUValGinLeuGlnGinSerGlyProGluLeuValAsnProGlyAlaSerValLysMet 39 TCCTGTGCAGCTAGCGGATTCACTTCAGTGGTAGTCTGGATGTCTGGGTCGCCCAGGCT 120	TACATCTGCAACGTGAATCACAAGCCCAACAACACCAAGGTGAACAAGAAGGGGGCCC 642
1 GAGGTGCAGCTGGAGTCTGGGAGTCTGGGGAGG 20 GluValGlnLeuGlnGlnSerGlyProGl 40 SerCysLysAlaSerGlyTyThrPhell 121 CCAGGGAAGGGGTCGAGTGGTTGCTGAGGGAAGTGTTGATTCAGTTCAGTGTGAGGGTTGCTGAGGGAATTCAGTTCAGTGTGAGGGGTTGCTGAGGGTTGCTGAGGGTTGCTGAAGGGAATTCAGTGAGTG	583 TACATCTGCAACGTGAATCACAAGCCCAAGCCCAACC 218 ValThrCysSerValalaHisProalaSe 643 AAATCTTGTGACAAACTCACACATC 238 SerGlyProlleSerThrlleAsnProby 682 GCACCTGAACTCGCGGGGGACCTCAGT 258 AlaProAsnLeuGluGlyGlyProSerVa 742 CTCATGATCTCCCGGACCCCTGAGTCACT 278 LeumetileSerLeuThrProLysValTh 802 CCTGAGGTCAAGTTCAACTGGTACGTGAGTCACT 278 ProAspValGln1leSerTrpPheValAs 862 CCGCGGGGGGCACCGTGGAGTCACACTGGTACGTGAGTCACTGGTACGTGAGTCACTGGTACGTGAGTCACTGGTACGTGAGTCACTGGTACACTGGTACACGGAGGAGCACGTACACGGAGGAGCACGTACACGGAGGAGCACGTACACGGAGGAGAGAGA

the cDNA sequences of a si

71- 71ne 745;	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-328 <kac> A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124 C;Genetics:</kac>	A;Gene: IgG2a C;Superfamily: immunoglobulin C region; immunoglobulin homology F;133-202/Domain: immunoglobulin homology <imm></imm>	Scores: 7.96e-62 Length: 1259.00 Marches: imilarity: 82.83% Conservati	Local Similarity: 70.18% Mishauches: Match: 2 2.35% Indels: C22 71(5) 10 (1 1305) v 1/2160 (1 200)	343 GCTCACCAAGGGCCCATCGGTC	ATACTORYSOLIFATERS TO SELECT A TROUGHAST TO SECRET SERVICES AS A GOCACOGG CONTROL OF SERVICES AND A SECRET S	463 TGGAACTCAGGGGCCCTGACCAGGGGGGGGGCCTTCCCGGCTGTCCTACAGTCCTCA FILL	523	583 TACATCTGCAACGTGAATCACAACACGCAACACCAAGAGGTGACAAGAAAAGTGGAAGCCC  [	643 AAATCTTGTGACAAAACTCACAAGCCCAGCCCAGCAGCACCTGACCTGGGGGGGA  [	101 Dysim:	763 GAGTICACATIGGGTGGTGGACGTGAGCCACAAGACCTGAGGTCAAGTTCAACTGG :::	823 TACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAC	883 AGCACGTACCGTCGTCAGCGTCCTCACCGTCCTGCACCAGACTGGCTGAATGGCAAG	943 GAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCATGAGAAAACCATCCC	1003 AAAGCCAAAGGGCAGCCCCAAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAG 110
337 TCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC    :::	<pre>rrSerValThrLeuGlyCysLeuValLysGlyTyrPhe! GAACTCAGGCGCCTGACCAGCGGCGTGCACACCTTCC  </pre>	517 TCCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCCACC	577 CAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACCACCAAGGACGACAAGGAAGTG 63 217 CInThrValThrCysSerValAlaHisProAlaSerSerThrThrValAspLysLysLeu 23	Qy 637 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCG	Oy 676 IGCCCAGCACCTGAACTCGCGGGGCCACCGTCAGTCTTCCTTC	OY 736 GACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC 795	Oy 796 GAAGACCCTGAGGTCAACTTCAACTGGTACGGGGGGGGGG	Oy 856 ACAAAGCCGCGGGAGGAGCAGTACAACAGCGTCGTGGTCAGCGTCCTCACCGTC 915	OY 916 CTGCACCAGACTGGCTGAATGGCAAGAGTACAAGGTCTCCAACAAAGCCCTC 975	OY 976 CCAGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTG 1035	OY 1036 TACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACTGCTG 1095	Oy . 1096 GTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGTGGGAAAGCAATGGCCAGGGG 1155  Db 397 AlavalGlyPheSerPxoGluAspileSerValGluTrpThrSerAsnGlyHisThrGlu 416	Oy 1156 AACAACTACAAGACCACGCCTCCCGAGCTCCGACGCCTCCTTCTTCTTCCTCTACAGC 1215	Oy 1216 AAGCTCACCGTGGACAAGAGCAGGTGGCAACAGGGGAACGTCTTCTCATGCTCCGTGATG 1275                 :::	Oy 1276 CAIGAGGCTCIGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAA 1332	RESULT 14 147159 Ig gamma 2a chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig)

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1002
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|101 LysThr------LysProProCysProlleCysProAlaCysGluSerProGly---
                                                                                                                                                                                                                                                           GAGTACAAGTGCAAGGCTCCCAACAAGCCCTCCCAGCCCCCCATCGAGAAAACCATCTCC
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                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                        .674-716B-18 (1-1335) x 147159 (1-328)
7.96e-62
1259.00
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70.18%
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            nt Similarity:
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Match:
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217 LysAlaLysGlyGlnThrArgGluProGlnValTyrThrLeuProProHisAlaGluGlu 236
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                                                                                                                                                                                                                                              197 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProlleThrArglleIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 ProGlnGlnAspValAspGlyThrTyrPheLeuTyrSerLysPheSerValAspLysAla
                                                                   117 ProSerValPheIlePheProProLysProLysAspThrLeuMet11eSerArgThrPro
                                                                                                                                                                                                                                                                                                           883 AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACGACTGGCTGAATGGCAAG
                                                                                                                                                                                                                                                                                                                                         177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuAsnGlyLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 LeuSerArgSerLysValSerIleThrCysLeuVallleGlyPheTyrProProAspile
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101 LysThr----LysProProCysProIleCysProAlaCysGluSerProGly---
                                          703 CCGTCAGTCTTCCTCCTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCT
                                                                                                                                763 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1003 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG
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R; Kacskovics, I.; Sun, J; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences A; Reference number: 147158; MUID:95015845; PMID:7930579
A; Accession: 147160
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mANA
A; Residues: 1-328 < KAC>
                                                                                                                                                                                                                                                                                      1237 AGGIGGCAGCAGGGAACGICTTCTCATGCTCCGIGATGCATGAGGCTCTGCACACAC 1296
                                                                                                                                                                                               1177 CCCGTGCTGGACTCCGACGCCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1236
                                                 237 LeuSerArgSerLysValSerIleThrCysLeuVallleGlyPheTyrProProAsplle 256
                                                                                                                                     257 AspValGluTrpGlnArgAsnGlyGlnProGluProGluGlyAsnTyrArgThrThrPro 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma 2b chain constant region - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                             ProGlnGlnAspValAspGlyThrTyrPheLeuTyrSerLysPheSerValAspLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTACCAAGAGCACCTCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

RESULT 1	GC1 HUMAN  10 GC1 HUMAN  AC COL HUMAN  AC PO1857,  DT 21-JUL-1986 (Rel. 01, Last sequence update)  DT 1-JUL-1986 (Rel. 01, Last sequence update)  DT 15-MAR-2004 (Rel. 43, Last annotation update)  DE 19 gamma-1 chain C region.  GN HOMO sapiens (Human).  CO ENKaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  CO Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NOBI TAXID-5606;	RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=82274238; PubMed=6287432; RA Ellison J.W., Berson B.J., Hood L.E.; RT "The nucleotide sequence of a human immunoglobulin C gammal gene."; RL Nucleic Acids Res. 10:4071-4079 [1982).	RN 121 RX MEDLINE71064024; Publed=5489771;		RN 131 RN SEQUENCE OF 136-329 (EU). RX MEDLINE=71064025; PubMed=5530842; RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., RA Edelman G.M.; RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; RL Biochemistry 9:3171-3181(1970).	KN 141 RN SEQUENCE (MYELOMA PROTEIN NIE). RX MEDLINE=77070269; PubMed=826475; RA Ponetingl H., Hischmann N.; RT "The rule of antibody structure. The primary structure of a RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The RT chymotryptic peptides of the H-chain, alignment of the tryptic
ברמנידת ברומנ אם מפשיים ברומנידים בר	Command line parameters:  MODEL=frame+ n.2P; model - DEV=x1p -Q-(cgn2 1/05FO 2P) - DEV=x1p -Q-(c	Database: SwissProt_42:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES \$ Query	Score Match Length DB ID  17.6 73.0 330 1 GCL HUMAN P01859 16.8 66.9 326 1 GC2 HUMAN P01859 1579.5 65.7 327 1 GC4_HUMAN P01861	50.7 323 1 GC_RABIT P01870 55.1 329 1 GCZ_CAVPO P01862 48.0 290 1 GCZ_HUMAN P01866 47.6 324 1 GCI_MOUSE P01866 47.4 333 1 GCIM MOUSE P01868 47.0 329 1 GCS_MAT P01869 47.0 329 1 GCS_MOUSE P01869	1119 46.5 398 1 1114.5 46.4 320 1 1114.5 46.3 322 1 1112.5 46.3 322 1 1112.5 46.3 335 1 1083 45.0 336 1

us-09-674-716b-18.rsp

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REMOVED POST-TRANSLATIONALLY.

K -> R (IN GIM(3) MARKER).

/FTIG=VAR 003886.

D -> E (IN GIM(NON-1) MARKER).

/FTIG=VAR 003887.

L -> M (IN GIM(NON-1) MARKER).

/FTIG=VAR 003888.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-dc1.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00047; ig; 3.
SWART; SN00407; IGc1; 2.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 Delsenhofer J.;

Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus are 2.9- and 2.8-A resolution.";

Biochemistry 20:2361-2370(1981).

-! MISCELLANBOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the GIM(3) marker and the GIM (1001-1) markers.

-! MISCELLANBOUS: Nie also differs in the amidation states of 15, 116, 129, 269 and 272.

-! MISCELLANBOUS: EU also differs in the amidation states of residues 155, 116, 177, 195, 198, 269, and 272 and in the order of residues
                                                                                                                                                                                                                         MEDINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
1961 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                 SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE=8328911; PubMed=6884994;
MEDLINE=83289111; PubMed=6884994;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268-272.
-!- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
                                                                                                                                    MEDLINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
 peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew, HGNC:5525, IGHG1.
MIM; 147100; -.
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
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PDB; 1FC2; 15-UUL-92.
PDB; 1FC2; 15-UUL-92.
PDB; 1D5B; 09-FEB-00.
PDB; 1D5B; 09-FEB-00.
PDB; 1D5B; 09-FEB-00.
PDB; 1D8C; 17-MAX-00.
PDB; 1E4K; 06-UUN-01.
PDB; 1E4K; 06-UUN-02.
PDB; 1HZH; 12-UUN-92.
PDB; 1HZH; 12-UUN-92.
PDB; 1HZH; 12-UUN-92.
PDB; 1HZH; 12-UUN-92.
PDB; 1HZH; 16-MAX-01.
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PDB; 111X; 16-MAY-01.
PDB; 116X; 10-APR-02.
PDB; 2RCS; 12-NOV-97.
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SEQUENCE OF 2-326 FROM N.A.
MEDLINE=82197621; PubMed=6804948;
Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                    TISSUE=Fetal liver;
MEDIINE=83001943; PubMed=6811139;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo 'Structure of human immunoglobulin gamma genes: implications evolution of a gene family.";
Cell 29:671-679(1982).
                                                                                                                                                                                                                SEQUENCE OF 99-177 AND 310-326 FROM
                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                           SEQUENCE OF 88-115 FROM N.A.
                 Ig gamma-2 chain C region.
IGHG2.
                                                              NCBI_TaxID=9606;
                                    Homo sapiens
21-JUL-1986
16-OCT-2001
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N.A.

Craniata, Vertebrata, Buteleostomi, Catarrhini, Hominidae, Homo.

(Rel. 01, Last sequence update) (Rel. 40, Last annotation update)

(Human)

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gamma
TISSUE=Fetal liver, MEDLINE=84235992; PubMed=6329676; Krawinkel U., Rabbitts T.H.; Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                               [5] SEQUENCE OF 1-85 AND 132-325 (MYELOWA PROTEIN ZIE).

SEQUENCE 90001557; Pubmed-113060;
Connell G.E., Parr D.M., Hofmann T.;
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GC2 HUMAN STANDARD; P01859; 21-JUL-1986 (Rel. 01, Created)

RESULT 2 GC2\_HUMAN ID\_\_\_GC2\_HT AC\_\_\_P01859 DT\_\_\_\_21-JUJ

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Catarrhini, Hominidae, Homo.
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"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Conservative:
Mismatches:
Indels:

        Immunoglobulin domain;
        Immunoglobulin C region.

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        219
        CH2.

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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; 1g-like.
InterPro; IPR007110; 1g-like.
InterPro; IPR003006; 1g_MHC.
Pfam; PF00047; 1g; 3.
SWART; SW00407; 1Gc1; 2.
PROSTIE; PS00295; 1G_MHC; 2.
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HSSP; P01857; 1FC1.
Genew; HGNC:5526; IGHG2.
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326 AA;
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                MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the
Constant region of a gama 4 chain.";
Biochem. J. 117:33-47(1970).
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PIR, A90933; G4HU.

PIR, A90933; G4HU.

PIR, A90933; G4HU.

BR Genew, HGNC:528; IGHG4.

MIM, 14130; ...

BR GO; GO:0003624; C:membrane fraction; NAS.

BR GO; GO:0003829; F:antigen binding; TAS.

BR GO; GO:0003829; F:antigen binding; TAS.

BR GO; GO:0003829; F:antigen binding; TAS.

BR GO; GO:0003829; Ig_MHC.

BR InterPro; IPR003006; Ig_MHC.

BR FEAM; PP00047; ig; 3.

BRART; PS00290; IG_MHC.

BROSITE; PS00290; IG_MHC; 2.

FROMITE; PS00290; IG_MHC; 2.

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Bernstein K.B., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
F-I haplotype.";
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P01870;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
IG gamma chain C region.
IG gamma chain C region.
Evytolagus cuniculus (Rabbit).
Evikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE-76135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of
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                                                                     SEGUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed=6193512;
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"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCCANDING TAXON, Ref.1 sequence has the D12 allotypic marker, 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15 markers and Ref.5 the E15 marker.
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
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MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the FG section of the heavy chain of rabbit immunoqlobulin G.";
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InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig_c1.
InterPro; IPR003306; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IG_Like.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Repeat.
NON TER 6 96 IG_LIKE; 1.
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V -> VE (IN REF. 3 AND 4).
V -> D (IN REF. 3 AND 5).
V -> D (IN REF. 5).
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Conservative:
Mismatches:
  immunoglobulin G of different allotype.";
slochem. J. 151:337-349(1975).
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B. Oliveira B., Lamm M.E.;

A. Oliveira B., Lamm M.E.;

B. Oliveira B., Lamm M.E.;

C. '- MISCELLANEOUS: This chain was isolated from pooled serum of strain

13 inbred guinea pigs.

B. PR.; A94553; G2GP.

B. Risp.; PRO030710; Ig-like.

B. InterPro; IPR003106; Ig_MHC.

B. InterPro; IPR00306; Ig_MHC.

B. Rosite; PS0083; IG_Like;

B. Rosite; PS0083; IG_Like; 3.

B. Rosite; PS00830; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

T. DISULFID 16 105 105 INTERCHAIN (WITH A LIGHT CHAIN).

B. DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
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the carboxyl-terminal
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MEDLINE=75036073; PubMed=4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2 antibodies.";
Biochemistry 13:4804-4811(1974).
                                21-JUL 1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-2 chain C region.
16 Gavia porcellus (Ginea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                      SEQUENCE OF 4-68.

MEDLINE-17058471; PubMed=5538606;

Birshtein B.K., Hussain Q.Z., Cebra J.J.;

Birshtein B.K., Hussain Q.Z., Cebra J.J.;

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Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig
antibodies.";
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MEDLINE=71058486; PubMed=5538616;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea jimmunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
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Submitted (APR-1975) to the PIR data bank.
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MEDLINE=71058474; PubMed=4922544;
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79 ------CysAsnValAlaHiSProAlaSerSerThrLysValAspLysThrValGlu
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Matches:
Conservative:
Mismatches:
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36074 MW;
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1205.50
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1177 CCCGTGCTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1236
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MEDDINE-SA102184; Pubmed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin B.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
1G gamma-3 chain C region (Heavy chain disease protein) (HDC)
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296 AsplysSeralaTrpAspGlnGlyThrValTyrThrCysSerValMetHisGluAlaLeu 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-89232738; PubMed=3149946;
Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UTL-1999 (Rel. 13, Last annotation update)
IG gamma-1 chain C region.
Rattus norvegicus (Rat).
Elwaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  # HSEP; PO1842; 7PNS.

# HSEP; PO1842; 7PNS.

# InterPro; IPR007110; Ig-like.

# InterPro; IPR003397; Ig_c1.

# InterPro; IPR00347; Ig_n.

# PROMITE: PS00407; IGc1; 2.

# PROSITE: PS00290; IG MHC; 1.

# PROSITE: PS00290; IG MHC; 1.

# RMMunoglobulin domain; Immunoglobulin C region; Glycoprotein.

# NON TER 1 1 7 CH1.

# DOMAIN 1 98 112 HINGE.
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013BAB45EF49B9DA CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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HINGE.
CH2.
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63.25%
47.98%
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PIR; PS0017; PS0017.
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106
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NCBI TaxID=10116;
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Best Local Similarity:
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P20759;
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H SSP; P01857; IFC1.

Genew; HGNC:5277; ICHG3.

R GO; GO:0005624; C:membrane fraction, NAS.

GO; GO:0003823; F:antigen binding; TAS.

GO; GO:0003825; F:antigen binding; TAS.

R GO; GO:0005925; P:antigen binding; TAS.

R GO; GO:0005925; P:antigen binding; TAS.

R GO; GO:0006955; P:antigen binding; TAS.

R GO; GO:0006957; IG_C1.

R InterPro; IPR00310; Ig_C1.

R FAMAT; SW00407; IG_2.

R FROSITE; PS00397; IG_LKE; 2.

R PROSITE; PS00290; IG_MHC; 1.

R PREDAIN (W Pyrrolidone carbox/lic acid, HINGE.

T DOMAIN (12 183 CH2.

T DOMAIN (14 289 CH3.

T REPEAT (29 43 CH3.

T REPEAT (39 73 PYRROLIDONE CARBOXYLIC ACID.

T MOD_RES (17 PROSITE) PS00290; IG_MHC; 1.

R REPEAT (39 73 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- MISCELLANBOUS: Disease protein WIS is lacking most of the V region and all of the CH1 region.
-I- MISCELLANBOUS: Disease protein ZUC lack most of the V region, all of the CH1 region, and part of the hinge compared with normal gamma-3 heavy chains.
-I- MISCELLANBOUS: Disease protein OWM may represent an allelic form or another gamma chain subclass.
-I- MISCELLANBOUS: The hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical 15-residue segments preceded by a similar 17-residue segment (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82247835, PubMed=6808505,
Alexander A., Steinmerz M., Barritault D., Frangione B.,
Alexander A., Steinmerz M., Barritault D., Frangione B.,
Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model.",
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982)
-!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
interchain disulfide bond at position 7 in addition to the 11
normally present in the hinge region.
-!- MISCELLANBOUS: The sequence of residues 42-76 was taken from the
Ref.2.
Ref.2.
                                                                      REVISIONS TO 12-97 (PROTEIN WIS).
MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin B.C.;
Wrimary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
MEDLINE=77021516; PubMed=823945;
MIDLENE=77021516; Frangione B., Prelli F., Franklin E.C.;
"The amino acid sequence of 'heavy chain disease' protein ZUC, Structure of the Fc fragment of immunoglobulin G3.";
Blochem. Blophys. Res. Commun. 71:907-914 (1976).
  Wis.";
gamma 3 heavy-chain disease protein
Biochemistry 19:4304-4308(1980).
REPRESENTATE STREET STR
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                        CHAIN DIMER).
CHAIN DIMER).
CCHAIN DIMER).
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E69CBC95705B2F46 CRC64;
N-LINKED (GLCNAC...).
INTERCHAIN (WITH HARAY OF INTERCHAIN (WITH HEAVY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
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S -> N (IN OWM)
/FTIG=VAR 002
MISSTY
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/FTIG=VAR_001e^-
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FTId=VAR 003890.

F -- L (IN OWN).

F -- Y (IN OWN).

F -- X (IN OWN).

T -- A (IN OWN).

FTId=VAR 003892.
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Biol. Chem. 253:6068-6075(1978).
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                          156 rpleuAspGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlleG 176
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869 AGGAGCAGTACAACAGCACGTACCGTGTGAGCGTCCTCACCGTCCTGCACCAGGACT 928
                                                                                  GGCTGAATGGCAAGGAGTACAAGTGCAAGACCAACAAAGAGCCCTCCCAAGAGCCCCCATCG
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MEDLINE=80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE=80205559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adetugbo K.; "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gammal chain.";
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21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
19 gamma-1 chain C region secreted form.
Mus musculus (Mouse).
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R EMBL; V00793; CAA24172.1; -.
R EMBL; V00793; CAA24173.1; -.
R EMBL; V00795; CAA24174.1; -.
R EMBL; V00795; CAA24176.1; -.
R MGD; MGI; MGI; Ig-like.
R InterPro; IPRO0310; Ig-like.
R InterPro; IPRO0306; Ig-MHC.
R Ffam; PF00047; Ig: 2.
R SWART; SW00407; IG-LIKE; 3.
R PROSITE; PS50835; IG-MK; 1.
R IMMLOGGObulin C region; Glycoprotein; Immunoglobulin C region; Glycoprotein;
                                                     Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126.837-850(1972).
-! SUBCELDULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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IsoId=P01868-1, Sequence=Displayed,
Note=May be the major isoform;
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                                                                                                                                                                                                                                                                                                      Name=Membrane-bound;
IsoId=P01869-1; Sequence=External;
DISULFIDE BONDS (MOPC 21)
MEDLINE=73008889; PubMed=5073237;
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47.57%
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                SEQUENCE OF 323-393 FROM N.A.
MEDLINE-22197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.
"Tyler B.W., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.
"mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                   SEQUENCE OF 323-366 FROM N.A.
MEDLINE=82115295; PubMed=6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl
Eisenberg D., Wall R.;
Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
                         NCBI_TaxID=10090;
                                                                                                                                                               domain.
 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGG 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1176
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                      TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
                                                       TrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp
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SEQUENCE OF 1-44 FROM N.A.
MEDIINE=80222190; PubMed=5283537;
MEDIINE=80222190; PubMed=5283537;
Mamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982).
-!- ALTERNATIVE PRODUCTS:
EVent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V00793; CAA24173.1; --
R EMBL; V00793; CAA24174.1; --
R PDB; 15C8; 23-MAR-98.
R PDB; 1F1; OF FBB-00.
R PDB; 1F2; 29-DEC-99.
R PDB; 1FC5; 24-UL-02.
R PDB; 1CC5; 24-UL-02.
R PDB; 1CC5; 24-UL-02.
R PDB; 1CC5; 24-UL-03.
R PDB; 1CC6; 1GD-4.
R InterPro; 1PR007110; 1G-1ike.
R InterPro; 1PR00710; 1G-1.
R InterPro; 1PR00710; 1G-1.
R PROSTIE; PS00290; 1G LIKE; 3.
R PROSTIE; PS00290; 1G LIKE; 3.
R PROSTIE; PS00290; 1G LIKE; 3.
R Immunoglobulin domail; Immunoglobulin C region; Glycoprotein;
M Immunoglobulin domail; Immunoglobulin C region; Glycoprotein;
M Alternative splicing; Transmembrane; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                       IsoId=P01869-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P01868-1; Sequence=External; Note=May be the major isoform;
                                                                                                                                                                                                                                                                                                                                      Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                              Name=Secreted;
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21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CUG-2003 (Rel. 12, Last annotation update)
IG-9Gamma-1 chain C region, membrane-bound form

Ą 393

STANDARD;

GCIM MOUSE P01869;

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TIGCCTGGTCAAAGGCTTCTATCCCAGC 1116
                                                     SCCGGAGAACAACTACAAGACCACGCCT 1176
                                                                                          TACAGCAAGCTCACCGTGGACAAGAGC 1236
                                                                                                                              COTGATGCATGAGGCTCTGCACAACCAC 1296
GlnValTyrThrIleProProProLys 232
                                                                                                                                                                                                                                                                                                                                                        heavy-chain gene family.";
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i, Muridae; Murinae; Rattus.
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Percent Similarity:
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GlyProProThrGluGlnLeuThrGluGlnThrValSerLeuThrCSerGly 257
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AspValGlnPheSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnPro 177
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                           GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG
                                                            SerThrValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrValThr
                                                                                    TGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
                                                                                              TrpAsnSerGlyAlaLeuSerSerAspValHisThrPheProAlaValLeuGln---Ser
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US-09-674-716B-18 (1-1335)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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SerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrValLysTrp
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P22436;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16 gamma-3 chain C region, secreted form.
1g gamma-3 chain C romouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(101 TaxID=10090;
                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A. MEDINES-8027161; PubMed-6092053; MEDINES-8027161; PubMed-6092053; Mels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.M., Blattner F.R.; Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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Mismatches:
Indels:
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Matches:
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PIR; B02156; G3MSC.
HSSP; P01857; 1FC1.
Interpro; IPR003110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003597; Ig_MHC.
Ffam; PR00047; ig_3 3.
Ffam; PR00047; ig_1 3.
PROSITE; PSS0835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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398 AA;
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                                                             --- IleProLysProSerThrProProGlySerSerCysProProGlyAsnIleLeudly 118
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G gamma-3 chain C region, membrane-bound form.
Mus muscaulus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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MEDLINE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 328-398 FROM N.A.
MEDLINE=84041483; PubMed=6314258;
Komarcomy M., Clayton L., Rogers J., Robertson S., Kettman J.,
Wall R.;
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structure of the mouse immunoglobulin in gamma 3 membrane gene
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R EMBL; V01526; CAA24767.1; ALT_SEQ.
R PIR; AOLS16; GSASM.
R HSSP; PO1857; 1FC1.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003597; Ig_C1.
R InterPro; IPR003065; Ig_MHC.
R Efam, PF00047; ig; 3.
R SWART; SM00407; Igc1; 2.
R PROSITE; PS50835; IG_LIKE; 3.
R PROSITE; PS00290; IG_MHC; 1.
M Transmembrane; Alternative splicing.
I NON TER.
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I 97 CH1.
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P -> F (IN REF. 2).
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                          segment.";
Nucleic Acids Res. 11:6775-6785(1983).
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REMEL, V00798; CRA24178.1; -.

R PDB; 1E4W; 12-UUL-01.

R PDB; 1E4W; 12-UUL-01.

R PDB; 1E4W; 12-UUL-01.

R PDB; 1E4W; 12-UUL-01.

R InterPro; 1PR003109; 1g_c1.

R InterPro; 1PR003597; 1g_c1.

R InterPro; 1PR003597; 1g_c1.

R FAMT; 8M00407; 1g; 2.

R RART; 8M00407; 1g; 2.

R RART; 8M00407; 1g; 2.

R RART; 8M00407; 1gc1.

R RART; 8M00407; 1gc1.

R RART; 8M00407; 1gc1.

R ROSITE; PS00230; 1G_MHC; 1.

R PROSITE; PS00330; 1G_MHC; 1.

R PROSITE; PS
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";
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                                                                                                                                                                  Bourgois A., Fougereau M., Rocca-Serra J.; "Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function."; Eur. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                           MEDLINE=73056887; PubMed=4565406;

de Preval C., Fougereau M.;

"Determination of the primary structure of a mouse gamma G2a "moreoglobulin. Identification of the disulfide bridges.";

Eur. J. Blochem. 30:452-462(1972).

-! - SIMILARITY: Contains 3 immunoglobulin-like domains.
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                                                                                 Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
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MEDLINE=74175517; PubMed=4831970;
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TrpPheValAspAsnLysGluValHisThrAlaTrpThrGlnProArgGluAlaGlnTyr 178
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MEDI-INE-Bill 18976; PubMed=6262729;
MEDI-INE-Bill 18976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer ";
Nucleic Acids Res. 9:1365-1381(1981).
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MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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PO1863;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g gamma-2A chain C region, A allele.

Buks mycota, Metazcos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
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            TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA 522
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                         41 TrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp
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P20762;
01-FEB-1991 (Rel. 17, Created)
11-72B-1991 (Rel. 17, Last sequence update)
11-72B-1999 (Rel. 38, Last annotation update)
11-72B-1999 (Rel. 38, Last annotation update)
11-72B-1991 (Rel. 38, Last annotation update)
Rattus norvegicus (Rat).
Rutinaei, Ruteleostomi;
NCBI_TaxID=10116;
                                                             GGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
MEDLINE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.,
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.,
Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).

Eur. J. Immunol. 18:317-319(1988).
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INTERCHAIN (WITH A LIGHT CHAIN).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGC1.
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PROSITE; PS00290; IG_MHC; 1.
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"Erueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
13 gamma-2A chain C region.
Rattus norvegicus (Rat).
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MEDLINE=89232738; PubMed=3149946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysLysleValPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 SerMetValThrLeuGlyCysLeuValLysGlyTyrPneProGluProValThrValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProAlaValLeuGln---Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 GGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCAGCTTGGGCACCCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 TACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAGTGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 ArgGluCys-----AsnProCys---GlyCysThrGlySerGluValSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCACGTACCGTGTGAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG
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                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
; E8EA136A9DE01EDB CRC64;
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INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
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206
49
67
8
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Matches:
Conservative:
Mismatches:
Indels:
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EMBL; M13804; AAA41376.1; ALT_INIT
PIR; PS0019; PS0019.
HSSP; P01842; 7FAB.
                                                                                                                                                                                           98 IG
212 IG
317 IG
82 IN
102 IN
105 IN
196 IN
350 IN
                                           InterPro; IPR00710; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfan; PF00047; Ig; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00299; IG_MHC; 1.
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1114.00
77.27%
62.42%
46.32%
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                1115
221
221
102
105
1105
1242
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943 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAACCATCTCC 1002

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1123 GCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 1182
                                                                                                                                          1183 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCTCACCGTGGACAAGAGCAGGTGG 1242
                                                                                                                                                                                253 TyrThrGluTrpLysMetAsnGlyGlnProGlnGluAsnTyrLysAsnThrProProThr 272
193 ThrPheLysCysLysValAsnSerGlyAlaPheProAlaProlleGluLysSerIleSer 212
                                                                                                                                                      CAGAAGAGCCTCTCCCTGTCTCGGGTAAA 1332
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Search completed: September 30, 2004, 08:43:02 Job time: 43.9645 secs

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MEDLINE=2288257; PubMed=12477932;
MEDLINE=2288257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jorden H., Moore T., Max S.L., Hane F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carancel T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Q72351 homo s
Q727p5 homo s
Q8n4y9 homo s
Q8t63 homo s
Q8171 homo s
Q813v9 mus n
Q86tt2 homo s
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O9bqb8 homo s
O8wux4 homo s
O96aa6 homo s
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086xx7 mus m
096ey0 homo s
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08bxv24 homo s
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08xy24 homo s
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Q72SW1.
Q72SW1.
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hymosaplens (Human).
Homo saplens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrinii, Hominidae, Homo.
                                                                                                             Q9rla4 mus
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 072351
0727P5
08N27P5
08N1N4
08N3V9
09STT2
099L134
099BL4
07TWK1
099R136
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Q7Z374
Q7Z379
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   SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
             RESULT 1
Q7Z5W1
   Command line parameters:
-MODBL=frame+ n2p; model -DEF=xlp
-MODBL=frame+ n2p: model -DEF=xlp
-G-cgn2 | 1/05PrO| spool | p/0809674716/runat | 30092004 | 070258 | 25867/app_query.fasta_1.3164
-DE-Cgn2 | 1/05PrO| spool | p/0809674716/runat | 30092004 | 070258 | 25867/app_query.fasta_1.3164
-DEF=SPTREMBL 25 -QFMT=fastan -SUFFIX=rspt -MINMATGH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRX=100 -MFR MIN=0 -ALIGN=15 -MODE=LOCAL
-OTFFMT=ptc - TRR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OTFFMT=ptc -NORM=ext -HEAPSIZE=560 -MINLEN -DAALDH=200000000
-USER=US09674716 @CGN 1 1 499 @runat 30092004 070258 | 25867 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES=0 -MAXIT -BSPBLCK=100 -LONGLOG
-DST TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                      September 30, 2004, 08:27:18; Search time 169.047 Seconds (without alignments) 4983.418 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                           - protein search, using frame_plus_n2p model
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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2405
1 gaggtgcagctggtgg
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AAGAGCAGGTGGCAGCAGCGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1290
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                                                                                                                                                                                                                                                                                                 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 930
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                      <u> AAAGTGGAGCCCAAATCTTGTGACAAAACTCACACGATGCCCACCGTGCCCAGCACCTGAA</u>
                                                                                                                                                                                         TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCCACGAAGACCCTGAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human),
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686N02209.
                                                                                                        CTCGCGGGGCCACCGTCAGTCT
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SEQUENCE FROM N.A.
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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Straubberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1; -.
Hypothetical protein.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                4407
110
124
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                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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2139.50
91.85%
89.65%
88.96%
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TISSUE=Spleen,
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1237 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGGACAACCAC
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                                                                                                                                                                                          378 AspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSer 397
                           318 TyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsn
                                                                               338 GlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlleGluLysThr
                                                                                                                     997 AICTCCAAAGCCAAAGGGAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
                                                                                                                                                                                                                                             398 AspileAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
                                                                                                                                     1177 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC
                                                                GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC
                                                                                                                                                                          1057 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTATCCCAGC
                                                                                                                                                                                                                                1117 GACATCGCCGTGGAGTGGGAAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
                                                                                                                                                                                                                                                                                                      QBN4Y9 PRELIMINARY; PRT; 521 AA.
QBN4Y9;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A Strausberg R.,
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Strausberg R.,
EMBL, BC033178; AAH33178.1; -.
REAL, BC033178; AAH33178.1; -.
RITA A60764; A60764.
RITA PRO0110; IPR003597; Ig_c1.
RITA PRO0170; IPR003596; Ig_v.
REAL, PRO0047; IGC1; 3.
REAL, PRO0407; IGC1; 3.
REAL, PROSITE; PS00290; IG_MHC; 2.
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Matches:
Conservative:
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Indels:
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2013.00
81.67%
76.69%
83.70%
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521 AA; 5
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                      CCAGGGAAGGGGCTCGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 180
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LysTyrAlaArgLysPheGlnGlyArgValThrMetThrThrAspThrSerAlaThrThr 97
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| ProGlyGlnGlyLeuGluTrpMetGlyTrpIle-----SerAlaHisAsnGlyAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG
                                                                                                                                                                                           C8D5BE12BAAF795C CRC64;
                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                        Gaps:
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              11 protein.
469 AA; 51395 MW;
                                                                3.26e-155
2053.00
90.27%
85.40%
85.36%
EMBL; BC051328; AAH51328.1;
                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
           Hypothetical
                                                    Alignment Scores:
Pred. No.:
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                                     TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT
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                                                               AAAGCCCTCCCAGCCCCCCATCGAGAAACCATCTCCAAAAGCCCAAAAGGGCAGCCCCGAGAA
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical protein.
Hypochetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Ghordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (MAR-2002) to the EWEL/GenBank/DDBJ databe
EWEL; BC02598; AAH5985.1; -
EWEL; BC02598; AAH5985.1; -
EWEL; BC02598; ACH5985.1; -
EWEL; BC02598; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEF
GO; GO:000518; P:electron transporter activity; IEF
GO; GO:000518; P:electron transport; IEA.
InterPro; IPR001033; BlueCu 1.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR0013596; Ig-v.
Pfam; PF00447; ig; 4.
SNART; SM00406; IG-v.
PROSITE; PS00196; COPPER BUUE; 1.
PROSITE; PS00196; COPPER BUUE; 1.
PROSITE; PS00290; IG-MEC; 3.
PROSITE; PS00290; IG-MEC; 3.
PROSITE; PS00290; IG-MEC; 3.
PROSITE; PS00290; IG-MEC; 3.
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                                                         382 GluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSer
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                               GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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TISSUB-Spleen;
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spleen.";
Submitteed (ULL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKG90464; BAC03445.1;
PIR; A45874; A45874.
InterPro; IPR007110; Ig-like.
InterPro; IPR003309; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SWART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00839; IG_LIKE; 3.
PROSITE; PS00839; IG_LIKE; 3.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Sciurognathi, Muridae, Murinae, Mus.
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Strausberg R.;
Submitted (MAR-2002) to the EMB EMBL, BC024405, AAH24405.1; --
PIR, B45837, B45837, --
MGD; MGI:96446; Igh-4.
InterPro; IPR003106; Ig-MrC.
InterPro; IPR003596; Ig-WrC.
Pfam, PF00047; ig; 3.
SMART; SM00406; IGY; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
HYDOthetIcal protein.
SEQUENCE 469 AA; 51976 MW;
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                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
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                                         679 CCAGCACCTGAACTCGCGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 738
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01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens
(Human) (Fragment).
                                                                                                                                            625 GACAAGAAAGTGGAGCCCAAATCTTGTGACAAAACTCACAACATGCCCACCG----TGC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Genoscope; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A. TISSUE=Placenta;

SEQUENCE FROM N.A. TISSUE=Placenta;

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121 CysProGluProLysSerCysAspThrProProProCysProArgCysProAlaProGlu 140
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Li W.B., Gruber C., Jessee J., Polayes D.;

"Full-length cDNA libraries and normalization.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BXZ48278; CAD62606.1; -.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

InterPro; IPR00710; Ig-like.

InterPro; IPR0031006; Ig-MC.

Rem; PF0047; Ig?, 1.

SMART; R004407; IGC1, 3.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 2.
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Matches:
Conservative:
Mismatches:
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde C.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde C. Discoulland C. Discoulland C. Discoulland Construction of a single chain antibody (RoFV).";

Wilde C. Misch C. Discoulland C.                                                                                                                                                                            1170
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              CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
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Sciurognathi, Muridae, Murinae, Mus.
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Last annotation update)
(Fragment)
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Conservative:
Mismatches:
Indels:
Gaps:
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01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-OCT-2003 (TrEMBLrel. 25, I
Gammal heavy chain of Mab7 (F
IGH-4.
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315 ThrGlnThrHisArgGluAspTyrAsnSerThrIleArgValValSerAlaLeuProIle
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156 ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluSerValThr
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235 GlubroSerGlyProlleSerThrIleAsnProCysProProCysLysGluCysHisLys
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350 LysAspLysValSerLeuThrCysMetlleThrAspPhePheProGluAspIleThrVal 369
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC101327; AAH10327.1; -.
KGJ, MGJ:2144919; -.
KGJ, MGJ:2144919; F:electron transporter activity; IEA.
GG, GG:0005189; F:electron transport; IEA.
InterPro; IPR00118; P:electron transport; IEA.
InterPro; IPR00118; P:electron transport; IEA.
InterPro; IPR001306; Ig-ike.
InterPro; IPR003006; Ig-ike.
InterPro; IPR003006; Ig-wHC.
InterPro; IPR0047; Ig-v.
FRAM; FR00404; Ig-v.
FRAM; FR00404; Ig-v.
FROSITE; PS00190; CYTOCHROME_C; I.
FROSITE; PS00190; CYTOCHROME_C; I.
FROSITE; PS00190; GYTOCHROME_C; I.
FROSITE; PS00190; GYTOCHROME_C; I.
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AU044919.
Mus musculus (Mouse).
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CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGCCCCCATCGAG
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LysSerAsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHisGluGlyLeuHis
138 SerAlaAlaLysThrThrProProSerValTyrProLeuAlaProGlySerAlaAlaGln
                                                                                                                                                                                       577 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACACCAAGGTGGACAAGAAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                        811 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGGGGAG
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                                                                                                                                 |||::: |||
237 ValProArgAspCysGly------CysLysProCysIleCysThrValProGlu
                                                                                                                                                                                                                                                                                                              :::::
253 ValSer-----SerValPheIlePheProProLysProLysAspValLeuThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG
                          397 TCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
                                            :::
158 ThrAsnSerMetValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr
                                                                              GTGTCGTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAG
                                                                                                                                                  637 GAGCCCAAATCTTGTGACAAAACTCACACACCCACCG-----TGCCCAGCACCTGAA
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                                         CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAA 1332
                                                          40 SerCysLysAlaSerGlyTyrThrPheThrGlyTyrGlyValSerTrpValLysGlnArg
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                                                                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                          A Strausberg R.;

L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; EC003435; AAH03435.1; -.

R PIR; B45837; B45837.

R HSSP; P01842; 7FAB.

R MGD; MGI:96446; Igh-4.

R InterPro; IPR00710; Ig MC.

R InterPro; IPR003106; Ig MC.

R InterPro; IPR003596; Ig_v.

R FAGM, PF00047; ig; 3.

DR SWART; SMO0406; IGV: 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; Id MHC; 1.

SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                  099Lc4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                        463 AA
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                                                                                                                        PRT;
                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.51e-109
1478.00
76.65%
59.91%
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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RA Azakawa T., Hara A., Shibata K., Kono H., Adachi J., Fukuda S.,
RA Azakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishik K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori. Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsud T., Gissi C., King B., Kochiwa H.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh J.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Hashibaan Y., Kawai Y., Kawaji H., Kohtsuki S.,
Hayashiashi Y.,
Hayashiashi Y.,
Hayashiashi Y.,
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1810060008Rik protein.
IGH-1 OR 1810060009RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Functional annotation of a full-length mouse cDNA collection.";
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Matches:
Conservative:
Mismatches:
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                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C57BL/6J, TISSUE-Pancreas;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, S26746; S26746.
HSSP; P01842; 7FAB.
MGD; MGI:96443; 1Gh-1.
INCEPPRO; 1PR007110; 1G-11Ke.
INCEPPRO; 1PR003106; 1G_MHC.
INCEPPRO; 1PR003596; 1G_V.
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EMBL; AK007918; BAB25349.1; -.
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PROSITE; PSS0835; IG LIKE; 4.
SEQUENCE 473 AA; 51699 MW;
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1444.00
75.49%
58.42%
60.04%
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Best Local Similarity:
                                                                              Mammalia, Eutheri
NCBI_TaxID=10090;
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                                                                                             197 SerGlyLeuTyrThrLeuSerSerValThrValThrSerAsnThrTpProSerGln
                                                                                                                                                                                                                                                                                                                                                                                       257 AlaProAspLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspVal
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317 ThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProlleGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 LeuProProAlaGluGluMetThrLysLysGluPheSerLeuThrCysMetIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 ArgValGlnLysSerThrTrpGluArgGlySerLeuPheAlaCysSerValValHilsGlu
                               118 SerGlyTyrAspTyrAspTxpPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSer
                                                                       340 TCAGCCTCCACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCT
                                                                                                                                                                                                                     460 TCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCGGCTGTCCTACAGTCC
                                                                                                                                                                                                                                                                                           TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCCACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TCTTGTGACAAACTCACACATGCCCACCGTGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProArgValProlleThrGlnAsnProCysProProLeuLysGluCysProProCysAla
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TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCC
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237 IleGluProArg---IleProLysProSerThrProProGlySerSerCysProProGly
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                                              GTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGCGG
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REALSOLOGIES FROW NA.

REALSDESSERVEN N. T. TISSUE=Breast tumor;

REALSDESSERVEN N. Feingold E.A., Grouse L.H., Derge J.G.,

REALSDESSER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Stausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Widen T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Chards S.A., McEwan P.J., McKernan K.J., Lu X., Gubbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

Ratesley R.W., Touchman J.W., Green E.D., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A., 99:16999-16903 (2002).
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Sciurognathi, Muridae, Murinae, Mus.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Submitted (AUG-2003) to the EMBL/GenBank/DDBU daremain; EC055910; AMH55910.1;
Hyporhetical protein: SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090
                      470 AA
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SEQUENCE FROM N.A.
STRAIN=CZECH II, TISSUE=Breast tumor;
                        PRT;
                                                         01-0CT-2003 (TrEMBLE). 25, Crea 01-0CT-2003 (TrEMBLE). 25, Last 01-0CT-2003 (TrEMBLE). 25, Last Hypothetical protein. Mus musculus (Mouse). Eukaryotta, Metazoa, Chordata; Cr Mammalia; Eutheria; Rodentia; SC 121-TaxID=10090;
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SEQUENCE FROM N.A.
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Best Local Similarity:
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520 TCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCAGCTTGGGCACCCAG
                                                                                                                                                                          694 GCGGGGGCACCGTCAGTCTTCCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC
                                                                                                                                                                                            256 LeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSer
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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R MBL, BC025447, AAH25447.1; -. MCD; MGT:2144967; AU044919.

MCD; MGT:2144967; AU044919.

GO:GO:0005489; F:electron transporter activity, IEA. GO:GO:0005418; F:electron transport; IEA. GO:0006118; P:electron transport; IEA. InterPro; IPRO0110; IG-11ke.

R InterPro; IPRO01396; IG-11ke.

InterPro; IPRO03906; IG-10ke.

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Search completed: September 30, 2004, 08:54:03 Job time: 192.047 secs

THE SHEET

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

2004, 08:19:42; Search time 159.041 Seconds (without alignments) 4743.430 Million cell updates/sec OM nucleic - protein search, using frame\_plus\_n2p model September 30, Run on:

US-09-674-716B-18 Title:

2405 1 gaggtgcagctggtggagtc.....ccctgtctccgggtaaatga 1335 Scoring table: Perfect score: Sequence:

0.5 BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 1586107 segs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s:\* 4.00 / 8 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aay32263 Humanised	Aar42162 Anti-HIV-	Aae33524 Human AQC	Aae33522 Human AQC	Abp58273 Humanised	Abp58275 Humanised	Aae35327 Humanised	Aae34876 BIWA4/8 a	Aae33523 Human AQC	Abr39465 Humanised
QI	AAY32263	AAR42162	AAE33524	AAE33522	ABP58273	ABP58275	AAE35327	AAE34876	AAE33523	ABR39465
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% Query Match	98.4	91.5	91.1	91.1	91.0	91.0	90.0	90.9	90.9	8.06
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## ALIGNMENTS

cod3; FCERII; igB receptor; monoclonal antibody; Cil; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lugus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria, nephrotic syndrome; glomerulonephritis; psoriasis; unflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; khihitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; Humanised anti-CD23 MAb C11 heavy chain. AAY32263 standard; protein; 444 AA. (first entry) 15-FEB-2000 AAY32263; AAY32263

1. .30
/note= "framework region 1" 36. .49 /note= "framework region 2" Location/Qualifiers "CDR 1" "CDR 2" 50. .68 31. .35 /note= Homo sapiens. Synthetic. cherapy. Region Region Region Region 

69. .100

Region

/note=

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480 160 540 200 960 720

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1081 AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGGTGGGAGAGC 1140
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101 PhelleAspTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro
                                                                                                                                                                                                                                                                                                                                                                             161 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyVeuTyrSerLeuSer
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                                                          CTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACAGAT
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CD23 (FCERII) monoclonal antibody C11, composed of a human framework
(HSIGKVII) and the heavy chain complementarity determining regions (see
AV22257-59) of murine antibody C11. The DNA was constructed by splice
overlap PCR. The invention provides altered antibodies, such as chimeric
or humanised antibodies, which comprise sufficient of the amino acid
sequences of the C11 light and heavy chain complementarity determining
regions to render them capable of binding to the CD23 type II molecule
expressed on haematopoietic cells. The antibodies are used to block
soluble CD23 formation in human therapy, for the treatment of arthritis,
lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
clomerallonephritis, inflammantory bowel disease, ulcerative colitis,
crohn's disease, Sjogren's syndrome, allergic asthma,
intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema,
thrinsic asthma, acute asthmatic exacerbation, rhinitis, and B-cell
malignancies (claimed). They are also useful for studying interactions
between CD23 and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGIGCAGCIGGAGICTGGGGGGAGCTIGGIAAAGCCCGGGGGGGTCCCTIAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                            Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
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Matches:
Conservative:
Mismatches:
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                                                       104. .111
/note= "framework region
                                                                                          112. .444
/note= "constant region"
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note= "framework
                 101. .103
/note= "CDR 3"
104. .111
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                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                      Bonnefoy JMP,
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Pred. No.:
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New recombinant human antibody - with HIV neutralising activity against at least two isolates, useful for preventing or treating infection in
SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu
                                                                                                                                                       Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; HIV-neutralising monoclonal antibody; immunoglobulin; AIDS; acquired immune deficiency syndrome; chimeric antibody; surface glycoprotein gp120; V3 loop.
                                                                                                                                                                                                                                                                                                                         Pfarr
                                                                                                                                         Anti-HIV-1 recombinant antibody 447-52D heavy chain.
                                                                                                                                                                                                                                                                                                                         Johnson LS,
                                                                          AAR42162 standard; protein; 461 AA.
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                    TCTCCGGGTAAA 1332
                                                                                                               (revised)
(first entry)
                               SerProGlyLys 444
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N-PSDB; AAQ49834.
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diagnosis, etc.
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                                                                                                                                                                                                                                                                   23-MAR-1993;
                                                                                                                                                                                                            Homo sapiens
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27-APR-1994
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bBV-transformed cell lines and mouse-human heterohybridomas producing human MAbs specific for the gpl20 V3 loop of HIV-1 NN isolate were obtained. WAb 447-52D was found to recognise the tetrapeptide motif GPGR, i.e. the Principal Neutralising Determinant common to the V3 loop of different HIV isolates. A recombinant Ab was produced in which the H chain intronic sequence are appended, fused to a fragment contg. a short intronic sequence are appended, fused to a fragment contg. a short intronic segment of the human gamma 1 cregion and the human gamma 1 encoding domain in its genomic form. (Updated on 25-MAR-2003 to correct PN field.)

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Sequence 461 AA;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                     (1-461)
                                                                                     US-09-674-716B-18 (1-1335) x AAR42162
           1.26e-130
2199.50
92.62%
90.24%
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 120 61

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1029 281 SerHisGluAspProGluValLySPheAsnTrpTyrValAspGlyValGluValHisAsn 300 606 320 240 260 789 280 849 549 200 609 220 699 729 240 309 120 369 140 429 160 489 80 AlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeu CAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTATCCCAGGGACATCGCCGTGGAGGGGGGAGAGCAATGGGCAG ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 241 ProbroCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLys ThrCysvalalaSerGlyPheThrPheSerAspvalTrpLeuAsnTrpValArgGlnAla :::::|||| | 101 AspGlyPheIleMetIleArgGlyValSerGluAspTyrTyrTyrTyrMetAspVal 730 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTG 261 ProlysAspThrLeuMetIleSerArgThrProGluValThrCysValValValAspVal 790 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAAT GCCAAGACAAAGCCGCGGGAAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTC CCAGGGAAGGGGCTCGAGTGGCTGCAATTAGATTGAAATCTGATAATTATGCAACA CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGAGATTCAAAATCTAGA GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGC TGGGGCCAGGGAACACTAGTCACCGTCTCAGCCTCCAACGGGCCCCATCGGTCTTC 850 1030 1090 670 301 910 361 181 241 81 310 121 490 19 301

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                                                                                                                                                                                                                                                                                    1270 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGT 1329
                                                                                                             401 ProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlySerPhePheLeu 420
                                                                                                                                                                                                           421 TyrSerLysLeuThrValAspLysSerArgTrpGlnGlyAsnValPheSerCysSer 440
381 CysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGln 400
                                                                                                                                                                                                                                                                                                                        441 ValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGly 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammacory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; crofns disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; agstritis; Hodgkin's disease; theumatic fever; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; asrcoldosis; Behoef's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriaals, eczema, burns, dermatitis and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel antibodies that specifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karpusas M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human AQC2 heavy chain mutant protein, hsAQC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE33524 standard; protein; 447 AA
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fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, bronchitis, tendonitis, bursitis, fever, migraine headaches, gastrointestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, gastrials, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anemia, periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid arthritis, systemic luque erythematosus and multiple sclerosis), renal failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, polymyositis, hypersensitivity (e.g. delayed type hypersensitivity), graft and transplant rejections, graft versus host disease, conjunctivitis, swelling occurring after injury, myocardial ischaemia or endocoxin shock syndrome. The present sequence is human AQC2 heavy chain mutant protein, haAQC2
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218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluAlaAlaGly 237
                                               238 GlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThr
                                                                                                                                                                                                     GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp
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                         700 GCACCETCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGGACC
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AAE33522 standard; protein; 447 AA AAE33522;

Human AQC2 heavy chain protein.

02-APR-2003 (first entry)

Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosolerosis; thyroditis; aplastic anemnia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteomic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyonitis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia. 

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CCAGGGAAGGGGCTCGAGTGGGTTGCTGAATTAGATTGAAATCTGATAATTATGCAACA CATTATGCGGAGTCTGTGAAGGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA

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CIGIAICHGCAAATGAACAGCCTGAAAACGGAGGACACAGCGGTGTATTACTGTACAGAT 300

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Homo sapiens

WO200283854-A2

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The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The cati-VLA-1 antibodies are useful for preventing or treating VLA-1-CC mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal compositis, tendonitis, respiratory distress syndrome, asthma, bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-concential conditions (e.g. inflammatory bowel disease, Crohn's disease, crohnist intrable bowel syndrome, colitis and colorectal cancer).

Contonimum diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, operiarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, carchides systemic lupus erythemacous and multiple sclerosis), renal failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, crimmediate hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft correctial isofamemia or endotoxin shock syndrome. The present sequence is hower where the syndrome is the present sequence is
                                                                                                                                                                                                                                                                   New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or
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                                                                                                                                                                                            Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 75; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human AQC2 heavy chain protein
                                                                                              13-APR-2001; 2001US-0283794P.
06-JUL-2001; 2001US-0303689P.
                                                        12-APR-2002; 2002WO-US011521
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                           -TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCC 339
                                                   98 GlyPheGlyAspGlyGlyTyrPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117
                                                                                              400 GGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG 459
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                                                                                                                                                                                                                                                                   SerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197
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78 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysThrArg 97
                                                                              340 TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCT
                                                                                                                                                   GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal
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The present sequence is that of a preferred heavy chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region originates from human germilate Wh segment DP-45 and 4D segment JM4 Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
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ABP58273 standard; protein; 449
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/note= "CDR1"
50. .66
/note= "CDR2"
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/note= "CDR3"
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Mismatches:
Indels:
Gaps:
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91.61%
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human; humanised antibody; antibody; Alzheimer's disease;
Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
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                                                                                                                       The present sequence is that of a preferred heavy chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline VH segment DP-45 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epicope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their calls, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
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            wew numanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plague in the brain.
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                                                                                                   Disclosure; Page 13-14; 54pp; English
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                                                                                                                                                                               The invention relates to a compound comprising CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions. The compound is used in pharmaceutical composition for the treatment of cancer, solid tumours, and as an adjuvant to surgical intervention to treat minimal residual disease. The present sequence is humanised murine antibody BIWA4 heavy chain protein used in the invention
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                                                                                                                          New compound useful for treatment of cancer comprises CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions.
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SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu
                                                                      TACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC
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                                                                                          TACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC
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                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel antibody molecules comprising a variable region of the heavy (WH) and/or light chain (VL) of CD44v6 specific humanised antibody called BTWAR and BTWAR. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck, ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BTWA4/8 antibody heavy chain mauure protein. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                      New antibodies specific for an epitope coded by the variant exon of tl
CD44 gene, useful for treating cancer, including non-small cell lung,
breast, head and neck, ovarian and lung cancer.
                                                                                                                                                                                                  Heider K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                       (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
(BOEH ) BOEHRINGER INGELHEIM PHARM INC
                                                                                                                                                                                                                                                                                                                                                   Claim 24; Col 44; 78pp; English
                                                                                                                                                                                                  Adolf G, Ostermann E, Patzelt Miglietta JJ, Van Dongen AAMS;
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2187.00
95.09%
92.63%
                                                                                17-MAY-2002; 2002WO-EP005467.
                                                                                                           18-MAY-2001; 2001EP-00112237
26-SEP-2001; 2001US-0325147P
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N-PSDB; AAD53212, AAD53215.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 444 AA,
                       WO200294879-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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Pred. No.:
                                                  28-NOV-2002
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1128

1008

888

1248

396

AQC2 heavy chain mutant protein, haAQC2 Homo sapiens 

Human, very late activation antigen, VLA-1; betal containing integrin, numunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema, burn, dermantitis; respiratory distress syndrome; fibroasis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; rever, migraine headache; inflammatory bowal disease; crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarreritis nodosa; agastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; astroidosis; Behoef's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.

24-OCT-2002.

12-APR-2002; 2002WO-US011521

13-APR-2001; 2001US-0283794P.

(BIOJ ) BIOGEN INC.

Karpusas M; Saldanha JW, Lyne PD, Garber EA,

WPI; 2003-093009/08

New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or fibrosis.

Example 23; Page 91-92; 248pp; English.

The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methodis of using these antibodies to treat immunological disorders. The anti-VLA-1 antibodies are useful for preventing or treating VLA-1 antibodies are useful and proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, prespiratory distress syndrome, asthma, bronditions (e.g. inflammatory bowel disease, Crohn's disease, checking and colorectal cancel), tratable bowel syndrome, colitis and colorectal cancel), periatteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, systemic lupus erythematosus and multiple sclerosis), renal arthitis, systemic lupus erythematosus and multiple sclerosis), renal muson host disease, conjunctivitis, swelling occurring after injury, myocardial ischaemia or endotoxain shock syndrome. The present sequence is human AQC2 heavy chain mutant protein, haAQC2

Sequence 447 AA;

1.04e-129 2185.00 94.22\* 92.67\* 90.85\* Percent Similarity:
Best Local Similarity:
Query Match:
DB:

4447 7417 710 110 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

180 240 459 157 197 639 217 669 759 819 277 939 337 120 300 399 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137 177 237 257 297 339 117 40 57 7 SerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 700 GCACCGTCAGTCTTCCTTCCCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACC TrpTyrValAspGlyValGluValHisAsnAlaLysTrrLysFroArgGluGluGluGluTyr AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlleGluLysThrlle TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla CCAGGGAAGGGCCTCGAGTGGCTTGCTGAATTAGATTGAAATCTGATAATTATGCAACA 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGAGGGG 640 CCCAAATCTTGTGACAAAACTCACACATGCCCAGCGTGCCCAGCACCTGAACTCGCGGGG 880 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC ------TTCATAGACTGGGGCCAGGGAACACTAGTCACGTCTCC 98 GlyPheGlyAspGlyGlyTyrPheAspValTrpGlyGlnGlyThrLeuValThrValSer 400 GGGGGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCCGAACCGGTGACGGTG TCGTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCCACCCAG ProlysserCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 238 GlyProSerValPheLeuPheProProLysProLysAspThrLeuWet1leSerArgThr CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC GlnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCCGGGGGGGTCCCTTAGACTC TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTAAGAGCACCTCT GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal US-09-674-716B-18 (1-1335) x AAE33523 (1-447) 258 1000 121 28 241 301 340 138 460 158 520 178 580 218 091 820 278 940 318 6 6 6 8 & 8 8 & 8 8 6 8 6 8 6 ò g 장염 8 8 8 8 6 8 6 6 6 6 8 8 8 8 8

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GTGCTGGACTCCGACGGCTCCTTCTTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 1239
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GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377
                                                                                                                             TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437
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beta peptide, e.g. Alzheimer's disease, vascular dementia or mild
cognitive impairment, comprises administering an anti-amyloid-beta
peptide antibody.
                                                                                                                                                                                                                                                              398 ValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg
                                                                                          ATCGCCGTGGAGGAGGAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCC
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28-MAY-2002; 2002US-0383851P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody; cognitive impairment; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; vascular dementia; nootropic; neurotropic; mild cognitive impairment; antibody 266; heavy chain; humanised; mutant; mutein.
SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysVal 318
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                                                                                                                                                                                                                                          PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe
                                      SerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnPro
                                                                                        SerLeuThrCysLeuValLysGlyPheTyrProSerAspileAlaValGluTrpGluSer
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The present invention relates to a method for effecting rapid improvement of cognition in a subject having a condition or disease related to the Abeta peptide. The method comprises administering an anti-Abeta antibody.

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The method is useful for treating cognitive impairments associated with Abeta peptide including those involved in Alzheimer's disease, Down's syndrome, cerebral amyloid angiopathy, craim vascular dementia, and certain forms of mild cognitive impairment. The anti-Abeta antibody is useful for preparing a medicament for effecting rapid improvement in cognition in a subject having Alzheimer's disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitive impairment. The present sequence represents a preferred heavy chain for a humanised 266 antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu
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                           Diagnosing preclinical or clinical Alzheimer's disease in a subject administering an antibody which specifically binds an epitope.
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                259 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu
                                                                           279 ValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValVal
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17-AUG-2001; 2001US-0313224P.
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to stem cell factor protein, treating asthma.

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The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c.kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain variable and constant region
                          New purified human antibody that binds useful for preparing a composition for
              WPI; 2003-523500/49
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                                                                                       CACACATGCCCACCTGCCCAGCACCTGAACTCGCGGGGGCACCGTCAGTCTTCCTTTC
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                              (1-445)
                                                              US-09-674-716B-18 (1-1335) x AAO31101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues syndrome or pre clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/revorse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized antibody for the treatment of Alzheimer's comprises the inhibition and reduction of the formation of amyloid plaques.
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/label= Mature_Hu266_heavy_chain
/nabe= "This sequence is specifically claimed in claim
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PheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrProGluValThr
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Alzheimer's disease, Down's syndrome, cerebral amyloid angiopathy;
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/label= Signal_peptide
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CDR;

Abeta; antibody 266; nootropic; neuroprotective;

(first entry)

Hu266 N56T heavy chain

Amyloid-beta;

Vasquez MJ

Tsurushita N,

Jia AY,

(ELIL ) LILLY & CO

WPI; 2003-278557/27. N-PSDB; ACC47228.

14-AUG-2002; 2002WO-US021322 17-AUG-2001; 2001US-0313224P.

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The invention relates to an anti-Abeta (amyloid-beta peptide) antibody 266. The antibodies are useful for treating and preventing conditions associated with the Abeta peptide, such as Alzhaimer's disease. Down syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in humans; for determining whether a human subject will respond to treatment using humanized antibodies against Abeta; for treating, preventing and reversing cognitive decline in clinical or pre-clinical Alzheimer's disease, Down's syndrome or erebral amyloid angiopathy; for inhibiting formation of amyloid plaques of the effects of toxic soluble Abeta (species in humans: Treatment of the patients with antibody will inhibit or prevent cognitive decline typically associated with disease progression and reverses it. The present sequence represents a humanised anti-Abeta antibody 266 N56T heavy chain
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and preventing
Alzheimer's disease
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Matches:
Conservative:
Mismatches:
Indels:
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93.24%
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Best Local Similarity: 5
Query Match:
DB:
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Pred. No.:
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Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 21, Appl
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Sequence 24, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 46, Appli
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Sequence 8, Appli
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Sequence 26, Appli
Sequence 27, Appli
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Sequence 16,
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US-10-474-832-6

US-10-150-474-832-6

US-10-150-474-832-6

US-10-150-475-812-6

US-10-26-435A-12

US-10-26-435A-12

US-10-326-3718-21

US-09-822-688A-26

US-09-822-688A-26

US-09-822-688A-26

US-09-822-688A-26

US-09-822-688A-3

US-10-461-148-1

US-10-461-148-1

US-10-461-148-1

US-10-461-148-1

US-10-25-108A-3

US-10-412-406-32

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US-10-412-406-32

US-10-412-406-32

US-10-412-406-32

US-10-291-256-395-3

US-10-291-265-395-3

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US-10-291-265-395-3

US-10-291-265-368-26

US-10-291-268-368-26

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Sequence 4, Application US/10474832

Sequence 4, Application US/10474832

Publication No. US20040081651A1

GENERAL INFORMATION:

APPLICAT: BIOGEN, INC.

TITLE OF INVENTION: ANTIBODIES TO VLA-1

FILE REFERENCE: A101 PCT

CURRENT APPLICATION NUMBER: US/10/474,832

CURRENT FILING DATE: 2001-0.14

PRIOR APPLICATION NUMBER: 60/283,794

PRIOR APPLICATION NUMBER: 60/283,794

PRIOR APPLICATION NUMBER: 60/283,794

PRIOR FILING DATE: 2001-07-06

NUMBER: OF SEQ ID NOS: 70

SEQ ID NO 4

LENGTH: 447
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ORGANISM: Artificial Sequence
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| cgn2_6/ptodata/1/pubpaa/DCT_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/DCT_MRW PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/USOF_NEW PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Match Length DB
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298 AsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317
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Publication No. USZO040081651A1;
GENEAL INFORMATION:
JAPLICANT: BIOGEN, INC.
TITLE OF INVENTION: ANTIBODIES TO VLA-1;
FILE REFERENCE: Al01 PCT
CURRENT FILING DATE: 2003-10-14;
PRIOR APPLICATION NUMBER: 60/283,794;
PRIOR PILING DATE: 2001-04-13;
PRIOR PLILNG DATE: 2001-04-13;
PRIOR PLILNG DATE: 2001-04-13;
PRIOR PLILNG DATE: 2001-06;
NUMBER OF SEQ ID NOS: 70.
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Mismatches:
Indels:
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                                                                                             Gaps:
                         6.93e-134
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94.44%
92.89%
91.10%
                                           Percent Similarity:
Best Local Similarity:
Query Match:
              Alignment Scores:
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Matches:
Conservative:
Mismatches:
Indels: US-09-674-716B-18 (1-1335) x US-10-474-832-6 (1-447) 

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398 ValleuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg
                                                     418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGlwAlaLeuHisAsnHisTyr
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                                                                                                                                                 NS-10-150-475A-6

| Sequence 6, Application US/10150475A |
| Sequence 6, Application US/10150475A |
| Publication No. US20030103985A1 |
| GENERAL INFORMATION: |
| APPLICANT: Adolf, G. et al. |
| TITLE OF INVENTION: Cyrotoxic CD44 Antibody Immunoconjugates |
| FILE REFERENCE: 1/121 |
| CURRENT APPLICATION NUMBER: US/10/150,475A |
| PRIOR APPLICATION NUMBER: US 60/307,451 |
| PRIOR PILING DATE: 2001-07-24 |
| NUMBER OF SEQ ID NOS: 9 |
| SEQ ID NO 6 |
| LENGTH: 444 |
| LENGTH: 444 |
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Matches:
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Indels:
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                    41 ProGlyLysGlyLeuGluTrpValAlaThrile-----SerGlyGlyHisThr
                                                                  CTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACAGAT
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Alignment Scores:
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Publication No. US20040120949A1
GENERAL INFORMATION:
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and methods for treating cancer using
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 1/1414

CURRENT APPLICATION NUMBER: US/10/704,522

CURRENT FILING DATE: 2003-11-07

PRIOR APPLICATION NUMBER: US 60/429,516

PRIOR FILING DATE: 2002-11-27

PRIOR FILING DATE: 2002-11-08

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1
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Best Local Similarity:
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Alignment Scores:
Pred. No.:
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CysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSer 236
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; Publication No. US2040126379A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AGOLf, Guenther
APPLICANT: Baum, Anke
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immu.
TITLE OF INVENTION: Cytotoxic CD4 Antibody Immu.
TITLE OF INVENTION: Cytotoxic CD4 Antibody Immu.
TITLE OF INVENTION: Cytotoxic CD4 Antibody Immu.
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immu.
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TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION WIMBER: US 0010 686.2
PRIOR APPLICATION NUMBER: US 004405,956
PRIOR APPLICATION NUMBER: US 004405,956
PRIOR PILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
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Mismatches:
Indels:
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Length:
Matches:
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1.26e-133
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1119 1120 ATCGCCCTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACCGCCTCCC 1179 939 666 358 GlubeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377 519 819 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240 157 177 579 669 237 759 257 241 CTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300 -----TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCC 339 340 TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTTCCTCCAAGAGCACCTCT 399 400 gegegenchecegecerregerrecriegerangenenacinetrececenacegrenene 459 41 ProGlyLysGlyLeuGluTrpValAlaThrIle------SerGlyGlyGlyHisThr 57 97 238 GlyProSerValPheLeuPheProProLysProLysAspThrLeuWetIleSerArgThr 298 GlnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlleGluLysThrlle 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluBroValThrVal 460 TCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCTGTCCTACAGTCC 520 TCAGGACTCTACTCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG 580 ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTGGAG 640 CCCAAATCTTGTGACAAAACTCACACGTGCCCACGTGCCCAGCACCTGAACTCGCGGGG 760 CCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 820 IGGIACGIGGACGCGIGGAGGIGCAIAAIGCCAAGACAAAGCCGCGCGGGAGGAGCAGIAC 880 AACAGCACGTACCGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC 940 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC 1060 GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC 218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 700 GCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACC

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299 SerValLeuThrValbeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer
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                  119 SerValPheProLeuAlaProSerSerLySSerThrSerGlyGlyThrAlaAlaLeuGly
                                                                                                                         481 ACCAGGGGGGGGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGG
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                                                                                                                                                                                                                                                     CACAAGCCCCAACCACCAAGGTGGACAAGAAAGTGGAGCCCCAAATCTTGTGACAAAACT
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, Sequence 79, Application US/10320231A
, Publication No. US20030194405A1
, GENERAL INFORMATION:
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| Sequence 1.2. Application US/10226435A
| Publication No. US20040043418A1
| GENERAL INFORMATION:
| APPLICANT ELL LILLY AND COMPANY and WASHINGTON UNIVERSITY
| TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
| FILE REFERENCE: 8792/293
| CURRENT FALLING DATE: 2002-11-13
| FILE REPLICATION NUMBER: US/10/226,435A
| CURRENT FILING DATE: 2001-02-26
| FRIOR FILING DATE: 2001-02-26
| FRIOR FILING DATE: 2000-02-24
| FRIOR PILING DATE: 2000-02-24
| FRIOR PILING DATE: 2000-12-08
| FRIOR APPLICATION NUMBER: 60/254,465
| FRIOR APPLICATION NUMBER: 60/254,465
| FRIOR APPLICATION NUMBER: 60/254,465
| FRIOR PILING DATE: 2000-12-08
| WINDER OF SEQ ID NOS: 16
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 12
| LENGTH: 442
                                             1240 TGGCAGCAGGGGAACCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACTAC 1299
418 TrpGlnGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437
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GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118
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TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 120
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                          FEATURE:
, OTHER INFORMATION: Humanized antibodies
US-10-226-435A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.29e-133
2183.00
95.72%
93.24%
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Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-226-435A-12
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APPLICANT: Neben, Steven
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Takeuchi, Toshihiko
TITLE OF TINUENTION: Addian
TITLE OF INVENTION: Addianody Inhibiting Stem Cell Factor Activity And Use For
TITLE OF INVENTION: Treatment Of Asthma
FILE REPERENCE: 7430*163
CURRENT APPLICATION NUMBER: US/10/320,231A
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTION NUMBER: 03.2
SOFTWARE: PATENTION NUMBER: 03.2
SOFTWARE: PATENTION NUMBER: 03.2
LENGTH: 445
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Conservative:
Mismatches:
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94.85%
92.84%
90.77%
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Best Local Similarity:
Query Match:
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Pred. No.:
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APPLICANT: Freewin, Mark
TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
FILE REFERENCE: Waldmann
CURRENT PELLION DAMBER: US/09/736,371B
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 9815909.8
PRIOR APPLICATION NUMBER: 9815909.8
PRIOR APPLICATION NUMBER: 977/GB99/02380
PRIOR APPLICATION NUMBER: 977/GB99/02380
PRIOR APPLICATION NUMBER: 977/GB99/02380
NUMBER OF SEQ ID NOS: 30
SOFFWARE: Patentin Ver: 2.1
SEQ ID NO 2.1 1312 CICICCCIGICICCGGGIAAA 1332 Sequence 21, Application US/09736371B; Patent No. US20020131968A1; GENERAL INFORMATION: 445

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319	1060 GB 15 G	379	9 6 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Db 419 TrpGlnGl)	Db 439 ThrGlnLy	#ESOUL 10 US-10-463-442-21 ; Sequence 21, Applica ; Publication No. US20	APPLICANT: Waldmann; APPLICANT: Frewin, TITLE OF INVENTION:	CURRENT APPLICATION CURRENT FILING DATE PRIOR APPLICATION N PRIOR PILING DATE:	PRIOR APPLICATION N PRIOR FILING DATE: PRIOR APPLICATION N PRIOR APPLICATION N	NUMBER OF SECTION OF SECTION SOFTWARE: Patentin SECTION OF SECTION	TYPE: PRT  CRGANISM: Homo sap US-10-463-442-21	Alignment Scores: Pred. No.: Score: Score: Constant Cimilarity.	Percent Similarity: Best Local Similarity: Query Match: DB:	US-09-674-716B-18 (1-1 Qy 1 GAGGGGCA	Db 1 GluValGl	21	OY 121 CCAGGGAA
Pred. No.: 9.46e-133 Length: 449 Score: 2173.50 Matches: 412 Percent Similarity: 94.01\$ Conservative: 12 Best Local Similarity: 91.35\$ Mismatches: 18 Query Match: 90.37\$ Indels: 9 DB: 90.47\$ Local Similarity: 91.35\$ Nos.09-736-371B-21 (1-449)	1 GAGGTGCAGCTGGAGTCTGGGGGAGGCTTG	61 TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCGCAGGCT 120	121 CCAGGGAAGGGCTCGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAAGA 180 	181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGTGATTCAAAATCTAGA 240 :::    :::    :::	241 CTGTATCTGCAAATGAACAGCCTGAAAACC	301 TTCATAGAC	340 TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCAAGAGCACCTCT 399	400 GGGGGCACCAGGCCCCTGGCCTGCTCAAGGACTACTTCCCCGAACCGGTGACGTG 459	Qy         460 TCGTGGBACTCAGGCCCCTGACCCAGCGCGTGCCACCCTCCCGGCTGTCCTACAGTCC 519           DD         159 SerTIPASnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 178	Oy 520 TCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG 579	Qy 580 ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACGTGGACAAGAAAGTGGAG 639	Qy 640 CCCAARICTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCGCGGG 699	Qy 700 GCACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACCCTCATGATCTCCCGGACC 759	Qy 760 CCTGAGGTCACATGCGTGGTGGTGGACGCACGAAGACCCTGAGGTCAAC 819	Qy         820         TGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGTAC         879           Ph	880 AACAGCACGTGCGTCGTCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC 93	Db 299 AlaserThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 318
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	Oy 1300 Db 439	O ACGCAGAAGACCTCTCCCTGTCTCCGGGTAAA 1332 
	RESULT 10 US-10-463-44; US-10-463-44; Publication; GENERAL IN APPLICANT APPLICANT TITLE OF FILE REFE; CURRENT A PRIOR PILE PRIOR FILE PRIOR FIL	RESULT 10 US-10-463-442-21 US-10-463-442-21 PUDICATION NO. US20040006216A1 GENERAL INFORMATION: APPLICANT: Waldmann, Herman APPLICANT: Waldmann, Herman APPLICANT: Brewin, Mark TITLE OF INVENTION: ACLYCOSYLATED ANTIBODIES FILER REPRENCE: Waldmann CURRENT APPLICATION NUMBER: US/10/463,442 CURRENT PILING DATE: 2000-06-18 PRIOR APPLICATION NUMBER: 991590.8 PRIOR APPLICATION NUMBER: 991590.8 PRIOR PILING DATE: 1999-07-21 PRIOR FILING DATE: 1999-07-21 PRIOR FILING DATE: 1999-07-21 SPRIOR FILING DATE: 1999-07-21 NUMBER: OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 21 LENGTH: 449 TYPE: PATENTE HOMO SAPIENS US-10-463-442-21
	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarit; Query Match:	ores: 9.46e-133 Length: 449 2173.50 Matches: 412 larity: 94.01% Conservative: 12 imilarity: 91.35% Mismatches: 18 15 Gaps: 2
	US-09-674-716	6B-18 (1-1335) x US-10-463-442-21 (1-449)
	è a	1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTC 60
	ò q	61 TCCTGTGCAGGTAGCGGATTCACTTTCAGTGGGTACTGGATGTCCTGGGTCCGCCAGGCT 120
	27	21 CCAGGGAAGGGGCTCGAGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 180

Qy         1240 TGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGAGGCTCTGCACAACCACTAC 1299           Db         419 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 438           Qy         1300 ACGCAGAAGAGCTCTCCCTGTCTCCGGTAAA 1332           Db         439 ThrGlnLysSerLeuSerForGlyLys 449           RESULT 11         US-09-822-698A-26           ; Sequence 26, Application US/09822698A           ; General INFORMATION:	APPLICANT: Hoogenboom, Hendricus R.J.M. APPLICANT: Henderikx, Maria P.G. TITLE OF INVENTION: MUCLUL Specific Binding Members and Methods of Use Theree; FILE REFERENCE: DYX-015.1 US CURRENT APPLICATION NUMBER: US/09/822,698A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 09/538,913 PRIOR PILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 112 SOFTWARE: Microsoft Word SEQ ID NO 26	; LENGTH: 451 ; TYPE: PRT ; ORGANISM: artificial sequence ; FEATURE: ; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1	Alignment Scores: Pred. No.: Pred. No.: Score: Scor	GAGGTGCAGCTGGTGGAGGCTTGGTAAGCCCGGGGGGTCCCTTAGACTC 60   1 G1nValG1	Qy         121 CCAGGGAAGGGGCTCGAGTGCTCAAATTAGATTGAAATTATGCAACA 180	CTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACA	
ProGlyLysGlyLeuGluTrpValSerThrIleSerThrSerGlyGlyArgThr 58  CATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 24  :::	340 TCAGCCTCCACCAAGGGCCCATGGGTCTTCCCCTGGCACCCTCCAAGAGGACCTCTT 399	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG 57	199 InriyrilecysasnvalasnHisbysProSerAsnThrLysValAspLysLyaIglu 218 640 CCCAAATCTTGTGACAAACTCACACAGGCCCGGCCCAGGCCTGAACTGGGGG 699 [11]	760 CCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAC 819 [	B80 AACAGCACGTACCGTGACGTCCTCACCGTCCTGCACGACTGACT	OTCCAAAGCCAAAGGGCAGCCCGAGAACCAGGTGTACACCCTGCCCCATCCCGGGGT 10	2 = 2 = 3 = 3 = 1

& 8	1240 IGGCAGCAGGGAAACGICTICTCAIGCTCCGIGATGCAIGAGCTCTGCACAACCACTAC 1299 	
oy D	1300 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1332 	
RESULT RE	Application US/09 S20020146750A1 RMATION: Hodgenboom, Hendri Henderikx, Maria VENTION: MUCIN-1 S NICK: DYX-015.1 US LICATION NUMBER: US G DATE: 2000-03-30 EQ ID NOS: 112 icrosoft Word	H.
, O	RGANISM: AILILLIA EATURE: THER INFORMATION: -822-698A-26	
Alignment Pred. No.: Score: Percent Si Best Local Query Matc	<pre>nment Scores:</pre>	
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6 6	121 CCAGGAAGGGCTCGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 180 	
\chi_{\text{q}}	181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240 :::      :::      ::: 59 TyrTyralaaspSerVallyGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 78	
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Sequence 3, Application US/09848832
Publication No. US20030165507A1
GENERAL INFORMATION:
APPLICANT: HOOPET, Douglas
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
FILE REFERENCE: HOOO1.NP0002
CURRENT APPLICATION NUMBER: US/09/848,832
CURRENT PILING DATE: 2001-05-04 RESULT 12 US-09-848-832-3

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Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/204, PRIOR FILING DATE: 2000-05-16, NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Ve; SEQ ID NO 3 LENGTH: 474
TYPE: PRT
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2172.50
93.228
89.938
                                              ; ORGANISM: Homo sapien
US-09-848-832-3
                                                                               Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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	982 CCCATCGAGAAAACCATCTCCAAAGCGAAAGGGCAGCCCCGAGAACCACACACA	1102 GGCTTCTATCCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1	GInGlyAsnValPheSerCysSerVa AAGAGCCTCTCCCTGTCTCCGGGTAA                   LysSerLeuSerLeuSerProGlyLy	; Sequence 3, Application US/10225108A; Publication No. US20030157112A1; Publication No. US20030157112A1; GENERAL INPORMATION: ; APPLICANT: HOOPER, Craig ; APPLICANT: DIPETSCROLD, Bernhard ; TITLE OF INVENTION: Recombinant Antibodies, and Compositions ; TITLE OF INVENTION: and Methods for Making Them ; FILE REPRENCE: 8321-110 ; CHEDRAL ADDITIONAL WINDOW: 10/10/2016 1008	CURRENT FILING DATE: 2003-04-10  PRIOR APPLICATION NUMBER: US 09/848,832  PRIOR APPLICATION NUMBER: US 09/848,832  PRIOR APPLICATION NUMBER: US 60/204,518  PRIOR PILING DATE: 2001-05-16  PRIOR PILING DATE: 2001-05-16  PRIOR FILING DATE: 2001-05-16  PRIOR FILING DATE: 2001-08-21	NUMBER OF SEQ ID NOS: 16  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO.3  LENGTH: 474  TYPE: PRT  ORGANISM: Homo sapiens US-10-225-108A-3	Pred. No.: 1.1e-132 Length: 474 Score: 2172.50 Matches: 411 Percent Similarity: 23.2\$ Conservative: 15 Best Local Similarity: 89.93\$ Mismatches: 16 Query Match: 16. 14.3\$ Indels: 2

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                                                  98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys
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78 TyrLeuAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr
                                 241 CIGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACA---
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                                         378 LeuproProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys
                                                                                                          GlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsn
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| Sequence 1, Application US/10461148
| Publication No. US20040013672A1 |
| GENERAL INFORMATION: |
| APPLICANT: Dietzschold, Bernhard |
| APPLICANT: Dietzschold, Bernhard |
| APPLICANT: Dietzschold, Bernhard |
| APPLICANT: Bioper, Douglas C. |
| TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS |
| TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME |
| FILE REFERENCE: 8321-110C11-185685 |
| CURRENT APPLICATION NUMBER: US 60/316/1148 |
| CURRENT FILING DATE: 2002-08-21 |
| PRIOR PILING DATE: 2002-08-21 |
| PRIOR PILING DATE: 2001-08-21 |
| PRIOR APPLICATION NUMBER: US 60/314,023 |
| PRIOR APPLICATION NUMBER: US 60/314,023 |
| PRIOR APPLICATION NUMBER: US 60/314,023 |
| PRIOR APPLICATION NUMBER: US 60/204,518 |
| PRIOR FILING DATE: 2001-05-04 |
| PRIOR FILING DATE: 2000-05-16 |
| NUMBER OF SEQ ID NOS: 24 |
| SEQ ID NO 1 |
| LENGTH: A74 |
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ORGANISM: Human
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         458 AlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
                                 RESULT 15

US-10-12-406-32

Sequence 32, Application US/10412406

Sequence 32, Application US/10412406

Publication No. US20040058394A1

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.

APPLICANT: GARBR, Ellen

APPLICANT: ALNE, Paul

TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINAJOGON

CURRENT APPLICATION NUMBER: US/10/412,406

CURRENT PILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: 60/240,285

PRIOR FILING DATE: 2001-013

PRIOR FILING DATE: 2001-03

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PESSEQ for Windows Version 4.0

SEQ ID NO 32

LEMPTH: 663
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US-10-412-406-32
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                                                                                                         ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu
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                                                                              <u> ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA</u>
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Solvia:
Use heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus
C;Species: Musculus
C;Accession: 338714
R;Cimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A;Reference number: 538713
A;Reference number: 538713
A;Reference number: S38714
A;Scatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIM>A;Cross-references: EMBL:X76014; NID:g416092; PIDN:CAA53601.1; PID:g1334076
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
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(c) 1993 - 2004 Compugen Ltd.
                                    protein search, using frame_plus_n2p model
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Db 41 GluLy,  Qy 270 TATGCC  Db 61 TYTALO  Qy 330 TACCTC  Db 101 LeuGly  RESULT 2  Species: Mus musec  C; Date: 30-Sep-1993  C; Accession: Prizzl3  R; Hong, H.J; Kim,  Gene 121, 331-335,  A; Accession: Prizzl3  R; Hong, H.J; Kim,  Gene 121, 331-335,  A; Residues: 1-139-R  A; Recented and and  A; References muser  A; Residues: 1-139-R  A; Accession: Prizzl3  A; Acce	GloubysGlyLeuGluTrpIleAlaGluIleArgLeuLysSerAspAsnTyrAlaThrHis 60   G29380   G29380   G1900 (BC-1000   G29380   G29380		PC1213 Ig heavy chain precursor V region (mAb H8) - mouse (fragment) C; Species: Mus musculus (house mouse) C; Species: Similarity: S18.00 Ray Match: Best Local Similarity: 74.63% Musculus (house mouse) C; Species: Similarity: Ray Musculus (house mouse) C; Species: Similarity: Ray Musculus (house mouse) C; Species: Similarity: Ray Musculus (house mouse) C; Matching and characterization of CDNAs coding for heavy and light chains of a mq A; A; Reference number: PC1213; MulDi:1446832 A; Raference number:		Scores:       2.92e-43       Length:       139       Oy       150       TGTGTAGCCTCTGGATTTACTTTCAGT         :       2.92e-43       Length:       101       Db       41       CyshlaAlaSerGlyPheThrPheSerT         imilarity:       88.37%       Mismacches:       15       Cy       210       GAGAAGGGCTTGAGTGGGTTGAA         ch:       68.79%       Indels:       8       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	(1-415) x PC1213 (1-139)       Qy       270         GGATTTTGGGCTGATTTTTTTTTTTTTTTTTATGGGGCTCCAGAGTGAA 89       Db       81         LTYLEuGlyLeuAsnTyxValPheilevalPheilevalPheilevalPheilevalPheilevalChyvalGlnSerGlu 20       Qy       330	GTGAAGCTTGAGGAGGAGGAGGAGGTTGGTGCAACCTGGAGGATCCATGAAACTTCTC 149	TGTGTAGCCTCTGGATTTACTTTGAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA 209	GAGAAGGGCTTGAGTGCTGAAATTAGATTGAAATCTGATAATTATGCAACAT 269 	270 TATGCGGGAAGTTGAAAGAGAAGATGATTCCAAAAGTCGTCTC 329   C. Accessaron: (92811, 40407/2   C. Accessa	TACCIGCAAAIGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
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.uLeuArgSerLysAlaHisAsnHisAlaThrTyr 80
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Db 41 ProGluLysGlyLeuGluTrpValAlaGluLleArgLeuLysSerHisAsnTyrAlaThr 60  Qy 267 CATTATGCGGAGTCTCTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326	NULT 6  MS51  heavy chain V-III region (U61) - mouse Species: Mus musculus (house mouse) Accession: 83818; A02072  Vrana, M.; Rudikoff, S.; Potter, M.  Title: Sequence variation among heavy chain Reference number: A93818; MUD:78158406; PW Accession: B93818  Rolling: Protein Residues: 1-113 <- VVRA Comment: This chain was isolated from a mye Superfamily: immunoglobulin Reywords: heterotetramer; immunoglobulin ReyNords: heterotetramer; immunoglobulin LS-100/Domain: immunoglobulin homology <- INW	Alignment Scores: Pred. No.: 5.14e-43	Db 41 ProGluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerHisAsnTyrAlaThr 60  Qy 267 CATTATGCGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326  Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  Qy 327 CTCTACCTGCAAATGAAAGACTGAAGACGAGAGATTATTACTGTACA 383  :::	S67945  Ig heavy chain BrE-3 - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C;Accession: S67945
Alignment Scores: Pred. No.: S17.50 Score: Score: Percent Similarity: Percent Similari	TTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCGGTCT	Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110 RESULT 5 AVMSAB GyPecies: Wus musculus (house mouse) C;Species: Wus musculus (house mouse) C;Species: Apr-1984 #sequence_revision 30-Jun-1993 #text_change 31-Mar-1997 C;Accession: A93818; A02072 C;Accession: A93818; A02072 R;Vanat. M.; Rudikoff, S; Potter, M. R;Vanat. M.; Rudikoff, S; Potter, M. R;Vaccence number: A93818; MUD:78158406; PMID:41734 A;Relecence number: A93818; MUD:78158406; PMID:41734 A;Relecence number: A93818 A;Molecule type: protein A;Rocession: A93818 A;Molecule type: protein A;Residues: 1-113 cyRa> C;Comment: This chain was isolated from a myeloma protein that binds inulin. C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;22-100/Domain: immunoglobulin homology  E;22-98/Disulfide bonds: #status predicted	Alignment Scores: Pred. No.: Score: S	

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Taylors (ABE-47N) - mouse (C.Species: Mus musculus (house mouse) (C.Species: Mus M.) (190400), A02072 (Musculus Musculus Musculus (Musculus Musculus Musculus (Musculus Musculus Musculus (house) (Musculus Musculus (house) (Musculus (house) (hou
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Ig heavy chain V region (251.3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C;Accession: A25803
R;Hebbst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.
R;Hebst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.
Biol. Chem. Hoppe-Seyler 367, 843-351, 1986
A;Title: The complete amino-acid sequence of the variable domain of a monoclonal A;Reference number: A25803; MUID:87076047; PMID:3539142
A;Accession: A25803
A;Molecule type: protein
A;Residues: 1-115 cHRR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Seywords: heteroterramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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  R;Couto, J.R.; Blank, E.W.; Peterson, J.A.; Ceriani, R.L.
Hybridoma 12, 15-23, 1993
A;Title: Cloning of CDNAs encoding the variable domains of antibody BrE-3 a
A;Reference number: S67944; MUID:93202671; PMID:8454302
A;Reference number: S67945
A;Reture: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <COU>
A;Cross-references: EMBL:222546; NID:g296066; PIDN:CAA80267.1; PID:g296067
C;Superfamily: immunoglobulin V region; immunoglobulin homology
E;25-110/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: C93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma prote A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: C93818
A;Molecule type: protein
A;Residues: 1-113 < VRAA
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;22-98/Disulfide bonds: #status predicted
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F;22-98/Disulfide
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C;Species Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: A92810; A02072
R;Rudikoff, S; Potterer, M.
J. Immunol. 127, 191-194, 1981
A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a A;Reference number: A92810; MUID:81216632; PMID:6787122
A;Accession: A92810
A;Molecule type: protein
A;Reference number: A92810
A;Molecule type: protein
A;Reference number: manusclobulin V region; immunoglobulin homology
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-100/Domain: immunoglobulin predicted
F;22-98/Disulfide bonds: #status predicted
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Ig heavy chain V-III region (W3082) - mouse
Ig heavy chain V-III region (W3082) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: D92811; A02072
R;Johnson, N; Slankard, J; Paul, L.; Hood, L.
G;Immunol. 128, 302-307, 1982
A;Title: The complete V domain amino acid sequences of two myeloma inulin-bi
A;Reference number: A92811; MUID:82099361; PMID:6798111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 1-115 <00Hs
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer
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5
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
    413
                         GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110
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    GATTTCATAGACTGGGGCCAAGGGACACTA
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507.50
91.82$
87.27$
67.40$
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Best Local Similarity:
Query Match:
DB:
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    384
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Ig heavy chain precursor V region (9-40) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 27-Uul-1990 #sequence_revision 27-Jul-1990 #text_change 23-Jul-1999 (A;Coession: D3490) A;Coession: D34903 A;N: Edmundson, A.B.; Voss Jr., E.W. A;Ritle: Active site structure and antigen binding properties of idiotypically cross-reach A;Reference number: A34903; MUID:90094387; PMID:2104617
                       Cypace: Instrugy 127 medicular procession: A02073

R) RudikOff, S.; Potter, M.

R) RudikOff, S.; Potter, M.

J. Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a new pyritie: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a new pyrecession: A02073

A) Reference number: A92810; MUID:81216632; PMID:6787122

A) Accession: A02073

A) Residues: 1-113 < RUD:
C) Comment: This chain was isolated from a myeloma protein that binds inulin.
C) Comment: This chain was isolated from a myeloma protein that binds inulin.
C) Superfamily: immunoglobulin V region; immunoglobulin homology
C) Reywords: heteroterramer; immunoglobulin homology claws
F) 15-100/Domain: immunoglobulin homology claws
F) 15-100/Domain: immunoglobulin homology claws
F) 2-98/Disulfide bonds: #status predicted
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A;Residues: 1-137 <BED.
A;Cross-references: GB:M32378; GB:J05237; GB:J05238; NID:g639652; PIDN:AAA61587.1; PID:g6
C;Superfemily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997
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496.50
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Cuery Match: 65.74*   Indels: 6   Gaps: 2   Caps: 3.6   Caps:																
1.09-674-716B-1 (1-415) x D34903 (1-137)   1.09-674-716B-1   1.09-674-716G-1   1.09-674-71																
ery Match: :-09-674-716E 36 1 90 21 150 41 210 210 61 101 121						4										
ery Match: :-09-674-716E 36 1 90 21 150 41 210 210 61 101 121			GAGTGA	l nCysGl	ACTOTO	 	GICTCC	 nSerPro	AACACA	:: ThrTy	rcgrcr	:: rServa	AGATTT	 rSerTy		
ery Match: :-09-674-716E 36 1 90 21 150 41 210 210 61 101 121			GGTCCA	yvalgl	CATGAA	OMetLy	CCGCCA	  ArgG1	TTATGC	 nTyrGl	CAAAAG	 rLysSe	CTGTAC	 rCysTh		
ery Match: :-09-674-716E 36 1 90 21 150 41 210 210 61 101 121			AAAAGG	uLysg1	AGGATC	 yArgPr	TTGGGT	:      nTrpVa	TGATAA	OTyras	TGATIC	 pAspSe	TTATT	:      eTyrTy		
ery Match: :-09-674-716E 36 1 90 21 150 210 61 270 81 101 121	901		TCTTT	erenre	ACCTGG	 nProGl	GATGTC	:: pMetAs	GAAATC	 nLysPr	AAGAGA	 rArgAs	TGGAGT	:: tGlyIl		
ery Match: :-09-674-716E 36 1 90 21 150 41 210 210 61 101 121	ω		TATTGI	evalPh	GGTGCA	 uValGl	CTACTG	PTYYT	TAGAT	 eArgAs	CATCTC	rllese	AGACAG	 uAspMe	GACACT	 yThrLe
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ery Match: :-09-674-716E 36 1 90 21 150 41 210 210 61 101 121	55.74%	x D349	GCTG	  YLeuSe	GGAGTC	:   : :pGluTh	TGGATI	rGlyPh	TGAGTG	 uGluTr	TGTGAA	rvally	GAACAG	: tAsnAs	-ATAGA	yAlaTy
ery Match: :-09-674-716E 36 1 90 21 150 210 61 270 81 101 121	Φ14	-415)	TTTTG	rLeuGl	GCTTGA	:  srenys	AGCCTC	  AlaSe	GGGGCT	  sGlyte	GGAGTC	rAspse	GCAAAT	 uGlnMe	1	rHisGl
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SEQUENCE.

The complete V domain amino acid sequences of two myeloma inulindrations N., Slankard J., Paul L., Hood L.;

Johnson N., Slankard J., Paul L., Hood L.;

The complete V domain amino acid sequences of two myeloma inulindrations of the complete V domain amino acid sequences of two myeloma inulindrations N. Immunol. 128:302-307(1982).

L. Immunol. 128:302-307(1982).

L. MICARIAN SELONA A MYELOMA PROTEIN THAT BINDS INULIN.

C. -- SIMILARITY: Contains 1 immunoglobulin-like domain.

PROST 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1980: 1
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region J606.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteleostomi; Remannalia; Buteleostomi; Mammalia; Buteleostomi; Marmalia; Buteleostomi; Mammalia; Buteleostomi; Marmalia; Rodentia; Sciurognathi; Muridae; Musinae; 
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98 BY SIMILARITY.
115
12810 MW; B67AD6638A121A5F CRC64;
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HV31 HUMAN
HV31 HUMAN
HV24 MOUSE
HV36 MOUSE
HV38 MOUSE
HV38 HV38 HV38
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HV41_MOUSE
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                  using frame_plus_n2p model
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HV36 MOUSE
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Listing first 45 summaries
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                                                                                                                                   207 CCAGAGAAGGGGCTTGAGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 266
                                                                                                                                                                                                          267 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
                                                                                                                                                                                                                                                                                  327 CICTACCIGCAAAIGAACAGCITAAGAGCIGAAGACAGIGGAGITIATIACIGI---ACA 383
                                                                             21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
                                                                                                                                                       41 ProGluLysGlyLeuGluTrpValAlaGlulleArgLeuLysSerHisAsnTyrAlaThr 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proceins.";
Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).
Proc. Matl. Acad. Sci. U.S.A. 75:1957-1961 (1978).
BINDS INULIN.
-I-SINLIARITY: Contains 1 immunoglobulin-like domain.
PIR; B93818; AVMS61.
HSSP; PO1810; 2FB0.
InterPro; IPR003596; Ig—v.
Fram; PF00047; ig, 1.
SWART; SM00406; IGV; 1.
SWART; SM00406; IGV; 1.
SWART; SM00406; IGV: 1.
Immunoglobulin V region.
IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV28 MOUSE STANDARD; PRT; 113 AA.
P01797;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region U61.
Ig heavy chain V-III region U61.
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=78158406; PubMed-417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
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Mismatches:
Indels:
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BY SIMILARITY.
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88.18%
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Best Local Similarity:
Query Match:
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                                                                                                                                                           21 SerCysValalaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.;

Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

-I. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOWA PROTEIN THAT BINDS INULIN.

-I. STATLARATY: Contains 1 immunoglobulin-like domain.

PIR., A93818; AVWSAB.

HSSP, P01810; 2FBJ.

InterPror IPR007110; 1g-like.

Pfam; PF00447; 1g; 1.

PROSITE: PS0086; Ig_v.

PROSITE: PS00835; IG_LIKE; 1.
                                                                                 41 ProGluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrAlaThr
                                                               GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC
                                                                                                                                         247 ICCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region A4.
If who musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. C.11 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76658C121C598285 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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BY SIMILARITY
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                           US-09-674-716B-1 (1-415) x HV32_MOUSE (1-115)
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113 AA; 12675 MW;
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SEQUENCE
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147 TCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCT 206

87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 146

CRC64;

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| Biochemistry 16:1170-1175(1977).
| Calchemistry 16:1170-1175(1977).
| Calchemistry 16:1170-1175(1977).
| Calchemistry 16:1170-1175(1977).
| EINDS INULINI.
| Calchemistry 17 Contains 1 immunoglobulin-like domain.
| Pir, A90400; ANMSB7.
| HSSP: PO1810; PR007110; Ig-like.
| RicePro; IPR007110; Ig-like.
| RicePro; IPR007110; Ig-like.
| RicePro; IPR008396; Ig_v.
| Pfam; PF00047; ig; 1.
| Ryart; SM00466; IGv; 1.
| Ryart; SM00466; IGv; 1.
| Proximal 1 > 113 IG-like.
| DisULFID 22 98 BY SIMILARITY.
| PON TER 113 113 113 113 | 113 A4; 12675 MW; 76658C16C779845E CRC64;
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CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT
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MEDLINE-77134726; PubMed=402936;
Vrana M. Rudikoff S., Potter M.;
"Heavy-chain variable-region sequence from an inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Als musculus (Mouse).
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MEDLINE=81216632; PubMed=6787122;
Radikoff S., Potter M.;
Rudikoff S., Potter M.;
Rudikoff S., Potter M.;
Rudikoff S., Potter M.;
Immunoglobulin heavy chains from anti-inulin myeloma proteins:
RT evidence for a new heavy chain joining segment.";
RT evidence for a new heavy chain joining segment.";
R. J. Immunol. 127.191-194(1981).
C. -! MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOWA PROTEIN THAT BINDS INULIN.
C. -! SIMILARITY: Contains 1 immunoglobulin-like domain.
RINGST. PROSTING 109-11.
RINGST. PROSTING 109-11.
RINGST. PROSTING 109-11.
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10-COT-1993 (Rel. 27, Last sequence update)
10-COT-2003 (Rel. 42, Last annotation update)
10 heavy chain V-III region T957.

Ig heavy chain V-III region T957.

Bukaryctains (Mouse).

Bukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
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101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110
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CALTAIGCGGAGICIGIGAAAGGGAAGIICACCAICICAAGAGAIGAIGCAAAAAGICGI 326

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81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrAlaIleTyrTyrCysSerThr 100

413

384 GATTTCATAGACTGGGGCCAAGGGACACTA

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proteins.";
Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

"In Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

"In MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT STRUCK IN THAIR 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 146
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region E109.
If heavy chain V-III region E109.
Bus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"Sequence variation among heavy chains from inulin-binding myeloma
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Matches:
Conservative:
Mismatches:
Indels:
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MEDLINE=78158406; PubMed=417344;
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WEDLINE=82099361; PubMed=6798111;
WEDLINE=82099361; PubMed=6798111;
WEDLINESSURE:
"Incomplete V domain amino acid sequences of two myeloma inulingrate binding proteins.";
"In immunol. 128:302-307(1982).
"In immunol. 128:302-307(1982).
"Incomplete V domains in immunoglobulin-like domain.
"In SIMILARITY: Contains I immunoglobulin-like domain.
"In SIMILARITY: Contains I immunoglobulin-like domain.
"In PROSIDE: PRO03505: Ig_v.
"InterPro; IPR003505: Ig_v.
"InterPro; IPR003506: Ig_v.
"InterPro; IPR003505: Ig_v.
"InterPro; IPR003505: Ig_v.
"InterPro; IPR003506: Ig_v.
"InterPro; IPR003
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                                                                                                              327 CTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT---ACA 383
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1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
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PO1802...
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region W3082.
Wus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; M
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REAL MEDLINE=81216632; PubMed=6787122;
RA MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
Rudikoff S., Potter M.;
Tramunoglobulin heavy chains from anti-inulin myeloma proteins:
Tramunoglobulin heavy chains from anti-inulin myeloma proteins:
RT Tranunoglobulin heavy chains from anti-inulin myeloma proteins:
RT Tranunoglobulin myeloma proteins:
RT Tranunoglobulin myeloma proteins:
RT Tranunoglobulin myeloma proteins:
RT Tranunoglobulin-like domain.
DR PRS A02073; HVMSAM.
DR PRS PO1739; IMCP.
RINGEPRO; IPRO0356; Ig.-v.
RINGEPRO; IPRO0356; Ig.-v.
RESP: PO1749; 19; 1.
RESP: PO1749; 10; 1.
RESP: RESP: RESPERS RESPE 206 87 GAAGUGAAGCITGAGGAGTGAGGGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 146 CCAGAGAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 266 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326 61 HisTyralaGluSerVallysGlyArgPheThrIleSerArgAspAspSerLysSerSer 80 40 RESULT B

RESULT B

RESULT B

ROUGE

1D 47944 MOUSE

STANDARD; PRT; 113 AA.

C 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

OC Mammalia S (Rel. 01, Last sequence)

NAMMALIA TAXID=10090;

RN MAMMALIA TAXID=10090;

RN MILL TAXID=10000;

RN MILL TAXID=10000;

RN MILL TAXID=10000;

RN MILL TAXID=10000;

RN MIL 147 TCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCT Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: GlyPheProSerTrpGlyProGlyThrLeu 110 GATTTCATAGACTGGGGCCAAGGGACACTA 413 US-09-674-716B-1 (1-415) x HV34\_MOUSE (1-113) 6.13e-49 496.50 90.91% 85.45% 65.94% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 207 41 267 384 21 Query Match: DB: g 셤 ò 임 임 ð ò ò ò ò

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SECURINE STORN N.A.

SECURINE STORN N.A.

MEDLINE=81013937; PubMed=6251474;

Bernard O., Gough N.M.;

MEDLINE=81013937; PubMed=6251474;

Bernard O., Gough N.M.;

MEDLINE=81013937; PubMed=6251474;

Bernard O., Gough N.M.;

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                                   11-07.,
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
If heavy chain V-III region HPC76 (Fragment).
Buks musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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111 AA

PRT;

STANDARD;

TUR Seb So TS:To:#7

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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region WH26 precursor.
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MEDLINE=81101090; PubMed=6450418;
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20 >117 IG
117 117
117 AA, 12582 MW;
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82.05%
68.38%
54.71%
                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                               NCBI_TaxID=9606;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 TyrGlyLysSerLeuLysGlyArgPheThrLeuSerArgAspAspSerLysSerIleVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||
| MetAspLeuArgLeuThrTyrValPheIleValAlaIleLeuLysGlyValLeuCysGlu
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                                                                                       Rāttus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                  MEDLINE-83064537; PubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                     Ducieic Acids Res. 10:6041-6049(1982).

-!- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
-!- MINOCYTOWA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.

R PIR; A02075; EVRTR2.
R HSSP; P01789; 1MCP.
R InterPro; IPR00310; Ig-like.
R InterPro; IPR003596; Ig_v.
R Pfam; PF00047; ig; 1.
R RMARY; SMO0406; IGv. 1.
R PROSITE; PS50835; IG LIKE; 1.
W Immunoglobulin V region; Signal.
T SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TyrGlyGlyTyrSerGluAsnTrpPheValTyrTrpGlyGlyThrLeu 137
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region IR2 precursor.
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63.50%
61.95%
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                                                                                                                                                      NCBI_TaxID=10116;
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Pred. No.:
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HV3C_HUMAN
ID HV3C_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human immunoglobulin
meavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E826733F1A3CB0F1 CRC64;
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EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; HGWU: 23-DEC-99.
Genew; HGWN:5545; IGHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000575; C:extracellular; NAS.
GO; GO:000555; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig-v.
Pfan; PF00047; ig; I.
EMART; SM00406; igv: 1.
PROSITE; PS50835; IG_LIKE; I.
Immunglobulin V region; Signal; 3D-structure.
SIGNAL
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                         213 AAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACATTAT
                                                          273 GCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltimore D.;
"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mus musculus (Youse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                     333 CTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT 380
                                                                                                                                                                                                                                                              99 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTyrCys 114
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D SEGMENT.
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MEDLINE=77100358; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
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PIR; E90809; GIMS21.
PDB; IIGC; 03-UTN-95.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; Ig-v.
Immunoglobulin V region; Signal; 3D-structure.
SIGNAL
SIGNAL 11 136 IG HEAVY CHAIN V RECHAIN IN INTERPORTED INTERPORTE
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Matches:
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405.00
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Pred. No.:
Score:
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ID HV16 MOUSE
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CONFLICT
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79 TyrGlyAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAspPheGlyLeullePhePheIleValAlaLeuLeuLysGlyValGlnCysGluVal
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                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V region 441 precursor.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                           330 TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT 380
                                                                                                          99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCys 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-82059449; PubMed-6795591;
MEDLINE-82059449; PubMed-6795591;
Ollo R., Auffray C., Sikorav J.-L., Rougeon F.;
"Mouse heavy chain variable regions: nucleotide sequence of germ-line VH gene segment.";
Nucleic Acids Res. 9:4099-4109(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION 441. IG-LIKE,
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19 >116 IG-LIKE.
116 116 AA: 12911 MW; 684FF3EF9A95D9F3 CRC64;
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Pred. No.:
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P18525;
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                                                                                                                                                                                                                                                                                          GGGAAGTICACCATCTCAAGAGATGATTCCAAAAGTCGTCTTCTACCTGCAAATGAACAGC 347
                                                                                                                                                                                                                                                                                                          102 LeuargSerGluaspIhralaMetTyrTyrCysalaargTrpGlyasnTyrProTyrTyr 121
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Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOWA PROTEIN
THAT BINDS PHOSPHORYLCHOLINE.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                        GlyGlyGlyLeuValGlnProGlyGlySerArgLysLeuSerCysAlaAlaSerGlyPhe
                                                                                                                                                                                                           64 ValAlaTyrIle----SerSerGlySerSerThrLeuHisTyrAlaAspThrValLys
                                                                                                    GGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTT
                                                                                                                                                                                         ACTITICAGIGGCIACIGGAIGICITIGGGICCGCCAGICTCCAGAGAGGGGCTIGAGIGG
                                                                                                                                                                                                                                          GTTGCTGAAATTAGATTCTGATAATTATGCAACACATTATGCGAGTCTGTGAAA
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Kim S., Davis M., Sinn E., Patten P., Hood L.,
"Antihody diversity: somatic hypermutation of rearranged VH genes.";
(211 27:573-581(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDILIDE76222762. PubMed=819932;
RUDIKOff S., Potter M.;
"Size differences among immunoglobulin heavy chains from
                                                                                                                                                                                                                                                                                                                                             348 TTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA------
 2 1 1 9 8 4 4 8
 Conservative:
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            Mismatches:
Indels:
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21-JUJ-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                             US-09-674-716B-1 (1-415) x HV16_MOUSE (1-136)
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171 TTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCAGAAGGGGGCTTGAGTGGGTT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 AAGTICACCATCICAAGAGAIGATICCAAAAGICGICTCTACCIGCAAAIGAACAGCTIA 350
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                     IG HEAVY CHAIN V REGION M167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 AGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATAGAC
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01-NOV-1990 (Rel. 16, Last sequence update)
11-NOV-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 5-84 precursor.
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MEDLINE=89279149; PubMed=2499654;
                                                                     Pfam, PF00047; ig; 1.
SMART, SM00406; IGy, 1.
PROSITE, PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
HSSP, P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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90 GIGAAGCIIGAGGAGICIGGAGGAGGCIIGGIGCAACCIGGAGGAICCAIGAAACICICC 149
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-!- MISCELLANBOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY. JT0505; HVWS84.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT 380
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                                                                                                                                                                                      IG HEAVY CHAIN V REGION 5-84.
REAMEWORK-1.
COMPLEXENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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117
12872 MW, 234055CB6A469861 CRC64;
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Matches:
Conservative:
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                                           HSSP; P01810; 2FBJ.
InterPor; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMARY; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V regīon; Signal.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                      Q96bb9 homo
Q8wukl homo
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Q921k1 n
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Straubberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC049143; AAH49143.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR00306; Ig-MHC.
InterPro; IPR00306; Ig-W.
RimterPro; IPR00309; Ig; 3.
SMART; SM00409; IG; 3.
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Q9UJ38
Q9UJ38
Q9UJ38
Q9UJ28
Q9UJ28
Q9UJ28
Q9UJ28
Q9UJ21
Q9UJ21
Q9UJ21
Q9UJ21
Q9UJ23
Q9UG3
Q7TMK4
Q8R3V9
Q96BB9
Q8WUK1
Q91WP5
Q99KA4
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01-JUN-2003 (TrEMBLrel. 24, C:
01-JUN-2003 (TrEMBLrel. 24, L:
01-OCT-2003 (TrEMBLrel. 25, Lie
Hypothetical protein.
Mus musculus (Mouse).
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     Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-G=CgnZ_1USFVO_spool_p/US09674716/runat_30092004_070258_25867/app_query.fasta_1.3164
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OCALIGN=200 -TRR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINNEN=0 -MAXLEN=2000000000
-USRE-USD6574716_GCGN 1 1 499_Grunat 30092004_070258_25867 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -MINLEN=1 -MATRIX=0 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -MARDEN=10 -MARDEN=0 -S -FGAPOP=6
-DEG_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -MARDEN=7
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1 aagctttacagttactcagc......tgggggccaagggacactagt 415
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                            - protein search, using frame plus n2p model
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p_vertebrate:*
p_unclassified:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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sp bacteria:*
sp fungl:*
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sp invertebrate:*
sp mammal:*
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sp phage:*
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and is derived by analysis of
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STRAIN=22188257, PubMed=1247932,

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RIGHER-22388257, PubMed=12477932,

RIGHER-22388257, PubMed=12477932,

RIGHER-22388257, PubMed=12477932,

RIGHER-22388257, Roader L., Schaefer G.P., Bhat N.K.,

Richerdo L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Richerds M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garciar A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garciar A.M., Gabbs R.A.,

Raha, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last amnotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 53019 MW;
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534.50
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 VallysLeuAspGluThrGlyGlyGlyLeuValGlnProGlyArgProMetLysLeuSer
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024405; AAH24405.1; -.
                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Breast tumor;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055905; AR55905.1; -.
Hypothetical protein.
SEQUENCE 479 AA; 52209 MW; 532DED9D46D0AEED CRC64;
                                                                                                                                                                                                                                                                      479
90
116
8
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Last annotation update)
                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                              US-09-674-716B-1 (1-415) x Q7TMK4 (1-479)
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21,
25,
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468.00
81.54%
69.23%
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01-JUN-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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IGH-4.
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Best Local Similarity:
Query Match:
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                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           Alignment Scores:
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Q8R3V9
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PROSITE; PS50835; IG_LIKE; 5. PROSITE; PS00290; IG_MHC; 3. Hypotherical protein. SEQUENCE 597 AA; 65039 MW;
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422.50
72.73%
59.44%
56.11%
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Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 AAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTCTACCTGCAAATGAACAGCTTA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 ArgPheThrileSerArgAspAsnSerGlnSerIleLeuTyrLeuGlnMetAsnAlaLeu 107
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Q96BB);
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2003 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-B-cell;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Stubmitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015/60; AAH15/60.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003806; Ig_MHC.
InterPro; IPR003896; Ig_V.
Pfam; PP00401; ig; S.
SMART; SM00406; IGV; 1.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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        PIR, B45837, B45837.

MGD; MOI:96446; IGh-4.

InterPro; IPR003106; IG-like.

InterPro; IRR03356; IG-WHC.

InterPro; IRR03556; IG-WHC.

Fram; PP00047; ig; 3.

SMART; SM00406; IG's 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG MHC; 1.

Hypothetical protein.

SEQUENCE 469 AA; 51976 MW; 5
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431.00
72.93%
62.41%
57.24%
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Best Local Similarity:
Query Match:
DB:
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AC 096BB
AC 096BB
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DT 
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383
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                                                                                                                                                                                                                                                                                                                                                                                 150 TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA
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01-MRA-2002 (TrEMBLrel. 20, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-TONSI;
SEQUENCE FROM N.A.
TISSUE-TONSI;
Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AAH20240.1; -.
FTR; PL0120; PL0120.
FTR; PL0120; PL0120.
FTR; PL0120; PL0120.
THE*SPO; S1S590; S1S590.
THE*PPCO; IPR003006; Ig_MHC.
THE*PPCO; IPR003006; Ig_MHC.
THE*PPCO; IPR00306; Ig_WHC.
FTAN; PF00047; Ig; S.
SYART; SM00406; IGV; I.
FROSITE; PS50835; IG_LIKE; 5.
4FCA3AD8ECE263D9 CRC64,
                                                        597
85
119
118
21
4
                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-09-674-716B-1 (1-415) x Q99KA4 (1-487)
76.92%
63.08%
54.12%
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                       Similarity:
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  Percent Similarity:
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                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                       90 GTGAAGCTTGAGGAGTCTGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GlyLysGlyLeuGluTrpValAlaValIleSerTyrAspGlySerAsn----LysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutherla, Rodentia, Sciurognathi, Muridae, Musinse, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Colon;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013656; AAH13656.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-V.
Pfam; PF00047; ig-4; 4.
SMART; SMO0406; IG-V.
PROSITE; PS00296; IG-MHC; 2.
                                          60C7F5950671E315 CRC64;
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84
117
123
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82
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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                     Hypothetical protein.
SEQUENCE 613 AA; 67296 MW;
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  PROSITE; PS00290; IG_MHC; 3.
                                                                                                             1.99e-38
420.00
74.26%
61.76%
55.78%
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407.50
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479 AA; 5
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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SEQUENCE 47
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Score:
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Q91WP5
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                                                                                                                                                                                                                                                                                           150 TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Strausberg R.;

Lu Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.)

R EMBL; BC004786; AAH44786.1; -.

R RASP; PO1810; ZFBJ.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003596; Ig-WG.

DR RAPER, SM00406; Ig-W.

DR SMRT; SM00406; Ig-V.

DR SMRT; SP50435; IG-Like; 4.

DR PROSITE; PS50435; IG-Like; 4.

SRQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Conservative:
              Mismatches:
Indels:
Gaps:
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                                                                                               US-09-674-716B-1 (1-415) x Q91WP5 (1-479)
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405.00
75.00%
59.29%
53.78%
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104

288 GGGAAGTICACCATCTCAAGAGATGATTCCAAAAGTCGTCTCTACCTGCAAATGAACAGC 347

228 GTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACCATTATGCGGAGTCTGTGAAA

∂ g & 8 |||||||:::|||||||::: 105 LeuArgSerGluAspThrAlaMetTyrTyrCysAlaArgGluLeuTrpLeuArgArg1le 124

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8 P 8

348 TTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA-------

287

84

227

46

99

167

108 GGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTT 168 ACTITCAGIGGCIACIGGAIGICIIGGGICCGCCAGICICCAGAGAGGGGCCTIGAGIGG

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7 LeuValPheLeuValLeuIleLeuLysGlyValGlnCysGluValGlnLeuValGluSer

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CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAAGTCGT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: ||| ||||||||||| 137 serProTyrGlyGlyTyrSerArgPheAspTyrTrpGlyGlnGlyThr 137
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  ATGGATTTTGGG-----CTGATTTTTTTTTATTGTTCTTTTAAAAGGGGTCCAGAGTGAA
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Strausberg R.;

L Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

E BMBL; BCOL01327; AAH10327.1; -.

R RGD; MG1:2144697; AU044919.

R GO; GO:0006118; P:electron transporter activity; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R InterPro; IPR000345; CytC, heme_BS.

R InterPro; IPR00345; CytC, heme_BS.

R InterPro; IPR00346; Ig_MG.

DR InterPro; IPR0036; Ig_W.

DR FROSTIF; PS00190; CYTOCHROME_C; 1.

DR PROSTIF; PS00190; CYTOCHROME_C; 1.

DR PROSTIF; PS00290; IG_MRC; 1.

KW Hypothetical protein.

KW Hypothetical protein.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Matches:
Conservative:
Mismatches:
Indels:
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404.00
76.74%
61.24%
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Percent Similarity:
Best Local Similarity:
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SEQUENCE FROM N.A.
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091205
AC 091205;
DT 01-DEC-20
DT 0
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996K68 PRELIMINARY, PRT, 494 AA.
096K68,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ14473.
Hypothetical protein FLJ14473.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CTISSUB=Mammary gland;

REGGITT. T. Otsuki T., Suzuki Y.,

RISSUB=Mammary gland;

RISSUB-Mammary Gland;

RISSUB-MA 36 ATGGATTTTGGGCTG-----ATTTTTTTTTTTTTTATAAAGGGGTCCAGAGTGAA 89 9A1D7AEB5AEE4C0E CRC64; Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-674-716B-1 (1-415) x Q96K68 (1-494) Hypothetical protein. SEQUENCE 494 AA; 53088 MW; 3.48e-36 400.00 72.46% 57.25% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: RESULT TO SEE THE SEE

107

Gaps:

US-09-674-716B-1 (1-415) x Q91Z05 (1-473)

Query Match: DB:

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310 GAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT
269
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                                                       21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GlySerGlySerTyrIleGlyTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThr 137
                                                                                                                                                                  330 TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA-----
                              TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
Mt. X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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18
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035024; AAD56260.1; -.
HSRB; PO1772; 2FB4.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003596; Ig-v.
R Fam; PF00047; Jg; I.
SNART; SM00406; IGv; I.
R SNART; SM00406; IGv; I.
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Matches:
Conservative:
Mismatches:
Indels:
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113 AA; 12437 MW;
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394.50
80.91%
70.91%
52.39%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAAGCTTGAGGAGTCTGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCC 149
                                                                                                                                                                                                                                                                                       210 GAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTCTGATAATTATGCAACACAT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 GIGAAGCITGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTC 149
                                                                                                             21 ValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeuSer 40
                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                             36 ATGGATTTTGGGCTG----ATTTTTTTTTTTTTAAAAGGGGTCCAGAGTGAA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGluLeuGlyLeuSerTrpIlePheLeuLeuAlaIleLeuLySGlyValGlnCysGlu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 ValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyArgSerLeuArgLeuSer 40
                                                                                                                                                                                                                                                                                                                         61 GlyLySGlyLeuGluTrpValSerSerIleSerSerArgSerAsp-----TyrIleTyr
                                                                                                                                                                                     150 TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGGCCAGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                               270 TATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GATTTCATAGACTGGGGCCAAGGGACACTA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BOC01276; AAH21276.1;
PTR; 231205; S21205.
R InterPro; IPR007110; Ig-11ke.
R InterPro; IPR003356; Ig-MHC.
R InterPro; IPR003356; Ig-WHC.
R PROMO406; Ig-V.
R PROSITE; PS00435; IG LIKE; 4.
PROSITE; PS00290; IG-MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
573 AA; 62967 MW;
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395.00
71.22%
58.99%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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SEQUENCE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
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DB:
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**08WU3** 

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Score:

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CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAAGTCGT 326 CICIACCIGCAAAIGAACAGCITAAGAGCIGAAGACAGIGGAGITITAITACIGIACA--- 383 ProGlyLysGlyLeuGluTrpValAlaPheIleArgTyrAspGlySerAsn----Lys 384 GATTTCATAGACTGGGGCCAAGGGACACTA 413 Thu Sep 30 13:18:42 2004 29 327 79 qq à d  $\delta$ ò

091XE1, 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein (Fragment). Hypothetical protein (Fragment). Bukaryota, Metazca, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinse, Mus. Z 480 PRT; PRELIMINARY; RESULT 12
091XE
10 091XE
10 091XE
DT 091XE
DT 01-0F
DT 01-0F
DT 01-0F
DE HYPO'
OC MARMY
OC MA

||| | AspleuAsnTyrTrpGlyGlnGlyThrLeu 108

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NCBI\_TaxID=10090;

SEQUENCE FROM N.A.

TISSUE=Colon;
Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003565; Ig-MHC.
InterPro; IPR003565; Ig-V.
Ffam; PF00647; Ig, 4.
SWART; SM00406; IGV; 1.
PROSITE; PS00290; IG MHC; 2.
PROSITE; PS00290; IG MHC; 2.
Hypotherical protein.
NOW TER
SEQÜENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.88e-35 393.50 75.57% 59.54% 52.26% Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:

US-09-674-716B-1 (1-415) x Q91XE1 (1-480)

93 AAGCTTGAGGAGGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTGCTGT 152 21 LysLeuValGluSerGlyGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeuSerCys 40 50 39 GATTTTGGG-----CTGATTTTTTTTTTTGTTCTTTTAAAAGGGGTCCAGAGTGAAGTG g d 8 ò ઠ

Op

g 8

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213 AAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACATTAT 272

99 LeuGlnMetThrSerLeuAsnSerGluAspThrAlaValTyrTyrCysThrArgGlyAsp 118 386 OBVEAO PRELIMINARY; PRT; 484 AA.

OBVEAO;
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 25, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
IGH-V0558 OR A1893585.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
U11-TaxID=10090; 333 CTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT--A STRUMBER FROM N.A.

SEQUENCE FROM N.A.

Strausberg R.;

Strumberg R.;

Strumberg R.;

EMBL, GenBank/DDBJ databases.

REMBL, BC019425; AAH19425.1; -..

REMBL, BC019425; AAH19425.1; -..

REMBL, BC019425; AAH19425.1; -..

REMBL, BC019425; AAH19425.1; -..

REMBL, BC03006; Igh-V0558.

REMBL, SWART; SW00406; Igy-V.

REMBL, PC0047; Igy-V.

REMBL, BC0047; Igy-V.

REMBL, BC0048; IGW-V.

REMBL, 484 75 17 28 6 Length:
Matches:
Conservative:
Mismatches:
Indels: -----TICATAGACTGGGGCCAAGGGACA 410 TyrTrpTyrPheAspValTrpGlyAlaGlyThr 129 3.6e+35 391.00 73.02% 59.52% 51.93% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 387 119 Query Match: DB: RESULT 13 

111 GGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTACT 170 

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US-09-674-716B-1 (1-415) x Q8VEA0 (1-484)

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351 AGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT-------TTCATA 392 

GACTGGGGCCAAGGGACA 393

18-08-4-118D-118D-

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SEQUENCE FROM N.A.
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Best Local Similarity:
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DB:
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TISSUESPECTOR N.A.

TISSUESPECTOR N.A.

TISSUESPECTOR N.A.

MEDINNE-2388257, PubMed=12477932;

MEDINNE-2388257, PubMed=12477932;

MEDINNE-2388257, PubMed=12477932;

MISCARL S.F., Zeeberg B. M. Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

MA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

MA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carannoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McGwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

M. Richards M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

T. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GAGAAGGGGCTTGAGTGGGTTGCTGAATTAGATTGAAATCTGATAATTATGCAACACAT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 ATGGATTTTGGGCTG----ATTTTTTTTTTTTTTAAAAGGGGTCCAGAGTGAA
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                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein...
Hypothetical protein...
Hypothetical protein...
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GlyLysGlyLeuGluTrpValSerLysIleGlyThrAlaGlyAspArgTyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases EMBL, BC053984; AAH53984.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            778CF34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                   470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
Gaps:
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                                                                                                   PRT;
AsnTrpGlyGlnGlyThr 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al protein.
470 AA; 51204 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.08e-35
390.50
70.29%
57.97%
51.86%
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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128
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                           210 GAGAAGGGGCTTGAGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT 269
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                                                                                      330 TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA-----
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| MetAsnPheGlyLeuArgleuIlePheLeuValLeuAlaLeuLysGlyValGlnCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ValHisLeuValGluSerGlyGlyGlyLeuValLysProGlyGlyGlySerLeuLysLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GluargargLeuGluTrpValAlaAlaIle-----ThrSerGlyGlyAsnThrTyr
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                                                                                                                                                                       384 -------GATTTCATAGACTGGGGCCAAGGGACACTA 413
                                                                                                                                                                                                              118 AlaGlyArgTrpAlaProLeuGlyAlaPheAspIleTrpGlyGlnGlyThrMet 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. BMBL, EC010324; AAH10324-1; InterPro; IFR007110; Ig-1ike. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_WHC.
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Mismatches:
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SWART, SM0406; IGV; 1.
PROSITE: PS00325; IG_LIKE; 4.
PROSITE: PS00290; IG_MC; 2.
Hypothetical protein.
SEOURNCE 486 AA; 52682 MW; 4
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091207
01-DEC-2001 (TrEMBLrel. 19, C3
01-DEC-2001 (TrEMBLrel. 19, L6
01-DEC-2001 (TrEMBLrel. 19, L6
Hypothetical protein.
Mis musculus (Mouse).
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Search completed: September 30, 2004, 08:53:35 Job time: 57.5503 secs

Dank Shed

Humanised Murine Br Murine Br

Antibody Variable Murine Mu VH region Amino aci

Anti-cata Lead bind

SM3 heavy

Heavy cha Humanised Antibody Lead bind Heavy cha 3B10xP5-2

Mouse ger P5-3 sing 113F1 hyb 2G3 hybri

Consensus Murine J4

Sequence:

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Searched:

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cod23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; chimeric antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nepirotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; sjogren's syndrome; allergy; asthma; rhinitis; eczema; insultits; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                         Aau72870 F
Abo10730 V
Abr44674 M
Aar72599 P
Abo10726 V
Abr44670 M
                                                                                                                                                                                                                     Aau72866 I
Aay90816
Aay90812
Abo10743
Abr44687 N
Aab50425 N
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Aae06973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                         ABO10743
ARB44687
AAB50425
AARB5908
AAU72870
ABC10730
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/note= "CDR H2"
129. .131
/note= "CDR H3"
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  Command line parameters:
-MODEL=frame+ h12p.mddell -DEV=xlp
-MODEL=frame+ h12p.mddell -DEV=xlp
-MODEL=frame+ h12p.mddell -DEV=xlp
-DeA-CgnZ_1/USFTO spool_p/US09674716/runat_30092004_070257_25848/app_query.fasta_1.3164
-DB=A_Geneeq_29Jan04 -QFWT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TTANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct - TTR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRE=US09674716_@CGN 1_1 475_@runat_30992004_070557_25848 -NCPU=6 -ICPU=3
-NO_WMAPP -LARGEQUERY -NGG_SCORES=0 -WARIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS12 -XGAPOP=10 -XGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aay32260 Mouse ant
Aab5529 Murine PS
Aaw6212 Mbb Br-3
Aaw85059 Wouse Br-
Abb:8893 Mouse Br-
Aar70829 Mb 4197X
Aar70829 Mb 4197X
Aar72358 Heavy Cha
Aar12336 Mouse MAB
                                                                               2; Search time 49.4398 Seconds (without alignments) 4743.430 Million cell updates/sec
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                                                                                                                                                          1 aagctttacagttactcagc......tgggggccaagggacactagt
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                        protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          1586107 segs, 282547505 residues
                                                                                  September 30, 2004, 08:19:42
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Maximum Match 100%
Listing first 45 summaries
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AAU76696
AAB35292
AAW66212
AAW85059
AAW85059
AAW85059
AAW85059
AAR09423
AAR12358
AAR12358
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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1. geneseqp1980s:*

2. geneseqp1990s:*

4. geneseqp2001s:*

5. geneseqp2012s:*

6. geneseqp2033s:*

7. geneseqp2033s:*

8. geneseqp2003bs:*
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Maximum DB seq length: 200000000
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Jatabase :

Result

P5-23 sin Variable Murine J4

Variable Murine J4 Variable Murine J4 Murine SC

SerGlyValTyrTyrCysThrAspPheIleAspTrpGlyGlnGlyThrLeu 137

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RESULT
                                                         This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCBRII) monoclonal antibody C11. The invention provides anti-CD23 (FCBRII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAY32262 and AAY32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on heamatopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus expthematious, psoriasis, urticaria, meltiple sclerosis, diabetes, uveltis, dermatitis, psoriasis, urticaria, mephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, croim's disease, Slogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic axacerbation, rhinitis, eczema, graftversus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 CAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTAC
                                                                                                                                             Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 AGTGGAGTTTATTACTGTACAGATTTCATAGACTGGGGCCAAGGGACACTA 413
                                                                                   Shearin J;
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Matches:
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                                                                                  Ellis JH,
                                                                                                                                                                                     Claim 8; Fig 1; 81pp; English.
           99WO-GB001434.
                                   98GB-00009B39.
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                                                          GLAX ) GLAXO GROUP LTD
                                                                                                           WPI; 2000-053101/04.
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Best Local Similarity:
                                                                                                                       N-PSDB; AAZ34745.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 137 AA;
                                                                                   Bonnefoy JMP,
                                   09-MAY-1998;
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The present invention relates to new antibodies that specifically bind a novel prostate stem cell antigen (PSCA), which is widely over-expressed across all stages of prostate cancer. The antibodies of the invention are useful to kill tumour cells expressing PSCA and as PSCA expression is observed in prostate tumour cells and in other human cancers, particularly bladder and pancreatic carcinomas, the antibodies are useful therapeutically to threat these diseases. In particular, monoclonal antibodies can be administered to subjects suffering from PSCA-associated cancers, e.g. prostate, bladder or pancreatic cancer or metastatic prostate, bladder or pancreatic cancer, or metastatic prostate, bladder or pancreatic cancer, or inhibit the cancer and prolong the subject's life. The antibodies can be combined with a therapeutic agent in immunoconjugates useful to treat subjects suffering from
                                                                                                                                                                                          Mouse; prostate stem cell antigen; PSCA; antibody; immunogen; prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate; PSCA-associated cancer; heavy chain variable domain region; PSCA antigen; PSCA antibody 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies binding to prostate stem cell antigen inhibit the growth of cancer cells and are used to detect and treat prostate, pancreatic or
                                                                                                                                                Mouse heavy chain variable domain region of PSCA antibody 2H9 protein
                                                                                                                                                                                                                                                                                                                                                                                                                     .54
e= "Complementarity determining region 1 (CDR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CDR2) "
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standard; protein; 151
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98US-0071111P.
98US-0074675P.
98US-0038261.
98US-013230P.
99US-0113230P.
99US-0120558P.
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SAFFRAN D C.
JAKOBOVITS A.
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                                                                                                      21-MAY-2002
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17-FEB-1999,
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AAU76696
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(JAKO/)
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malignant diseases, characterised by cells having FSCA antigen on the cell surface e.g. cancers, by killing the cells. The antibodies and commonconjugates may also be included with a carrier in pharmaccutical compositions useful to kill human cells expressing PSCA antigen on the cell surface. The antibodies are also useful diagnostically to detect cancers, especially prostate cancer, to isolate prostate cancer cells e.g. to enable culture growth to evaluate candidate therapeutic compounds, assist in identification of rare genes associated with prostate cancer, and to isolate and purity PSCA and PSCA homologues. The present amino acid sequence represents the mouse heavy chain variable domain region of the PSCA monoclonal antibody 2H9 of the invention
                                                                                                                                                                                                                                                                                                                                                  92
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109
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Matches:
Conservative:
Mismatches:
Indels:
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573.50
92.31%
83.85%
76.16%
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Best Local Similarity:
                                                                                                                                                                           Sequence 151 AA;
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The present invention describes a method of treating cancer associated with prostate stem cell antigen (PSCA) by administering an antibody which selectively binds to PSCA and inhibits the growth of the cancer cells. The PSCA gene is found on human chromosome 8Q24.2. The invention provides the human and murine PSCA protein and coding sequences, which can be used not only in the treatment of, but also in detection and prognosis of
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                                                                                                                                  Antibodies binding to prostate stem cell antigen inhibit the growth of cancer cells and are used to detect and treat prostate, pancreatic or
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                                                                        Saffran DC,
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20-JUL-1999; 99US-00359326.
03-MAY-2000; 2000US-00564329.
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573.50
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UROGENESYS.
                                                                                              WPI; 2001-159478/16.
N-PSDB; AAF27975.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                 prostate cancer
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12-FEB-1997
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Sequence 142 AA;
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06-MAY-1991;
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16-APR-1999
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13-SEP-1988
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21-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers.
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                         Chimeric antibody, monoclonal antibody, Br-3; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma; ovary carcinoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                              Horwitz AH,
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4 0
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Matches:
Conservative:
Mismatches:
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MAb Br-3 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 15; 102pp; English.
                                                                                                                                                                                              88US-00240624.
88US-00241744.
88US-00243739.
89US-00353002.
89US-003827641.
89US-00382768.
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89.31%
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N-PSDB; AAT43437.
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Best Local Similarity:
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                                                                                                                                                                       27-DEC-1994;
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No.:
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The present sequence represents the heavy chain variable region of murine antibody Br-3. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytotoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                       81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSerVal 100
                                                                                                                                                                                                                               TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGly1leTyrTyrCysThrPheGly 120
61 GluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrAlaThrHis 80
                                                                                                                                                                                          TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGGAGTTTATTACTGTACA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain variable region; murine antibody Br-3; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robinson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Br-3 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW85059 standard; protein; 142 AA
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88US-00243739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
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Mouse; human tumour antigen; anti-human tumour antigen-antibody; ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis; tumour therapy; cytostatic; heavy chain variable region.
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                                                                                                                                                       TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA 209
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                                                                                                                              ValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
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                                                               US-09-674-716B-1 (1-415) x AAW85059 (1-142)
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88US-00241744.
88US-00241743.
89US-00253002.
89US-00367641.
89US-00382768.
89WG-00059401.
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3.42e-53
561.50
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82.44%
74.57%
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                   Percent Similarity:
Best Local Similarity:
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08-SEP-1988;
13-SEP-1988;
04-OCT-1988;
19-JUN-1989;
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06-SEP-1989;
06-MAY-1991;
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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the InG-1 antibody, where the ING-1 is produced by cell line is 199812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an immunoassay method for detecting an antigen in a sample by contacting at label and relating the detected label to the presence of the antigen; for use in an immal by contacting the presence of a label-detectable attigen in the sample with the artibody, detecting the attigen in an animal by contacting the antibody with a part of the antigen; cuse in an immal by contacting the cattering the label and relating the cells attigen in an antigen by contacting the cattering the label and relating the carting an antigen by contacting the cattering the antibody with a part of the antigen; carting an antigen by contacting the cattering the antibody and relating the killing to occur. The antibodies are useful in tumour allowing the killing to occur. The antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothelial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against thuman tumour cell lines combined with minimal reactivity with normal tissues of malignant tissue. The presence of human rather than murine mabs: This creatisance to caparance thousances the potential utility of these chimeric antibodies, as well as their derivatives; in tumour diagnosis and the chimeric antibodies, in tumour diagnosis and the chimeric determinable region used in the creation of an anti-human tumour antigen-
                                                                Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody.
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                                                                                                                                                               Example 3; Fig 15; 101pp; English.
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561.50
89.31%
82.44%
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Pred. No.:
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VallysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA

GIGAAGCITGAGGAGTCTGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCCTCC

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36 ATGGATTTTGGGCTG----ATTTTTTTTTTTTTTTAAAAGGGGTCCAGAGTGAA

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269

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TACCTCCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA-----

330

101

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TAIGCGGAGICTGTGAAAGGGAAGITCACCATCTCAAGAGATGATTCCAAAAGTCGTCTC 329

81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSerVal

GAGAAGGGGCTTGAGTTGCTTGAAATTAGATTGAAATCTGATAATTATGCAACAC

80

9

384

(revised)

25-MAR-2003 04-MAR-1993

AAR09423;

AAR09423

Mus musculus

WO9002569-A 22-MAR-1990

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An immunotoxin (given in AAR70827) comprises the heavy (VH) and light chain (VL) variable regions of anti-lens epithelium IgG3 MAb 4197\mathrm{X} linked
                                                                                                                                                                                                                                                              101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrPheGly 120
                                                                                                                                                                      270 TATGCGGAGICTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTC 329
                                                                                                                                                                                                                                          IACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383
21 ValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
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                                                                                                                         61 GluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrAlaThrHis
                                                                                                                                                                                         TGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCA
                                                                     41 CysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSerPro
                                                                                                    210 GAGAAGGGGCTTGAGTGCGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New single chain immuno:toxin - binds specifically to epithelial of for inhibiting development of sec. cataracts after extra:capsular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139. 144 / Abbel = CD3 /note = "complementarity determining region 3" /note = "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "complementarity determining region 1"
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/label= CDR2
/note= "complementarity determining region"
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                                                                                                                                                                                                                                                                                                                                             121 AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu 131
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N-PSDB; AAQ85388.
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31-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour antigen.
                                                                                                                                                                                                                                                                           Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 ATGGATTTTGGGCTG-----ATTTTTTTTTTTTTTTTTAAAAGGGGTCCAGAGTGAA
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                                                                                                                                                                                                                                                                                            antigen; diagnosis; cancer; tumour
                                                                                                                                                                                                                                            Br-3 Heavy Chain V Region (mouse).
                                                                                                                       AAR09423 standard; protein; 143
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88US-00253002.
89US-00367641.
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74.57%
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INT GENETIC

(ITGE-) (INGE-)

04-OCT-1988; 19-JUN-1989; 21-JUL-1989;

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08-SEP-1988;

08-SEP-1988

WPI; 1990-115825/15. N-PSDB; AAQ08605.

Best Local Similarity:

Query Match:

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Percent Similarity:

Sequence 143 AA;

Alignment Scores:

Pred. No.:

Score:

118 383 206 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 146 CCAGAGAGAGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 266 GluValLysLeuGluGluSerGlyGlyGlyGlyLoeuValGlnProGlyGlySerMetLysLeu 58 78 86 ACCATGGATTTTGGGCTG-----ATTTTTTTTTTTTTTTAAAAGGGGTCCAGAGT 86 to ricin-A. cDNAs encoding the VL and VH regions of 4197X (AAQB5387-88, respectively) were obtained from hybridoma mRNA, amplified by PCR, and engineered for inclusion in the immunotoxin construct (AAQB5386). (Updated on 25-MAR-2003 to correct PN field.) HisTyralaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer ProGluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrProThr CTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA---CTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCT Heavy chain variable region of murine 1C11 immunoglobulin. 160 110 110 2 Horwitz AH, Ghoshdasti P, Robinson R; 413 Chimeric antibodies; immunoconjugates; HIV; AIDS Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: ----GATTTCATAGACTGGGGCCAAGGGACACTA US-09-674-716B-1 (1-415) x AAR70829 (1-160) Æ AAR12358 standard; protein; 134 89US-00433730 89US-00433730 2.69e-52 553.50 88.64% 80.30% 73.51% (revised)
(first entry) (XOMA ) XOMA CORP. Best Local Similarity: 160 AA; Percent Similarity: 13-NOV-1989; musculus 13-NOV-1989; Alignment Scores: 25-MAR-2003 15-AUG-1991 WO9107493-A 30-MAY-1991 Better MD, Seguence 33 87 39 147 50 79 327 384 139 13 207 267 9 AAR12358 Query Match: DB: No. RESULT 9 Mus 8x33333 ò g g 임 a d g ò g ò à ò ò à

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This is the heavy-chain variable (V) region of a mouse mono- clonal antibody (MAb), 1C11, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also AAQ12056-59 and AAQ12061. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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103
110
113
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Mismatches:
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Matches:
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                                                                       Disclosure; Fig 12; 107pp; English
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(first entry)
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531.50
87.60%
79.84%
                                   New chimeric mouse-hums
-1 antigen from sample
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Best Local Similarity:
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19-AUG-1991
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mouse-human antibodies - used to detect, kill and remove HIV

WPI; 1991-178105/24

N-PSDB; AAQ12060,

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AAY32263 standard; protein; 444 AA.
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Synthetic.
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                                                                         15-FEB-2000
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                                            AAY32263;
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   AAY32263
                                                                                                                                                                                                                                                                                                                                                                           The mouse VH gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCC 149
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                                                                                                                                                                                                                                                                                                     New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 ATGGATTTTGGGCTG-----ATTTTTTTTTATTGTTCTTTTAAAAGGGGTCCAGAGTGAA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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531.50
87.60%
79.84%
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GREC ) GREEN CROSS CORP.
ZOMA-) ZOMA CORP.
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N-PSDB; AAQ12106.
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                                                                                                      13-NCV-1989;
                                                                                                                                    13-NCV-1989;
                                            WO9107494-A.
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CD23; FCBRII; IgE receptor; monoclonal antibody; CII; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcrariue colitis; Crohn's disease; slogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This amino acid sequence represents the heavy chain of humanised anti-
CD23 (FCERII) monoclonal antibody C11, composed of a human framework
(HSIGKVII) and the heavy chain complementarity determining regions (see
AAY32257-59) of murine antibody C11. The DNA was constructed by splice
overlap PCR. The invention provides altered antibodies, such as chimeric
or humanised antibodies, which comprise sufficient of the amino acid
sequences of the C11 light and heavy chain complementarity determining
regions to render them capable of binding to the CD23 type II molecule
expressed on haematopoietic cells. The antibodies are used to block
soluble CD23 formation in human therapy, for the treatment of arthritis,
lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
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/note= "framework region 4"
112. .444
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                                                                          Humanised anti-CD23 MAb C11 heavy chain.
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36. .49
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/note= "framework
101. .103
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'note= "CDR 1"
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N-PSDB; AAZ34748.
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                     graft-
         Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                        GluValGlnLeuValGluSerGlyGlyGlyLeuValLysFroGlyGlySerLeuArgLeu
                                                                                                                                                                                                                                                                                        CCAGAGAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA
                                                                                                                                                                                                                                                                                                                                CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT
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                                                                                                                                                                                                                            GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC
glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; BrE-3 VH-chain.
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47
47
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Matches:
Conservative:
Mismatches:
Indels:
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/label= BrE-3_VH-chain
50. 54
/label= CDR1
69. 87
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120. 123
/label= CDR3
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88.99%
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(first entry)
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
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24-JAN-1995
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Chimeric human-murine polypeptide(s) specific for human mammary fat globule antigen - for imaging, diagnosing and treating neoplasia, with less undesirable immunogenic response.

Example 10; Page 32; 54pp; English.

(CANC-) CANCER RES FUND CONTRA COSTA

WPI; 1994-183509/22.

N-PSDB; AAQ62750

92US-00977706. 92US-00977707. 93US-00128015.

13-NOV-1992; 13-NOV-1992; 28-SEP-1993; 15-NOV-1993;

93WO-US011316

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210 GAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACT
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Pred. No.:
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                                                   Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; BrE-3 VH-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New analogue peptide(s) comprising antibody variable regions - a develop prods. for use in the detection, diagnosis, therapy and
                           Murine BrE-3 immunoglobulin heavy chain variable domain.
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Mismatches:
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Gaps:
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|label= BrE-3_VH-chain
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                                                                                                                Location/Qualifiers
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/label= CDR1
69. .87
/label= CDR2
120. .123
/label= CDR3
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93US-00134346.
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08-OCT-1993;
                                                                                         Aus musculus
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 24-JAN-1995
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This sequence represents the heavy chain of the antibody ABX-CXL. The invention relates to a monoclonal antibody (MAb) with an isotype that itses complement and a variable region that binds to the epitope on CD147 bound by the IgM MAb ABX-CBL, providing that the antibody is not CBLI. The MAb can selectively kill activated T-cells, activated B-cells or resting or activated monocytes. The products and methods can be used for treating diseases involving activated T-cells or B-cells or monocytes, e.g. graft versus host disease (GVHD), organ transplant rejection diseases (e.g. renal transplant, ocular transplant), cancers (e.g. anners of the blood (e.g. leukaemia's and lymphomas) and pancreatic), arthritis)
                                                                                     329
                                                                                                                                                                                                                                                     330 TACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA---GAT 386
                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody, CD147; IgM, ABX-CBL, activated T-cell killing, leukaemia; activated B-cell, monocyte; graft versus host disease; therapy; cancer; organ transplant rejection disease; lymphoma; panoreatic disease; autoimmune disease; inflammatory disease; arthritis; binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Culwell AR, Green LL, Hales J;
Liu Q, Weber RF, Yang X;
61 GluLysGlyLeuGluTrpValAlaGlulleArgAsnLysAlaAsnAsnHisAlaThrTyr
                                                                                                                          TATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGAGATGATTCCAAAAGTCGTCTC
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Lipani JA,
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, Ivanov VE,
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Disclosure; Fig 7C; 254pp; English

18-08-6/4-/TOD-T.rad

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                                                                                         GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 146
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Mismatches:
Indels:
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101 TyrAspAlaTyrTrpGlyGlnGlyThrLeu 110
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88.18%
69.26%
Percent Similarity:
Best Local Similarity:
Query Match:
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ABO10742 standard; protein; 123 AA

ABO10742;

20-AUG-2003 (first entry)

Variable region of murine antibody MuVHIIIC.

Modified antibody, deimmunised antibody; anti-PMSA antibody; prostate specific membrane antigen; immunogenic; CDR; murine; complementarity determining region; J591, J415, J533, E99; mouse; prostatic disorder; cancerous disorder; genitourinary inflammation; prostatitis; benign enlargement; prostatic cancer; testicular cancer; solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic; antinflammatory; cytostatic; tramework region; variable heavy chain; variable light chain; VH; VL; variable region. 

musculus Mus WO200298897-A2

12-DEC-2002

completed: September 30, 2004, 08:40:50 ne : 54.4398 secs

Search col Job time

30-MAY-2002; 2002WO-US017068.

01-JUN-2001; 2001US-0295214P. 20-SEP-2001; 2001US-0323585P. 08-MAR-2002; 2002US-0362810P.

(CORR ) CORNELL RES FOUND INC.

Carr FJ, Hamilton A;

Bander N,

WPI; 2003-156839/15

or New modified anti-prostate specific membrane antigen (PSMA) immunoglobulins, useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatits, prostatic or testicular cancer.

The present invention relates to modified (e.g. deimmunised) antibodies are less immunogenic compared to the unadified anti-PSVA antibodies are less immunogenic compared to the unmodified anti-PSVA antibodies. The modified antibodies complementarity determining regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415, J53 or B99), and framework sequences that are less immunogenic in humans (e.g. less antigenic than the murine frameworks in which a murine CDR human PMSA, with high affinity and specificity. The anti-PMSA antibodies are useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatitis, benign enlargement, prostatic cancer or testicular cancer, or solid tumours, soft tissue tumours or metastatic lesions, and its associated pain. The present sequence represents a variable region from a murine antibody 206 266 326 386 20 40 9 80 TCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCT CTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT CCAGAGAAGGGGCTTGAGTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer 123 98 6 5 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-674-716B-1 (1-415) x ABO10742 (1-123) 1.88e-48 518.50 88.14% 83.05% 68.86% Percent Similarity: Best Local Similarity: Sequence 123 AA; Alignment Scores: Pred. No.: 327 147 21 207 267 387 Query Match: ò g à g ₹ g 8 Ωp g ò

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573.5 76.2 151 9 573.5 76.2 151 9 573.5 76.2 151 9 573.5 76.2 151 9	573.5 76.2 151 9 573.5 76.2 151 10 573.5 76.2 151 10	573.5 76.2 151 14 573.5 76.2 151 14 573.5 76.2 151 14	11 573.5 76.2 151 15 12 524.5 69.7 134 10 13 518.5 68.9 123 14 14 518.5 68.9 123 16	15 518.5 68.9 123 1 16 503 66.8 114 1 17 500 66.4 285 9 18 497.5 66.1 503 1 19 495 65.7 100 9 20 495 65.7 100 9	495 65.7 100 16 495 65.7 100 16 493 65.5 256 12	489.5 65.0 123 14 489.5 65.0 123 16 489.5 65.0 123 16	488 64.8 298 9 484.5 64.3 262 14	483 64.1 255 12.481 63.9 133 14	3.2 481 63.9 133 16 3.3 481 63.9 133 1 3.4 480 63.7 116 14	:a_1.3164 35 480 63.7 116 16 37 37 476 63.2 116 14	38 476 63.2 116 16 39 476 63.2 116 16 20 475 63.2 116 16	41 475 63.1 507 12 42 473 62.8 116 14 42 473 62.8 116 14	44 473 62.8 116 16	ALIGNMENTS	RESULT 1 US-09-564-329A-15 ; Sequence 15, Application US/09564329A	; Facell No. OSCOLOOS/JIAI ; GENERAL INFORMATION: ; APPLICANT: Reiter, Robert E.	; APPLICANT: Witte, Owen N.; ; APPLICANT: Saffran, Douglas C.; ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES	4, 32	a inted,	; PRIOR APPLICATION NUMBER: 60/074,675 ; PRIOR FILING DATE: 1998-02-13 ; PRIOR APPLICATION NUMBER: 60/113.230	
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model	Run on: September 30, 2004, 08:54:09; Search time 54.4329 (without alignments) 4906.833 Million cell up	Title: US-09-674-716B-1 Perfect score: 753 Sequence: 1 aagctttacagttactcagctggggccaagggacactagt	table: BLOSUM62 XGapop 10.0 , XGapext 0.5 YGapop 10.0 , YGapext 0.5 YGapop 10.0 , YGapext 7.0 YGapop 6.0 , PGapext 7.0 PGapop 6.0 , PGapext 7.0	1351062 segs, 321799191 residues	umber of hits sa DB seq length:	Maximum DB seq length: 2000000000	FOSE_PIOCESSING: MILLIAMM MACCH 100% Listing first 45 summaries	Command line parameters: -MODEL=frame+_n2p.model -DEV=xlp	-Q=-cgn2 1/USPTO spool p/USO9674716/runat 30092004 070302 26027/app -DB-Published_Applications AA -OFWIT-fastam -SUFFIX=rapb -MINWATCH=C -LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62	-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=1 -THR_MIN=0 -ALIGN=15 -MODE=LOCALOUTFWT=150 -NORM=ext -HEAP0TZE=50 -MXYIN-200000000 -HEAP0TZE=50	-NCPD=6 ICPU=3 -NO WAAP -LARGEQUEST -NEG SCORRES - WAIT -DSPENCK=100 - NCPD=6 ICPU=3 -NO WAAP -LARGEQUEST -NGG SCORRES - WAIT -DSPENCK=100 - NGAP TIMEQUEST -NGG SCORRES - WAIT -DSPENCK=10 - NGAP TIMEQUEST - NGAP TIMEGUEST - NGA	Database : Published Applications AA:*	1: /cgn2_6/ptodata/// 2: /cgn2_6/ptodata/// 3: /cgn2_6/ptodata/// 4: /cgn2_6/ptodata////	5: /cgn2_6/ptodata/1/pubpaa/US07_NBW_PUB.pep:* 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:* 7: /cgn2_6/ptodata/1/pubpaa/US08_NBW_PUB.pep:*	o: /cgnio/prodata/1/pubpad/USO9B_PUCOMB.pep:* 0: /cgn2_o/prodata/1/pubpad/USO9B_PUCOMB.pep:* 10: /cgn2_o/prodata/1/pubpad/USO9B_PUCOMB.pep:*	<pre>11: /cgn2_6/ptcdata/1/pubpaa/US09C_PUBCOMB.pep:* 12: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:* 13: /cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*</pre>	14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:* 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.ppp:* 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.ppp:* 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.ppp:* 18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.ppp:*	Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description

Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 36, Appl Sequence 27, Appl Sequence 24, Appl Sequence 47, Appl Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 60, Appl Sequence 61, 
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APPLICANT: Reiter, Robert E. APPLICANT: Witte, Owen N. APPLICANT: Saffran, Douglas C.
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US-09-855-153-15
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Best Local Similarity:
Query Match:
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Sequence 15, Application US/09855153
Sequence 15, Application US/09855153
Sequence 15, Application US/09855153
Septemal Information US/09/05/01026641
APPLICANT: Reiter, Robert E.
APPLICANT: Witter, Own N.
APPLICANT: Witter, Own N.
APPLICANT: Witter, Deuglas C.
ITLE REFERENCE: 30435.440314
FILE REFERENCE: 30435.440314
CURRENT FILING DATE: 2001-05-14
PRIOR PALICATION NUMBER: 09/564,329
PRIOR PLING DATE: 2000-05-03
PRIOR PLING DATE: 2000-05-03
PRIOR PLING DATE: 1990-07-20
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR PLING DATE: 1990-07-20
PRIOR PLING DATE: 1990-07-20
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/23,939
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-17
PRIOR PAPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 27
SEQ ID NO S:
LENGTH: 151
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573.50
92.31%
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76.16%
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ORGANISM: SCID Mice
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Best Local Similarity:
Query Match:
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PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VAF. 2.0
SEQ ID NO 15
LENGTH: 151
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US-00-854-811-15
Sequence 15, Application US/09854811;
Patent No. US20020119157A1
GENERAL INFORMATION:
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Federat No. US20020136689A1

GENERAL INFORMATION

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Seffran, Douglas C.

TILLE PEFERRACE: 30435.54US14

CURRENT APPLICATION NUMBER: US/09/934,773

CURRENT FILING DATE: 2001.08-21

PRIOR PILICATION NUMBER: 09/564,329

PRIOR PILICATION NUMBER: 09/564,329

PRIOR PLICATION NUMBER: 09/564,329

PRIOR PLICATION NUMBER: 09/359,326

PRIOR PLICATION NUMBER: 08/359,326

PRIOR PLICATION NUMBER: 08/359,326

PRIOR PLICATION NUMBER: 08/359,326

PRIOR PLICATION NUMBER: 08/359,326

PRIOR PLICATION NUMBER: 06/071,141
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        THEREOF
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THERE
CURRENT PAPLICATION NUMBER: US/09/884,811
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR PILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 151

TYPE: PRI
CRANICAL: SCID Mice
US-09-854-811-15
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US-09-934-773-15
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Fatent No. US20020141941A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
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PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR PRIOR APPLICATION NUMBER: 60/124,658
PRIOR PRIOR DATE: 1999-02-17
PRIOR PRIOR DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR PRIOR DATE: 1999-02-17
PRIOR PRIOR PRIOR NUMBER: 09/308,503
PRIOR PRIOR PRIOR NOW: 2.0
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN USE: 2.0
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Query Match:
76.16$
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US-09-963-620-15
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APPLICANT: Reiter, Robert E.
APPLICANT: Wite, Owen N.
APPLICANT: Wite, Owen N.
APPLICANT: Wite, Owen N.
APPLICANT: Saffran. Douglas C.
ITILE OF INVANION: PROM: PROGRATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFRENCE: 30435-54051
FILE REFRENCE: 30435-54051
CURRENT PILING DATE: 2001-05-14
FRIOR APPLICATION NUMBER: 09/359,326
FRIOR RILING DATE: 1999-07-310
FRIOR RILING DATE: 1999-07-310
FRIOR PELICATION NUMBER: 06/071,141
FRIOR PELICATION NUMBER: 06/071,141
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-02-13
FRIOR PELICATION NUMBER: 60/113,230
FRIOR PELICATION NUMBER: 60/113,230
FRIOR PELICATION NUMBER: 60/120,536
FRIOR PELICATION NUMBER: 60/120,536
FRIOR FILING DATE: 1998-03-10
FRIOR FILING DATE: 1999-03-16
FRIOR FILING DATE: 1999-03-10
FRIOR FILI
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42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu
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                         Sequence 15, Application US/0985532 Publication No. US20030113818A1 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/963,620 CURRENT FILING DATE: 2001-09-26
                   CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PELLING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR PRIOR DATE: 1998-01-21
PRIOR FILING DATE: 1998-01-21
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3:
LENGTH DATE: 151
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CORGANISM: SCID Mice
US-09-963-620-15
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APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435 54US14
CURRENT PAPLICATION NUMBER: US/09/359,326
PRIOR PAPLICATION NUMBER: US/09/359,326
PRIOR APPLICATION NUMBER: 08/01/1,141
PRIOR APPLICATION NUMBER: 06/011,141
PRIOR PLING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/011,141
PRIOR PLING DATE: 1998-01-12
PRIOR PLING DATE: 1998-01-12
PRIOR PLING DATE: 1998-01-12
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-02-17
PRIOR PLING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 60/13,230
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR PLING DATE: 1999-03-16
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR PLING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
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PRIOR PLING DATE: 1999-02-17
   62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGluAsnTyrAlaThrHisTyr
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US-10-224-720-15
Sequence 15, Application US/10224720
Publication No. US/20030147806A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-15
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93 AAGCTTGAGGAGTCTGGAGGATGCTGCAACCTGGAGGATCCATGAAACTCTCTGT 152
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US-10-25-784-15

Sequence 15, Application US/10225784

Publication No. US20030113820A1

GENERAL INFORMATION:

APPLICANT: Reiter, Nebert E

APPLICANT: Reiter, Owen N.

APPLICANT: Mitte, Owen N.

TITLE OF INVENTION: PSCA: PROSTRIE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S4

CURRENT APPLICATION NUMBER: US/10/25,784

CURRENT PLING DATE: 2000-08-21

PRIOR APPLICATION NUMBER: US/09/564,329

PRIOR APPLICATION NUMBER: US/09/564,329

PRIOR PLING DATE: 1999-07-20

PRIOR PLING DATE: 1999-07-20

PRIOR FILING DATE: 1997-03-10

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR PLING DATE: 1998-01-13

PRIOR PLING DATE: 1999-02-13

PRIOR PLING DATE: 1999-02-13

PRIOR PLING DATE: 1999-02-13

PRIOR PLING DATE: 1999-02-13

PRIOR PLING DATE: 1999-03-16

PRIOR PRIOR PLING DATE: 1999-03-16

PRIOR PLING DATE: 1999-03-16

PRIOR PLING DATE: 1999-03-16

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Mismatches:
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ORGANISM: SCID Mice
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Best Local Similarity:
Query Match:
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Pred. No.:
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RESULT 10

RESULT 10

Sequence 15, Application US/10374381

Publication No. US20030228318A1

Sequence 15, Application No. US20030228318A1

SEQUENCE 15, Application No. US20030228318A1

SAPPLICANT: Witte, Owen N

APPLICANT: Witte, Owen N

APPLICANT: Witte, Owen N

APPLICANT: Saffran, Douglas C.

ITITE OF INVARIATION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 3043-6.25

FILE REFERENCE: 30435.54US14

CURRENT APPLICATION NUMBER: US/10/564,329A

PRIOR APPLICATION NUMBER: US/09/564,329A

PRIOR APPLICATION NUMBER: 08/014,279

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1998-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR PRIOR FILING DATE: 1999-03-16

PRIOR PRIOR FILING DATE: 1999-03-16

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2 AspPheGlyLeuSerTrpValPheIleIleValLeuLeuLysGlyValArgSerGluVal
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; LENGTH: 151
; TYPE: PRT
; ORGANISM: SID Mice
US-10-374-381-15
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Sequence 15, Application US/10225779

Sequence 15, Application US/10225779

Sequence 15, Application US/10225779

Sequence 15, Application Sequence 15, Application Work US Office 10 on the control of Care Interesting Wite, Owen N.

APPLICANT: Saffan, Douglas C.

TITLE OF INVENTION: BCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFRENCE: 30435.54418.

FILE REFRENCE: 30435.54518.

CURRENT APPLICATION NUMBER: US/09/564,329

PRIOR APPLICATION NUMBER: US/09/564,329

PRIOR APPLICATION NUMBER: US/09/59.07-20

PRIOR APPLICATION NUMBER: 00/359,326

PRIOR APPLICATION NUMBER: 60/074,479

PRIOR APPLICATION NUMBER: 60/074,479

PRIOR APPLICATION NUMBER: 60/074,475

PRIOR APPLICATION NUMBER: 60/12,536

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/12,536

PRIOR PLILING DATE: 1999-03-10

PRIOR PLILING DATE: 1999-03-10

PRIOR PLILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-03-10

PRIOR PLILING DATE: 1999-03-1
                                             42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu
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ORGANISM: SCID Mice
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Score:

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153 GTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCTCCAGAG 212
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Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padian Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
Carcinoma Specificity, and Kit and
Diagnostic Vaccination and
Therapeutic Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: READABLE FORM:

REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/947,839
FILING DATE: 06-Sep-2001
CLASSIFICATION CATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/976,288
FILING DATE: «Unknown: 77/977,696
APPLING DATE: 07/977,696
FILING DATE: No. US20030138428Alember 16, 1992
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CORRESONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: Callfornia
COUNTRY: USA
                                                                          Conservative:
Mismatches:
Indels:
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US-09-947-839-13
US-09-947-839-13
Sequence 13, Application US/08947839
Publication No. US20030138428A1
GENERAL INCORMATION:
                                             573.50
92.31%
83.85%
76.16%
                                                                       Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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SEQUENCE 15, Application US/10446542

Publication No. USZO040018571A1

GENERAL INPORMATION:

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

TILE OF INVANTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

TILE OF INVANTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

TILE REFERENCE: 30435.54014.

PRIOR APPLICATION NUMBER: US/09/85,153

PRIOR APPLICATION NUMBER: US/09/85,153

PRIOR APPLICATION NUMBER: 09/564,329

PRIOR APPLICATION NUMBER: 09/564,329

PRIOR APPLICATION NUMBER: 09/564,329

PRIOR APPLICATION NUMBER: 09/564,329

PRIOR APPLICATION NUMBER: 06/071,141

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR PLILNG DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR PLILNG DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR PLILNG DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR PLILNG DATE: 1999-01-16

PRIOR PLIL
                                                                                                                                                                                                                                                                                                                                                      42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu
                                                US-09-674-716B-1 (1-415) x US-10-374-381-15 (1-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 -----GACTGGGGCCAAGGGACACTA 413
  Gaps:
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CORGANISM: SCID Mice
US-10-446-542-15
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; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-69
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US-10-449-379-69
                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-160-506-69

Sequence 69, Application US/10160506

Publication No. US20030161832A1

Sequence 60, No. US20030161832A1

SEGUENCE OF USED 
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102
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Matches:
Conservative:
Mismatches:
Indels:
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   ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amrel Ph.D.
REGISTRATION UNMER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFEAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-947-839-13
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acid
TYPE: amino acid
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79.07%
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Best Local Similarity:
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                                                                                                                                                                               87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC
                                                                                                                                                                                                                                                            147 TCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGGTCCGCCAGTCT
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Sequence 69, Application US/10449379

Publication No. US20040120958A1

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

TITLE OF INVENTION NUMBER: 10/160,505

PRIOR PELING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: 60/323,885

PRIOR PILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-06-01

NUMBER OF SEQ ID NOS: 128

SEG ID NO 69

LENGTH: 123

TYPE: RET
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Mismatches:
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
FILE REPERENCE: 10448-19601
CURRENT PAPLICATION NUMBER: US/10/688,015
CURRENT PILING DATE: 2002-10-30
FRIOR APPLICATION NUMBER: 60/422,396
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 128
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 69
LENGTH: 123
LENGTH: 123
TYPE: PRT
CORGANISM: Mus musculus
US-10-688-015-69
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                                       87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 146
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US-09-674-716B-1 (1-415) x US-10-449-379-69 (1-123)
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US-10-688-015-69
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RESULT 1
US-09-544-129A-15
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US-09-544-129A-15

BACHOL No. 6541212

GANEAL INFORMATION:
APPLICANT: Reiter, Robert B.
APPLICANT: Reiter, Robert B.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFRENCE: 3045.540S4

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT PLING DATE: 1995-02-03

PRIOR APPLICATION NUMBER: 00/071,141

PRIOR APPLICATION NUMBER: 00/071,141

PRIOR APPLICATION NUMBER: 00/071,141

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-12

PRIOR FILING DATE: 1998-02-12

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 00/201,939

PRIOR PILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/201,939

PRIOR PILING DATE: 1999-03-16

PRIOR PILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/201,939

PRIOR PILING DATE: 1999-03-16

PRIOR PILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/201,939

PRIOR PILING DATE: 1999-03-16

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US-08-192-102-5

US-08-324-799-5

US-08-133-119-5

US-09-133-119-5

US-09-133-119-5

US-09-136-315-6

US-09-136-315-6

US-09-136-315-6

US-09-136-315-6

US-09-136-315-6

US-09-136-315-6

US-09-136-318A-23

US-09-166-093-23

US-09-166-093-23

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US-09-166-093-23

US-09-166-093-13

US-08-328-113-13

US-08-328-113-13

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US-09-166-093-13

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US-09-166-093-15

US-09-166-093-15

US-09-166-093-15
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     Command line parameters:
-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-C=Cgn2_1/USF7O_spool_PUS09674716/runat_30092004_070259_25901/app_query.fasta_1.3164
-D=Lsgued_Patents AA -QFWT=fastan -SUFFIX=xi -MINMATCH=0.1 -LOOPCL=0
-LDOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR EXCRE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OOTFMT=pto -NORM=ext -HEAPSIZE=500 -MILLEN MIN=0 -ALIGN=15
-NORM=CATAL6 @CGN 1 1 107 @runat 30092004 070259 25901 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 13, Appl
Sequence 13, Appl
Sequence 28, Appl
Sequence 4, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                               September 30, 2004, 08:41:28; Search time 10.1499 Seconds (without alignments) 4221.672 Million cell updates/sec
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1 aagctttacagttactcagc......tgggggccaagggacactagt
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11. /Ggn2_6/ptodate2/iaa/5A_COMB.pep:*
12. /Ggn2_6/ptodate3/iaa/5B_COMB.pep:*
31. /Ggn2_6/ptodata3/iaa/6A_COMB.pep:*
41. /Ggn2_6/ptodata3/iaa/6B_COMB.pep:*
42. /Ggn2_6/ptodata3/iaa/PCTUS_COMB.pep:*
61. /Ggn2_6/ptodata3/iaa/PCTUS_COMB.pep:*
62. /Ggn2_6/ptodata3/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                - protein search, using frame_plus_n2p model
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US-07-977-696C-13
US-08-976-28BA-13
US-08-76-28BA-13
US-09-318-661-4
US-09-318-661-4
US-08-767-128-26
US-08-767-128-26
US-08-483-749A-10
US-08-483-749A-2
US-09-318-61-2
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                                                                                                                                                                                                                                                                                                                                                    389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                   Title:
Perfect score:
                                                                                     OM nucleic
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                                                                                                                                                                                                                    Sequence:
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429789711

Result 8

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ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Vivia
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Best Local Similarity:
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US-08-129-930B-13
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Patent No. 5/92852

GENERAL INFORMATION:
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GENERAL September 10.
GENERAL September 10.
APPLICANT:
APPLICANTION:
APPLICANTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 11-16-92
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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Matches:
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CITY: Los Angeles
STATE: California
                             LENGTH: 151
TYPE: PRT
ORGANISM: SCID Mice
                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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      SEQ ID NO 15
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APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEB: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
                                                                                                                                                                                                                                                                                                                                          134
112
112
23
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STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMUNICATION INFORMATION:
TELEPHONE: (510) 748-6688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08129930B; Patent No. 5804187; GENERAL INFORMATION:
                                                                                                                                                    13:
                                                                                                        TELEFAX: (510) 748-6688
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acids
TOPOLOGY: linear
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88.37%
79.07%
69.65%
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Thu Sep 30 13:18:40 2004
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us-09-674-716b-1.rai

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210 GAGAAGGGCTTGAGTGCGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT 269
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CUDINIKI: USA

CIP: 94596

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER IBM PC compatible
COMPUTER IBM PC compatible
COMPUTER BEADELE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAYS:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
FLING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: AMACHIER PAD.
REFIRENCE/DOCKET NUMBER: CRFCC-008A
TELEZEMONIACIONIN POR NOT 13:
TELEZEMONIA: (510) 521-1331
TELEZEMONIA: (510) 521-1333
TELEZEMONIA: (510) 521-1354
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acids
TYPE: Amino acid
TYPE: peptide
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Best Local Similarity:
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US-08-976-288A-13
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210 GAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACAC 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GluLysGlyLeuGluTrpValAlaGluIleArgAsnLysAlaAsnAsnHisAlaThrTyr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 ATGGATTTTGGGCTG----ATTTTTTTTTTTTTTTAAAAGGGGTCCAGAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 Tergradocretegarrracrireagregeracregargrerregerececearcrea
APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pertty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                     COMPUTER RELABBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
CLASSIFICATION DATA:
FILING DATE: No. 631597ember 21, 1997
CLASSIFICATION NUMBER: 08/129,930
FILING APPLICATION DATA:
PPLICATION NUMBER: 07/977,696
FILING DATE: No. 631597ember 16, 1992
ATTORNEY/AGBRI INFORMATION:
NAME: VIVIA and Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
TELEFRAM: (213) 489-4210
TELERY: (213) 489-4210
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102
12
23
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-13
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88.37*
79.07*
69.65*
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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149

209

Sequence 13, Application US/08976288A
Patent No. 6315997
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.

Thu Sep 30 13:18:40 2004

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154 GluValMetLeuValGluSerGlyGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 CCAGAGAAGGGGCTTGAGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 CAITATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
                                                                                                                                                                                                                                                 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer 80
                                                                                                                                                                                                                       87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC
                                                                                                                                                                                                                                                                                                                                                              21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpWetAsnTrpValArgGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 TCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 CTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGGAGTTTATTACTGTACA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Nucleotide OTHER INFORMATION: residue sequence of catalytic fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shabat. III, Carlos F. APPLICANT: Shabat. Doron APPLICANT: Shabat. Doron APPLICANT: Rader. Christoph APPLICANT: List, Benjamin APPLICANT: PLF00118 CURRENT FILE REPERBORE: PLF00118 CURRENT APPLICATION NUMBER: US/09/318,661
CURRENT APPLICATION NUMBER: US/09/318,661
CURRENT FILE OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 -------GATTTCATAGACTGGGCCCAAGGGACACTA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 TyrGlyArgGluGlyGlyPheAlaTyrTrpGlyGluGlyThrLeu 115
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                            Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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     Matches:
                                                                                                               Gaps:
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, Sequence 4, Application US/09318661
, Patent No. 626848
, GENERAL INFORMATION:
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500.00
87.61%
84.96%
66.40%
507.00
89.57%
82.61%
67.33%
                         Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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LENGTH: 285
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DB:
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                               ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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APPLICANT: WOREAY, PETER JOSEPH
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            387 TTCATAGACTGGGGCCAAGGGACACTA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION 10 DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION NUMBER: PCT/US96/09258
PRIOR APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-UN-1996
PRIOR APPLICATION NUMBER: 08/41,373
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
ATTORNEY/AGBNT INFORMATION:
NAME: CATEARY ON NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
PRIOR PERIOR OF THE STANDARY OF THE STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
STUDENT PASTEM DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 612/332-9081
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEC
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Pred. No.:
                                                                                                                                                                                                                                                    RESULT 5
US-08-767-128-28
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234 LeuTyrLeuGlnMetAsnSerLeuArgThrGluAspThrGlylleTyrTyrCysLysIle 253
                                                                                                                                        Sequence 26, Application US/08767128
; Sequence 26, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLE, DWANE E.
; APPLICANT: WYLE, DWANE E.
; APPLICANT: WIRRAY, PETER JOSEPH
APPLICANT: WORBAL, PETER
ITILE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCES: 46
; CORRESPONDENCES: 46
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079**est Center, 90 South Seventh St
CITY: Minneapolis
CITY: Minneapolis
STATE: MN
COUNTRY: USA
                                                                        384 -----GATTTCATAGACTGGGGCCAAGGGACACTA 413
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Matches:
Conservative:
Mismatches:
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CCUMIXA:
CCUMIXA:
CCUMIXA:
CCMPUTER READABLE FORM:
MEDIUM TYPEE: Diskette
COMPUTER. IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FASESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PTLING DATE:
FILING DATE:
FILING DATE: O4-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PTLING DATE: PTLING DATE: O5-UN-1996
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: 08/461,373
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: 08/461,373
FILING DATE: 10-OCT-1995
ATTORNEY/AGENT INFORMATION:
AMERICANTON NUMBER: 05-UN-1995
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 612/31-578
TELERAX: 612/31-578
TELERAX: 612/332-9081
TELERAX: 612/332-9081
TELERAX: 612/332-9081
TELERAX: AIND AMINO ACIDS
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89.57%
82.61%
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STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
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Best Local Similarity:
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ORIGINAL SOURCE:
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Pred. No.:
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                                                                           266
                                                                                                                 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAAGAGATGATTCCAAAAGTCGT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
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174 SerCysValValSerGlyLeuThrPheSerArgPheTrpMetSerTrpValArgGlnSer 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09883758
Fatent No. 6677435
GENERAL INFORMATION:
APPLICANT: Barbar, Doron
APPLICANT: Barbar, Doron
APPLICANT: List, Benjamin
APPLICANT: List, Benja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide COTHER INFORMATION: residue sequence of catalytic fragment US-09-883-758-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 TyrPheTyrSerPheSerTyrTrpGlyGlnGlyThrLeu 266
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM: Artificial Sequence
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84.96%
66.40%
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Best Local Similarity:
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US-09-883-758-4
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DB:
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267 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
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                                                                                                                                                                                                                                                                       21 SercysvalAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
                                                                                                                                                                                                                                                                                                                                                      87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC
                                                                                                                                                                        61 HisTyralaGluSerValLysGlyArgPheThrAlaSerArgAspAspSerLysSerSer
                                                                                                                                                                                                                                                                                                                                207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA
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Patent No. 6054561

GENERAL INFORMATION:
APPLICANT: RING, DAVID B.

TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSES CHIRON CORPORATION
STREET: INVELECTUAL PROPERTY - R440, PO BOX 8097
CITY: BMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

COUNTRY: USA

ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A

FLING DATE: 07-JUN-1995

CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REFERENCE/DOCKET NUMBER: 0508.008

TELECOMMUNICATION NUMBER: 0508.008
                                                                                           US-09-674-716B-1 (1-415) x US-08-483-749A-10 (1-114)
Mismatches:
Indels:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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amino acid
  Best Local Similarity: 82.41%
Query Match: 65.21%
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Pred. No.:
Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 CTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
                                                                                                                                                         1 GluValLysLeuGluGluSerGlyGlyGlyGlyLoeuValGlnProGlyGlySerMetLysLeu 20
                                                                                                                                                                                                                                           41 ProGlubysGlyLeuGluTrpValAlaGluValArgLeuLysSer---AsnTyrAlaThr 59
                                                                                                                                                                                                                                                                                                                                                                                                                                80 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGly11eTyrTyrCysThrArg 99
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Sequence 10, Application US/08483749A

Sequence 10, Application US/08483749A

Sequence 10, Application US/08483749A

Patent No. 605450A

TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY

TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097

CITY: EMBRYVILLE
STATE: CA

COUNTRY: USA

ZIP: 94662-8097
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100 TyrGlyArgGluGlyGlyValAlaTyrTrpGlyGlnGlyThrLeu 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
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Matches:
Conservative:
                                                                       US-09-674-716B-1 (1-415) x US-08-767-128-26 (1-119)
    Indels:
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ATTORNEY AGENT INN: 333
NAME: SAVERIDE PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/POCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPAX: (510) 601-2585
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 10:
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92.59%
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amino acid
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Pred. No.:
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Db 196 ProdlutysGlyLeuGluTrpValAlaGluIleArgLeuArgSerAspAssTTyrAlaThr 215  Oy 267 CATTATGCGGAGTCTCTGAAAGGGATGATTCACAAAGGTGT 326  Db 216 HisTyrAlaGluSerValLysPheThrIleSerArgAspAspSerLysSerArg 235  Oy 327 CTCTACCACAATGAACGCTTAAAGGGAGTGAAAGATGATTCACATACA 363  Db 226 LeuTyrLeuGlaMetAsnSerLeuArgThrGluAspThrGlyIleTyrTyrCysLysThr 255  Oy 384CATTCATAAGACGGAGCACA 413  Db 226 TyrPheTyrSerPheSerTyrTrpGlyGluAspThrGlyIleTyrTyrCysLysThr 255  Oy 384CATTCATAAGACTGGAGGACACA 413  Db 226 TyrPheTyrSerPheSerTyrTrpGlyGluGlyThrLeu 268  RESULT 12  US-09-883-758-7  Pacent No. 6677435	Alignment Scores:  Alignment Scores:  Alignment Scores:  Back Conservative: 93  Score:  Back Similarity: 82.34  Conservative: 4  Beet Local Similarity: 82.34  Mismatches: 12  Guery Match: 4  Beet Local Similarity: 82.34  Indels: 1  US-09-674-716B-1 (1-415) × Us-09-883-758-2 (1-298)  Cy  By GaAGTGAAGTTGAGGAGTTGAGGAGGTTGGTGCACTGGAGGATCCATGAACTC 146  Db 156 GluvalMetLeuvalGluSerGlyGlyLeuvalGlnProGlyGlyThrMetLysLeu 175  Cy  147 TCCTGTGTGAGCTTCTGGATTTACTTTCAGTGGATGTCTCAGGTCCCCAGTTC 206  Db 156 GluvalMetLeuvalGluSerGlyGlyLeuvalGlnProGlyGlyThrMetLysLeu 175  Cy  176 SecCyellulseerGlyGlyLeuvlarAgtGAGTGGAGATGTGAAATTGAATAGAAGGLSET 195  Cy  207 CCAGAGAAGGGGTTGGTGAAATTGATGAAATTGAATAGAAGGLSET 195  Cy  208 CATTATGCGGAGTTGTGAAATTGATGAAATTGAATATATAGAAACA 266  Db 156 ProGluLysGlyLeuvlarAgtGAGTTGACAGAGATGATTATATATATATATATA 215  Cy  209 CCATTATGCGGAGTTGTGAAAGGAGTTCACAAAGAGATGATTATATATA
	APPLICANT: Rader, Christoph APPLICANT: List, Benjamin A. APPLICANT: List, Benjamin A. APPLICANT: Lister, Richard A. APPLICANT: Lister, Repland Activation USING CATALYTIC ANTIBODIES FILE REPERBNCE: PLFOOLIN NUMBER: Ug/09/318,661 CURRENT APPLICATION NUMBER: Ug/09/318,661 CURRENT PRING DATE: 1999-05-25 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin Ver. 2.1 LENGTH: 299 L

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. 1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
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Patent No. S698195
GENERAL INFORMATION:
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Vilcek, Jan
Daddona, Peter E.
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APPLICANT:
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                                           GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Daddona, Peter E.
APPLICANT: Manage, John
APPLICANT: Right, David M.
APPLICANT: Right, David M.
APPLICANT: Right, David M.
APPLICANT: Right, Scott A.
TITLE OF INVENTION: ANTI-THY ANTIBODIES AND ASSAYS EMPLOYING
TITLE OF INVENTION: ANTI-THY ANTIBODIES
NUMBER OF SECUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: FIDDRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,102
FILING DATE: 04-FEB-1994
PRIOR APPLICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/192,093
FILING DATE: 04-FEB-1994
APPLICATION NUMBER: US 08/013,413
FILING DATE: 02-FEB-1993
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US 08/010,406
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: US 07/943,852
FILING DATE: 1-SEP-1992
FILING DATE: 1-SEP-1992
FILING DATE: 18-MAR-1992
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BLOOK, DATA: NATIONAL BERSEENER INFORMATION NUMBER: 22,592
FREGERRATION NUMBER: 22,592
FREGERRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE DOCKET NIMBER: NYU93-01M3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                            Sequence 5, Application US/08192102
Patent No. 5656272
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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amino acid
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83.62%
77.59%
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CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity:
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267 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAAGAAGATGATTCCAAAAGTCGT 326
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                                                                                         21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40
147 TCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCCCAGTCT
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ADDRESSE: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: Massachusetts
CONDUTRY: Was achusetts
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CONDUTRY: Is a proper to the conduct of the conduct of the condutry of
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APPLICANT: Ghrayeb, John
APPLICANT: Ghrayeb, John
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES
TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSED: Hamilton, Brook, Smith & Reynolds, P.C.
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FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
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Thu Sep 30 13:18:40 2004
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207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATTGGAACA 266
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APPLICANT: Utlcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Odddona, Peter E.
APPLICANT: Ghrayeb, John
APPLICANT: Rnight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: METHODS OF TREATING TNF'-MEDIATED DISEASE ITILE OF INVENTION: CHMBERIC ANTI-TNF ANTIBODIES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESCONDENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 -------GATTTCATAGACTGGGGCCAAGGGACA 410
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STREET: Two Militia Drive
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200
200
110
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAZ-1991
NAME: BROCK, DAVIG E.
REGISTRATION NUMBER: 22.592
REGISTRATION NUMBER: 22.592
REFERENCE/DOCKET NUMBER: DAVIG E.
FELECOMMUNICATION INFORMATION:
TELEPAN: (617) 861-9540
TELEPAN: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACATERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: proctin
US-08-324-799-5
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Patent No. 5919452
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77.59%
61.49%
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CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-08-192-861A-5
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Conservative:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM
SPETATING SYSTEM
SPETATING SYSTEM
APPLICATION UNDER: US (08/192,861A
FILING DATE: 04-FEB-1994
PRIOR APPLICATION NUMBER: US (08/13,413
PRIOR APPLICATION NUMBER: US (08/013,413
PRIOR APPLICATION NUMBER: US (08/010,406
PRIOR APPLICATION NUMBER: US (08/010,406
PRIOR APPLICATION NUMBER: US (07/943,852
PRIOR APPLICATION NUMBER: US (07/943,852
PRIOR APPLICATION NUMBER: US (07/670,827
FILING DATE: 11-SEP-1992
PRIOR APPLICATION NUMBER: US (07/670,827
FILING DATE: 18-MAR-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US (07/670,827
FILING DATE: 18-MAR-1991
APPLICATION NUMBER: US (07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT NUMBER: US (07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT NUMBER: 22,592
REFERENCE/POCKET NUMBER: WITU93-01M2
TELEPHONE: (731) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPEC, NATERIAL NATERIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463.00
83.62%
77.59%
61.49%
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Best Local Similarity:
Query Match:
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Pred. No.:
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earch completed: September 30, 2004, 09:31:33

Job time : 13.1499 secs

us-09-674-716b-2.rpr

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RESULT 1

KUMS67

Ig Wasca

Ig Wasca

Ig Wascassion. With musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

R; Selsing; E; Storb, U.

R; Selsing; E; Storb, U.

A; Reference number: A01909; MUID:82002223; PMID:6791832

A; Reference number: A01909

A; Reference number: A01909

A; Residues: 1-120 < SEL-A;

A; Residues: 1-120 < SEL-A;

A; Residues: 1-120 < SEL-A;

A; Introns: 17/

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp. hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into land; Reywords: heterotetramer

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer

F; 1-20/Domain: signal sequence #status predicted < SIG>
F; 1-120/Product: Ig kappa chain V V region (VK167) #status predicted <MAT>
F; 36-115/Domain: immunoglobulin homology 
Ig kappa chain - h
Ig kappa chain - h
Ig kappa chain prec
Ig kappa chain pre
Ig kappa chain vr
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Matches:
Conservative:
Mismatches:
Indels:
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     Percent Similarity:
Best Local Similarity:
Query Match:
     Alignment Scores:
Pred. No.:
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-MODEL=frame+ n2p.model -DEV=xlp
-DE_CORD_1/USPTO_spool_p/USO9674716/runat_30092004_070259_25882/app_query.fasta_1.3164
-DE_CORD_1/USPTO_spool_p/USO9674716/runat_30092004_070259_25882/app_query.fasta_1.3164
-DE_CORD_1/USPTO_SPOOL_P/USO9674716/runat_30FFXT=0
-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
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-UNITS=Dits -START=1 -END=-1 -MATRIX=100 -TRANS=human40_cdi -LIST=45
-UNITS=Dits -START=1 -END=-1 -MATRIX=100 -TALGN=15 -MODE=LOCAL
-USER=US09674716 @CGN 11 1.52 @runat 30092004 070259 25882 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                      US-09-674-716B-2
785
1 aagctttacagttactcagc.....agttggaaataaaacgtacg
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                  283366 segs, 96191526 residues
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                                                                                         September 30, 2004, 08:29:27
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Delop 6.0 , Delext 7
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A29775
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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Maximum DB
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A, Molecule type: protein
A, Residues: 1-112 < RUD>
C, Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. 7
C, Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. 7
C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan C; Superfamily: immunoglobulin V region; immunoglobulin homology
E, Reywords: heterotetramer
F; 16-95/Domain: immunoglobulin homology < IMM>
F; 23-93/Disulfide bonds: #status predicted
                                                                                                           Mol. Immunol. 17, 711-718, 1980
Ayîtite: Amino acid sequence of the light chain variable region of M511, a phosphorylchol A;Reference number: A01910; WUID:81052016; PMID:6776396
A;Accession: A01910
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C;Accession: A01910
R;Appella, B.
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A;Residues: 1-113 <APP>
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                       81 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGlulle
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A; Molecule type: DNA
A; Motors: Lhis sequence was determined from the germline gene
C; Genetics:
A; Introns: 17/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Superfamily: signal sequence #status predicted <SIG>F; 21-20/Paroduct: Ig kappa chain V region 24.2 #status predicted <MAT>F; 36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                               - shrew mouse
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R; Jouvin-Warche, E.; Rudikoff, S.
Immunogenetics 4, 191-201, 1986
A; Title: Evolution of a V-kappa gene family.
A; Reference number: A91751; MUID:87006895; PMID:3093373
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840357
19 kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-200
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-200
C;Accession: 840354 #sequence_revision and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Accession: S40357
A;Accession: S40357
A;Accession: Storian and their hypermutation.
A;Accession: S
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
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C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. C;Complex: An immunoglobulin heterotetramer submit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the submits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
E;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
192775
19 kappa chain precursor V region (mouse 24.1) - shrew mouse C; Species: Mus pahari
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000 C; Accession: B29775
R; Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A; Title: Evolution of a V.kappa gene family.
A; Reference number: A91751; MUID:8706895; PMID:3093373
A; Accession: B29775
A; Molecule type: DNA
A; Residues: 1-120 -4004
A; Residues: 1-10 -40
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G.; Zachau, H.G.

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J. Exp. Med. 173, 1033-1036, 1991
AyÎtîle: Novel Chromosome translocation caused by fusion of immunoglobulin heavy and lig?
A;Reference number: S23230; MUID:91178438; PMID:1840606
A;Accession: S23230
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23230
                                                                                         A; Accession: 52682
A; Status: preliminary; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C; Genetics:
A; Introns: 17/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: hererotetramer; immunoglobulin
F; 36-115/Domain: immunoglobulin homology < INM/>
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R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H. Nature 347, 90-92, 1990
A;Title: Megabase inversions in the human genome as physiological events.
A;Reference number: S26882; MUID:90370099; PMID:2118596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <KEN>
A;Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
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S403/2

S403/2

Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: 540372

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: 840312; MUID:94080891; PMID:8258341

A;Accession: S40372

A;Accession: S40372

A;Residues: 1-131 < KLE>

A;Cross-references: EMBL:X72482; NID:9441432; PIDN:CAA51150.1; PID:9441433

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology < IMM>
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Db 30 SerGlyAspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnPro 49  Qy 150 GTTTCCATCTGCAGGTCTAGTAAAGAGTCTCTGTATAAAGATGGAAGAACATACTTG 209  Db 50 AlaSerIleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeu 69  Qy 210 AATTGGTTTCTGCAAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACC 269  Qy 210 AATTGGTTTCTGCAAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACC 269  The statement of the sta	Oy 270 CGTGCALCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGGCACAGATTTCACCCTG 329	Qy 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTTTACTGTCAACAACTTGTAGAG 389 :::	Qy 390 TATCCATTCACGTTCGGCTCGGGACAAAGTTGGAATA 428 :::	RESULT 11 S40342 Ig kappa chain - human	C.) Species: Homo sapiens (mail) C.) Species: none sapiens (mail) C.) Date: 06-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C.) Accession: S40342 R.) Klein, R.; Jaenichen, R.; Zachau, H.G.	Eur. J. Immunol. 23, 3248-3271, 1993 A;Tile: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341 A;Accession: S40342	A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-135 <kle> A;Cross-references: EMBL:X72452; NID:g441372; PID:g441373</kle>	C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;29-108/Domain: immunoglobulin homology <imm></imm>	Alignment Scores: 4.47e-40 Length: 135 Pred. No.: 485.00 Matches: 93 Percent Similarity: 85.04\$ Conservative: 15 Best Local Similarity: 73.23\$ Mismatches: 19 Query Match: 61.78\$ Indels: 0	2 Gaps: -674-716B-2 (1-437) x 840342 (1-135)	Oy 57 CTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGAT 116	Qy 117 GAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCTAGTAAG 176	Db 21 ProleuSerLeuProValThrProdlyGluProAlaSerTleSerCysArgSerSerGin 40	4. SerieuleuHisSerAsnGlyTyrAsnTyrLeuAspTrpTyrLeuGlnLysProGlyGln	Qy 237 TCTCCTCAGCTCCTGATATTTGATGTCCACCCGTGCATCAGAGGACTCTCAGACGGTTT 296	297 AGTGGCAGTGAGGCACAGAATTTCACCCTGGAAATCAGTAGAGTGAAAGGCTGAGGAT 3	Db 81 SerGlySerGlyThrAspPheThrLeuLysIleSerArgValGluAlaGluAsp 100	Qy 357 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCATTCACGTTCGGCTCGGGGACA 416
Alignment Scores:  Pred. No.:  Pred. No.:  Pred. No.:  Pred. No.:  Pred. No.:  Pred. No.:  Pered. Similarity:  Percent Similarity:  Per	Oy 36 ATGAGGTTCTGTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95	Qy 96 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155	Oy 156 ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215	Oy 216 TITCTGCAGAGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGGGCA 275	Qy 276 TCAGAGICTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335	OY 336 AGTAGAGTGAAGGTGAGGATGTGGGTGTGTATTACTGTCAACATTGTAGAGTATCCA 395	Qy         396         TTCACGTTCGGCGGACAAAGTTGGAAATAAAACGT         434           Db         121         TyrThrPheGlyGlnGlyThrLysLeuGlulleLysArg         133	RESULT 10 522902	Ig kappa chain V region - human C,Species: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S22902 R;Chastagner, P: Theze, J.; Zouali, M. Gene 101, 305-306, 1991	•	A.Residues: 1-142 <cha> A.Residues: 1-142 <cha> A.Cross-references: EMBL:X56510 C.Superfamily: immunoglobulin V region; immunoglobulin homology</cha></cha>	C;Keywords: Acterotetramer; 1mmunoglobulin F;47-126/Domain: immunoglobulin homology <imm></imm>	Dength:	/: 90.00 /: 90.45% rity: 69.1% 61.91%	2 Gaps: -674-7168-2 (1-437) x S22902 (1-142)	30	Db 10 LeuThrMetArgLeuProAlaGInLeuLeuGlyLeuLeuMetLeuTrpValProGlySer 29	Qy 90 AGTGGGGATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCA 149

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Alignment Scores:
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                                                                                                                                                                                                                                                        Ig kappa chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: S29593
R;Seymour, R.
Submitted to the BMEL Data Library, February 1991
A;Reference number: S29593
C;Residues: 1-197
C;Residues: 1-197
C;Residues: 1-197
C;Repwords: heterotetramer; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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Conservative:
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                                                                                                                             121 LysvalGlulleLysArgThr 127
                                                                                              417 AAGTTGGAAATAAAACGTACG 437
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483.00
82.03%
73.44%
61.53%
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| TCAGGAGTCTCAGACCGGTTTAGTGGCACTGGGGTCAGGCACAGTTTCACCCTGGAAATC 335
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A;Molecule type: DNA
A;Residues: 1-133 <KLO>
A;Note: the sequence was determined from the differentiated gene
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479.00
79.70%
68.42%
61.02%
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A;Map position: 2p12-2p12
A;Introns: 17/1
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US-09-674-716B-2 (1-437) x S40321 (1-130)
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S40321
Ig kappe chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40312
R;Klein, R: Jaenichen, R: Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40321
A;Status: preliminary; translation not shown
A;Residues: 1-130 cKLES
A;Cross-references: EMBL:X72431
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCATTCACGTTCGGCTCG 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 CAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCT
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-133 < CKLUS
A;Cross-references: EMBL:X72434
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;33-112/Domain: immunoglobulin homology <IMM>
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Conservative:
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60.83%
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P01627;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
11 g kappa chain V-II region VKappa167 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 mouse | Musinae; M
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINIG-1.
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                               P065311
P065312
P016513
P011651
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P011658
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EMBL; 400562; AAA39051.1; -
FIRE, A01909; KVMS67.
HSSP; P80362; 1WTL.
HREPPOC; IPR007110; Ig-like.
INTERPOC; IPR003566; Ig_v.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LKE; 1.
IMMUNOGlobulin V region; Signal.
SIGNAL 21 120 IG KAPPA CH
DOMAIN 21 120 IG KAPPA CH
DOMAIN 21 43 COMPLEMENTA
KV3M HUMAN
KV4E MOUSE
KV3K HUMAN
KV1M HUMAN
KV3I HUMAN
KV3I MOUSE
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KV3T MOUSE
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-DE-SW18SFTOC 42 - QFWT=fastan - SUFFTX=rsp - MINNATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-OCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE=LOCAL
-OCALIGN=200 - NORM=ext - HEAPSIZE==500 - MINNEN0 - MAXIEN=200000000
-USRE=US0674716_GCGN 1 1 82 @TUNAT 130022004_070257_25855 - NOPU=6 - ICPU=3
-NO_MMAPP - LARGEQUERY - NGG = SCORES=0 - WARIT - USPBLOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPDEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AL BIOCHAMISTRY 17:2703-2707(1978).

BIOLOGISTRY 17:2703-2707(1978).

- I- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WYELOWA PROTEIN THAT CC EALSO BERN DEFERMINED.

CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY CC CHARLY A01904; KWWS16.

DR HSSP, P80362; 1WTL.

BR HSSP, P80362; 1WTL.

DR HSSP, P80362; 1G-1:

BR MART; SM00407; ig; 1.

BR SMART; SM00406; IGV; 1.

BR SMART; SM00406; IGV; 1.

BR FRAMENOSITE; PS50835; IG LIKE; 1.

FT MOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                          96 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
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Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
          COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
19-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region MOPC 167.
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FRAMEWORK-2.
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Mol. Immunol. 17.711-718 (1980).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.
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FRAMBWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMBWORK-4.
BY SIMILARITY.
54 FRAMEWORK-2.
61 CONFLEMENTARITY-DETERMINING-
93 CONFLEMENTARITY-DETERMINING-
102 CONFLEMENTARITY-DETERMINING-
112 FRAMEWORK-4.
93 BY SIMILARITY.
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region MOPC 511.
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MEDLINE=81052016; PubMed=6776396;
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HSSP, P80362, 1WTL.
InterPro; IPR00710, Ig-like.
InterPro; IPR003596; Ig_v.
Pfam, PF00047; ig; 1.
SWART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=86641852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.,
"Human immunoglobulin Kappa light chain genes of subgroups II and
       COMPLEMENTARITY-DETERMINING-1.
                                                   COMPLEMENTARITY-DETERMINING-2.
                                                                      PRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
39 COMPLEMENTARITY-DETERMINING-
54 FRAMENORK-2.
61 COMPLEMENTARITY-DETERMINING-
93 COMPLEMENTARITY-DETERMINING-
112 FRAMEWORK-3.
93 BY SIMILARITY.
93 BY SIMILARITY.
113 BY EFBODC4DA2BD3450 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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01-07N-1998 (Rel. 06, Last sequence update)
15-07U-1999 (Rel. 38, Last annotation update)
Kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human)
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Best Local Similarity:
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Pred. No.:
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KV2F HUMAN

AC P06310,

DT 01-JAN,

DT 01-JAN,

DT 11-JUL,

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TO KVZD HUMAN

STANDARD; PRT; 113 AA.

TO 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1998 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

C 15-JUL-1999 (Rel. 38, Last annotation update)

DE 16 kappa chain V-II region TEW.

S Homo sapiens (Human).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            KAPPA CHAIN V-II REGION RPMI
                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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Mismatches:
Indels:
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Matches:
HSSP, PR0362; 1WTL.
GO, GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR00710; Ig-11ke.
Pfam; PF00047; ig; 1
SWART; SW00406; IGv; 1.
FR051TE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                          IG KAPPA CH
FRAMEWORK-1
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No
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396 TTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT
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P01630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
                                                                                                                                                                                                                    patient with plasma cell dyscrasia and amyloidosis.";
J. Chin. Invest. 52.1276-1281 (1973)
J. Chin. Invest. 52.1276-1281 (1973)
J. Chin. Invest. 52.1276-1281 (1973)
J. MISCELLANEOUS: THE MAJOR ANYLOID PROTEIN APPEARS TO BE IDENTICAL
WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
J. MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
J. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                        identity of Bence Jones and amyloid fibril proteins in
                                                                               ij
                                        MEDLINE=7414840) PubMed=4596149;
Putnam F.W., Whitley B.J. Jr., Paul C., Davidson J.N.,
"Amino acid sequence of a kappa Bence Jones protein from a case
primary amyloidosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 1.
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FRAMEWORK-3.
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                                                                                                                                                         MEDLINE=73166638; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Glenner G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; irav...
Pfam; PF00047; ig; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
FRAMEWORK-1.
FRAMEWORK-1.
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Matches:
Conservative:
Mismatches:
Indels:
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HSSP, PO1607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                            SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW)
                                (BENCE-JONES PROTEIN JEW)
                                                                                                             ochemistry 12:3763-3780(1973).
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72.57%
55.41%
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Query Match:
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                          "Structural
                                                                                                                                                                                                                                                                                                                                     MARKER
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NON TER
SEQUENCE
                                QUENCE
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9
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MEDLINE=33256427; PubWed=6409088;

MEDLINE=33256427; PubWed=6409088;

Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;

The desired sequence (V kappa 27) of the variable region of kappa-
ight chains from a mouse hybridoma-derived anti-(streptococcal group

A polysaccharide) antibody containing an additional cysteine residue.

Application of the dimethylaminoazobenzene isothiocyanate technique
for the isolation of peptides.";

Biochem J. 21:1173-180 (1983).

L in MISCELLANBOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL

ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

R AND AND AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

R INTERPROPINGE 1980362; IG-V.

R INTERPROPINGE 1890363; IG-LIKE; 1.

R SWART; SMO0406; IG-V.

R Pfam: PF00047; ig: 1.

R ROSSITE; PS50835; IG-LIKE; 1.

POWALING IMPRODIATION OF SEGURE AND SEGURE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAlaPheThrLeuArgile 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspileValMetThrGinThrAlaProSerAlaLeuValThrProGlyGluSerValSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 IleSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyAsnThrTyrLeuTyrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 TITCIGCAGAGCCAGGACAATCICCICAGCICCIGATGIAITTGAIGICCACCGIGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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87
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101 IleThrPheGlyGlnGlyThrArgLeuGluIleLysArg 113
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                    21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region 7834.1.
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12496 MW;
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82.30%
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203

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84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGA 143

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21 GluProAlaSerIleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsn 40
                                                                             144 GAATCAGTTTCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACA
1 GlySerSerGlyAspileValMetThrGlnSerProLeuSerLeuProValThrProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBI_TaxID=9606;
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P01614;
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                                      81 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlnArgGluTyrPro 100
  336 ACTAGAGGTGAAGGTTGTGGGTGTGTTTACTGTCAACAACTTGTAGAGTATCCA 395
                                                                                                                                                                                                                                                                                                                                     01-JAN 1988 (Rel. 06, Created)
1-JAN 1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 39, Last annotation update)
15-JUL-1999 (Rel. 39, Last annotation update)
16 kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-84191506; PubMed-6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG KAPPA CHAIN V-II REGION GM607.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                               TyrThrPheGlyGlyGlyThrLysLeuGluIleLysArg 113
                                                                                                                 TTCACGTTCGGCTCGGGGACAAGTTGGAAATAAAACGT
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Conservative:
Mismatches:
Indels:
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PIR; A01889; KZHUGM.
HSSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0005825; F:antigen binding; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR00756; Ig-1.
SMART; SM00406; Ig-1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
NON TER.
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431.00
83.76%
72.65%
54.90%
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                        HUMAN
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DISULFID
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SEQUENCE
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P06309;
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DB:
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264 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTC 323
                                                                                                    324 ACCCIGGAAAICAGIAGAGIGAAGGCIGAGGAIGIGGGGIGIGIAIIACIGICAACAACII 383
                                                                                                                    80
204 TACTIGAATIGGITICIGCAGAGACCAGGACAATCICCICAGCICCIGAIGIATITGAIG
            MEDLINE=62242259; PubMed=5586923;
Hilschmann N.;
"The complete amino acid sequence of Bence Jones protein Cum (kappa-
type).";
                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
1-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-II region Cum.
16 kappa chain V-II region Cum.
17 kappa chain (Human).
18 karyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
18 Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                        434
                                                                                                                                                                    384 GTAGAGTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
85
11
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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427.50
84.21$
74.56$
54.46$
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-674-716B-2 (1-437) x KV2A\_HUMAN (1-115)

Thu Sep 30 13:18:44 2004

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155
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                                                           156 ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAG---GATGGGAAGACATACTTGAAT 212
                                                                                                                                                                                273 GCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAA 332
                                                                                                                                                                                                                                          333 ATCAGTAGAGGTGAAGGCTGAGGATGTGGTGTATTACTGTCAACAACTTGTAGAGTAT 392
                                                                                                                                                                                                                                                             2 AsplieValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 21
                                                                                        41
                                                                                                                                                                                                           62 AlaSerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 81
96 GATATTGTGATAACCCAGGATGAACTCTCCCAATCCTGTCACTTCTGGAGAATCAGTTTCC
                                                                           22 IleSerCysArgSerSerGinSerLeuLeuAspSerGlyAspGlyAspThrTyrLeuAsn
                                                                                                                     213 TGGTTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=85128968; PubMed=6441768; AbbErsold R., Herbart H., Grutter T., Chang J.Y., Braun D.G.; Abbersold R., Herbart H., Grutter T., Chang J.Y., Braun D.G.; Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6 origin: monoclonal antibodies 17829.1 and 22825.1 specific for the group A-streptococcal polysaccharides."; Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
-i- MISCELLANBOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                       393 CCATTCACGTTCGGCTCGGGGACAAGTTGGAAATAAAACGT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4E93797046F8DB33 CRC64;
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Conservative:
Mismatches:
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23-OCT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G Kappa chain V-II region 17829.1.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                               113 AA
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PRGART, SM00406; iGv; l.
PROSTE; PS50835; iG LIKE; l.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01912; KYMS17.
HSSP; P01607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12390 MW;
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427.00
82.30%
74.34%
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Best Local Similarity:
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Pred. No.:
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NON TER
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                                                                        1 AspilevalMetThrGlnAlaValPheSerAsnProValThrLeuGlyThrSerAlaSer
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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12660 MW; 0C0DA39E46DB96BE CRC64;
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                               US-09-674-716B-2 (1-437) x KV2E_MOUSE
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113 AA;
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Alignment Scores:

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Pred. No.:
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REPURNE.

X MEDLINE=10030;

X HEADLINE=10030;

X HEADLINE=2055101; PubMed=7141411;

REDLINE=3055101; PubMed=7141411;

REDLINE=3055101; PubMed=7141411;

HEADLINE=3055101; PubMed=7141411;

HEADLINE=3055101; PubMed=7141411;

THE GROUP A SIEPPROCOCCAL GROUP A FOLYSACCHARDE.

THE GRANSCT THE STREPTOCOCCAL GROUP A POLYSACCHARDE.

PIR; A01911; KWMSS1.

PRSP; PO1607; IREI.

RESP; POMAIN CONPERMENTARITY-DETERMINING-2.

REPRESP; POMAIN CONPERMENTARITY-DETERMINING-3.

REPRESPRESP; POMAIN CONPERMENTARITY-DETERMI
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
Mus musculus (Mouse)
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
11 TaxID=10090;
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83.19%
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Best Local Similarity:
Query Match:
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P01629;
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SEQUENCE:

XX MEDLINE=83178921; PubMed=6404298;
XX MEDLINE=83178921; PubMed=6404298;
XX MEDLINE=83178921; PubMed=6404298;
XX MEDLINE=83178921; PubMed=6404298;
XX "Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
XX "Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
XX "AMISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT BINDS DIGOXIN.
XX "ANSSE"
XX "
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21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
15-UTL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region 26-10.
Buks musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TD KV2G MOUSE

DT 21-JULI

DT 21-JULI

DE 19-JULI

DE
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E5B22E2FA7ABE481 CRC64;

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EMBL; X02990; CAA26733.1; -.
HSSP; P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
            112 AA; 12055 MW;
                                                                                         5.29e-35
398.50
83.19%
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                                                                   Alignment Scores:
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Dreyer W.J., Gray W.R., Hood L.E.,

The genetic, molecular, and cellular basis of antibody formation:

"The genetic, molecular, and cellular basis of antibody formation:

"The genetic and a unifying hypothesis.",

Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).

"I MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

"I MISCELLANEOUS: This is a Bence-Jones protein.

PIR, A01887; RZHUML.

RISCELLANEOUS: This is a Bence-Jones protein.

RISCP: PR003710; Ig-like.

RINGERPO: IPR007110; Ig-like.

RINGERPO: IPR007110; Ig-like.

RINGERPO: IPR0047; Ig-like.

REMART: SMO446; IG-V.

REMART: SMO446; IG-V.

REMART: PS050835; IG-LIKE; I.
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15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region MIL.
1g kappa chain V-II region MIL.
Elwaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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      12273 MW;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the buropean Bioinformatics Institute. There are no restrictions on institute by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@igb-sib.ch).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Marsh P., Mills F., Gould H.;
Detection of a unique human V kappa IV germline gene by a cloned
CDMA probe.".
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Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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          "Subgroup IV of human immunoglobulin K light chains is encoded by single germline gene."; Nucleic Acids Res. 13:6515-6529(1985).
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COMPLEMENTARITY-DETERMINING-3.
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PIR, A01904; K4HUJI.
HSPP, R00362; URATUJI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1;
InterPro; IPR007110; Ig-1;
Pfan; PF00047; Ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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  Zachau H.G.;
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MEDLINE-86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                 IG KAPPA CHAIN V-IV REGION B17
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                              COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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Last annotation update)
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BY SIMILARITY
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01-07N-1988 (Rel. 06, Last sequence upda 15-UUL-1999 (Rel. 38, Last annotation up 1g kappa chain V-IV region JI precursor.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG LIKE; 1.
Immunoglobulin V regIon; Signal.
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Thu Sep 30 13:18:44 2004

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Search completed: September 30, 2004, 08:42:45 Job time : 11.4813 secs

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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa, Cordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 aagctttacagttactcagc.....agttggaaataaaacgtacg
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                   - protein search, using frame_plus_n2p model
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PIR; A32248; A32248.
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PIR; SH1044; PH1044.
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QSTCD0;
QSTCD0;
QSTCD0;
QSTCD0;
QSTCD0;
QSTCD0;
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                                                                                                                                                                   F5E20AD3B0552C0A CRC64;
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Matches:
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Mismatches:
Indels:
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Pfam; PF00047; ig; 2.
SWART; SM00407; iGG1; 1.
SWART; SM00406; iGv; 1.
PROSITE; PSC935; IG_LIKE; 2.
PROSITE; PSC9090; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26024 MW; F
                                                                                                                                                                                                                                              1.35e-48
497.00
82.84%
70.90%
63.31%
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Best Local Similarity:
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TISSUE=Lung;
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Pred. No.:
Score:
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DB:
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Q8TCD0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-070-2001 (TrEMBLrel. 17, Created)
01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-070-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musine; Mus.
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FACEDC3A3B03871D CRC64;
                                                                 233
91
16
27
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                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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EMBL/GenBank/DDBJ

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216
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAGGTTCTCTGTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG
                                                                                                                                                                                                                                                                                       GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBVCI6 PRELIMINARY; PRT; 238 AA.

OBVCI6;

O1-MAR-2002 (TEMBLrel. 20, Last sequence update)

O1-MAR-2003 (TEMBLrel. 25, Last annotation update)

O1-OCT-2003 (TEMBLrel. 25, Last annotation update)

Hypothetical protein.

Hypothetical protein.

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

O11-TAXID=10090;
                                                                                                                                                FB2B06A0B801330A CRC64
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87
20
20
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PIR; S24529; S24529.
PIR; S24532; S24532.
PIR; S24533; S24533.
PIR; S24536; S24533.
PIR; S24536; S24536.
PIR; S24536; S24536.
PIR; S24536; S24536.
PIR; S24536; S24536.
PIR; S24538; S24536.
PIR; J102; 31-UUL-02.
PIR; J104; 31-UUL-02.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_NHC.
InterPro; IPR003596; IG_NHC.
PROMITE; PS0047; ig; PROMITE; PS00406; IGV: IRR; PROSITE; PS00290; IG_MHC; I.R.
PROSITE; PS00290; IG_MHC; I.R.
PROSITE; PS00290; IG_MHC; I.R.
SEQUENCE 238 AA; 26344 MW; F
                                                                                                                                                                         7.62e-43
447.50
80.45%
65.41%
57.01%
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TISSUE=Colon;
Strausberg R.;
                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                        96
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Q8VCI6

110 Q88

AC Q88

DDT O11

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TTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeulleTyrLysValSerAsnArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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EMBL, BCO19760; AAH19760.1; --
EMBL, BCO19760; AAH19760.1; --
PIR, AA27887, A27887.
PIR, AA27887, BA2248.
PIR, AA3933, A3933.
PIR, B30577, B30577.
PIR, B31485; B31485.
PIR, B31485; B31485.
PIR, B31485; B31485.
PIR, B3248; B32248.
PIR, C32487; C3248.
PIR, C34904; C34904.
PIR, C34904; C34904.
PIR, C34904; C34904.
PIR, E28833, E3883.
PIR, PHO3987; D27887.
PIR, PHO3987; D27887.
PIR, PHO3987; D27887.
PIR, PHO3987; D40106.
PIR, PHO398; PHO390.
PIR, PHO398; PHO390.
PIR, PHO399; PHO390.
PIR, S07455; S07455.
PIR, S07455; S07455.
PIR, S16112; S16112.
PIR, S53750; S33750, S33750.
InterPro; IPR003196; IG_MC.
InterPro; IPR003596; IG_WC.
InterPro; IPR003596; IG_MC.
InterPro; IPR003596; IG_MC.
InterPro; IPR003596; IG_MC.
InterPro; IPR003596; IG_MC.
InterPro; IPR003596; IG_WC.
PROSITE; PS00305; IG_MC.
INTERPRO; IPR003596; IG_MC.
INTERPROSITE; PS00395; IG_MC.
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442.50
79.70%
64.66%
56.37%
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Percent Similarity:
Best Local Similarity:
Query Match:
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336 AGTAGAGTGAAGGCTGAGGATGTGGGGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395 PRELIMINARY; Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: QBKOF8 QBKOF8; No.: RESULT 6 A CONTRACTOR OF THE CONTRACTOR ઠે a ò 임 g à à g ઠે Db GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395

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96 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetMetSerProAlaGinPheLeuPheLeuLeuValLeuSerileGlnGluIleAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 ATGAGGTTCTCTGTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                            PSCUENCE FROM N.A.

TISSUE=Freast tumor;

A Strausberg R.;

Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.

L Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; EC031498; AAH31498.1; -..

PIR; A3393, A3393, A33933.

R PIR; A33933, A33933, PIR; -..

R OJ GO:0016491; F:omerabolism; EA.

GO; GO:0016491; F:omerabolism; EA.

InterPro; IPR001599; ADH short.

R InterPro; IPR003599; IG.-1.

R EMPRI; SM00407; IG.1; IG.-1.

R SMART; SM00409; IG.1; IG.-1.

R SMART; SM00409; IG.1; I..

R SMART; SM00409; IG.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00061; ADH SHORT; 1.
PROSITE; PS00061; ADH SHORT; 1.
PROSITE; PS00290; IG LIKE; 2.
PROSITE; PS00290; IG LIKE; 1.
SEQUENCE 239 AA; 26366 MW; D7BE84398AA31F0 CRC64;
Last sequence update)
Last annotation update)
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Matches:
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                                                                                                                                                PRT;
                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein. Mus musculus (Mouse).
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418.00
76.69%
61.65%
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CCATTCACGTTCGGCTCGGGGACAAGTTGGAAATAAAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 148 AA; 16345 MW;
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400.00
75.78%
62.50%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934; MEDLINE=98277139; PubMed=9614934; Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Mu X., Liu B., Van der Merwe P.L., Kalis n.N., arditis and n
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                                                                     396 TTCACGTTCGGCTCGGGACAAAGTTGGAAATAAAACGT 434
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                         TyrThrPheGlyGlyGlyThrLysLeuGlulleLysArg
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EMBL, AF035034; AAD56270.1; -.
PIR; B49002; B49002.
PIR; S23638; S23638.
PIR; S34094; S34094.
PIR; S34095; S34095.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM0406; IGv; 1.
NON TER 114 114 114
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01-0CT-2002 (TEMBLrel. 22, Created)
01-0CT-2002 (TEMBLrel. 22, Last sequence update)
01-0CT-2003 (TEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Homo sapiens (Human)
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Mammalia; Eutheria; Rodentia; Sçiurognathi; Muridae; Murinae; Mus
                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
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Hypothetical protein.
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Attaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhard N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soarsa M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
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Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-0CT-2003 (TEMBLE) 25, Created)
01-0CT-2003 (TEMBLE) 25, Last sequence update)
01-0CT-2003 (TEMBLE) 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                 MEDINE=93383497; PubMed=8372513; Troige D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.; Choige D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.; Cloning and characterization of 1116K819.9 heavy and light chain cDNAs and expression of antibody fragments in Escherichia coli."; Fars Immunol. 7:56-62[193].

EMBL, S65921; AAB28160.1; -
SEQUENCE 236 AA, 26454 MW, 2CS86EBF5EA10F4C CRC64;
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 TrpThrPheGlyGlnGlyThrLysValGluIleLysArgThr 129
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                             Anti-colorectal carcinoma light chain.
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SEQUENCE FROM N.A.
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Percent Similarity:
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01-OCT-2003
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Q7TS98;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., A Itausrer R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., ARICHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Garlist E. Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Garlist E. Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Garlist E.D., Schnerch A., Schein J.E., Marra M.A., Jones S.J., Marra M.A., Touchman J., Smailus D.E., Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Garlist E. Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Garlist E. Schnerch A., Schein J.E., Marra M.A., Jones S.J., Marra M.A., Touchman J.W., Garlist E. Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Garlist E. Schnerch A., Schein J.E., Marra M.A., J. Jones S.J., Marra M.A., Touchman J. W., Garlist E. Schnerch A., Schein J.E., Marra M.A., J. W. M., Garlist E. J., Schnerch A., Schein J.E., Marra M.A., M. J. J., M. J. J., M. J., S., M. J., J. J., M. J., J., J. J.,
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SEQUENCE 236 AA; 25702 MW;
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Submitted (MAR-2001) to the
EMBL; BC005332; AAH05332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.";
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TISSUE=Skeletal muscle;
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Best Local Similarity:
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US-09-674-716B-2 (1-437) x Q7SZ36 (1-237)
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                                                                                                                                                                                                            STRAIN=CZECH II; TISSUE=Breast tumor;

MEDLINE=2288257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Wodin T.B., Toshiyuki S., Carnino P., Prange C.,

Raha S., Loquellano N.A., Peters G.J., Abramson R.D., mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Richingez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 CTCACCATGAGGTTCTCTGTTCAGTTTCTGGGGGGTGCTTATGTTCTGGATCTCTGGAGTC
                            01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Musmanla, Eutheria, Rodentia, Sciurognathi, Muridae, Mus., Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BCO559906; AAH55906.1; -. Hypothetical protein.
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oc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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236 AA; 26299 MW;
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47.41%
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PRELIMINARY;
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Q7TMK3
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330 GAAATCAGTAGAGTGAAGGCTGAGGATGTGGGGTGTGTATTACTGTCAACAACATGTAGAG 389
                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                            Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                              434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO54155; AAHS4155.1; -.
Hypothetical protein:
SEQUENCE 237 AA; 26300 MW; 47BBDDD2639CB436 CRC64;
                                                           390 TATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                 237 AA
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86 IleSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgMetGluAlaGlu 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 GAIGIGGGIGIGIAITIACIGICAACAACAGIAGAGIAICCAITICACGITICGGCTCGGGG 413
CTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCCAGGAT 116
                                                                                                                        117 GAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCTAGTAAG 176
                                                                                                                                                                                                                                                    AGTOTOCOGTATAAGGATGGGAAGACA - - TACTTGAATTGGTTTCTGCAGAAGACCAGGA 233
                                                                                                                                                                                                                                                                                                                                                                            CAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 ITTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATCAGTAGAGGTGAAGGCTGAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 AspAlaAlaAspTyrTyrCysGlnGlnSerArgSerAspProLeuThrPheGlyLysGly 125
                                                                                                                                                                ProAspTyrValSerValSerProGlyGluThrValThrLeuThrCysLysAlaSerSer 47
                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, MuschI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strauberg R.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR001101; Ig-1ike.
InterPro; IPR00306; Ig-MHC.
InterPro; IPR00306; Ig-W.
Pfam; PF00047; Ig's.
SMART; SM00406; IGV; I.
PROSITE; PS00290; IG/MHC; I.
PROSITE; PS00290; IG/MHC; I.
Hypothetical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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48.87%
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57
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GATATIGEGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155

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36 AIGAGGIICICIGIGIICAGIIIICIGGGGGGGGCIIAIGIICIGGAICICCIGGAGICAGIGGG 95

US-09-674-716B-2 (1-437) x Q8R062 (1-234)

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Percent Similarity: Best Local Similarity: Query Match: DB:

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216 TITCIGCAGAGCCAGGACAATCICCICAGCICCIGAIGIATIIGAIGICCACCCGIGCA 275
                                                                                                                                                                                                                               TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335
                                                                                                                                                                                                             336 AGTAGAGTGAAGGCTGAGGATGTGGTGTGTTTACTGTCAACAACTTGTAGAGTATCCA 395
                                                                                                          -----SerAsnTyrLeuAsnTrp 55
21 AsplleGlnMetThrGlnThrThrSerSerLeuSerAlaSerLeuGlyAspArgValThr 40
                                156 ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
                                                                                                                                                                    TTCACGTTCGGCTCGGGGACAAGTTGGAAATAAAACGT 434
                                                 |||||||||||
41 IleSerCysSerAlaSerGlnGlyIle----
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Job time : 59.3361 secs
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DIMK Shelt

us-09-674-716b-2.rag

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Aay32262 Humanised
Aae06969 Mouse ger
Ade22461 Human ant
Aay82617 Human PTH
Aay82615 Human PTH
Aay82618 Human PTH
Ade28405 Human ant
Ade28407 Human ant
Abp64972 Human ant
Abp64972 Human ant
Abp64972 Human PTH
Aar3641 C242 Kapp
Aay82610 Human PTH
Aar3641 Human PTH
Aar3681 Human PTH
Ade28409137 Feline Int
Ade28611 Human ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabstes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; psoriasis; inflammatory bowel disease; ulcrarive collitis; Crohn's disease; sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                         AAK82541
AAK82614
AAK82614
AAK33951
AAK56874
ADE28463
ADE28477
ADE28610
AADE2801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
55. .70
/note= "CDR L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32261 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83. .92
/note= "CDR L2"
125. .134
/note= "CDR L3"
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   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09958679-A1
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   AAY32261;
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    Mouse ant
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                                                                                       (without alignments)
4743.430 Million cell updates/sec
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                                                                             September 30, 2004, 08:19:42; Search time 52.0607 Seconds
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785
1 aagctttacagttactcagc......agttggaaataaaacgtacg 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aay32261 Nar12354 Aar12354 Aaw39882 Aaw39801 Aaw39801 Aaw39801 Aaw39802 Aaw39802 Aaw39802 Aaw39862 Aaw39886
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                        - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
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0.7
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AAR12354
AAR12232
AAW39804
AAW39882
AAW39803
AAW39801
AAY70790
AAW39802
                                                                                                                                                                BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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1. geneseqp1980s:*

3. geneseqp2000s:*

4. geneseqp2001s:*

5. geneseqp2001s:*

6. geneseqp203s:*

7. geneseqp203as:*

8. geneseqp203bs:*
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seq length: 2000000000
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Database :

1264507860

Result Š.

Minimum DB Maximum DB

Searched:

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96 GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
121 ValTyrTyrCysGlnGlnLeuValGluTyrProPheThrPheGlySerGlyThrLysLeu 140
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric mouse-human antibodies -1 antigen from sample.
                                                                                                             AAR12354 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 1; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                89US-00433730
                                                                                                                                                                                                                                                                                                                                                                            89US-00433730
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631.00
96.21%
92.42%
80.38%
                                                                                                                                                                                 (first entry)
                                           (XOMA ) XOMA CORP. (GREC ) GREEN CROSS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                              Better MD, Horwitz AH,
                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ12056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 132 AA;
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                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                13-NOV-1989;
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                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                 15-AUG-1991
                                                                                                                                                                                                                                                                                           WO9107493-A.
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                             423
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                                                                                                                                                                                                                               This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see A173262 and AAV32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAV32264-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of antiritis, lupus erythematosus, Habineovo's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Slogren's syndrome, altergic asthma, acute asthmatic exacerbation, rhinitis, eczema, graftverbroticis asthma, acute asthmatics, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and Brcell mallignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIGCTTATGTICTGGATCTCTGGAGTCAGTGGGGGATATTGTGATAACCCAGGATGAACTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ICCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCTAGTAAGAGTCTC 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTGGGTCAGGCACAGATTTCACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTATAAGGATGGGAAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCT
                                                                                                                                                                 receptor specific antibodies useful for treating e.g. arthritis,
                                                                                                  Shearin J;
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Matches:
Conservative:
Mismatches:
                                                                                                  Rapson NT,
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                                                                                                Ellis JH,
                                                                                                                                                                                                           8; Fig 2; 81pp; English
                99WO-GB001434.
                                          98GB-00009839
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100.00%
100.00%
93.89%
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                                                                      (GLAX ) GLAXO GROUP LTD
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N-PSDB; AAZ34746.
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Best Local Similarity:
Query Match:
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                                                                                                  Bonnefoy JMP,
                07-MAY-1999;
                                          09-MAY-1998;
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This is the light (kappa) - chain variable (V) region of a mouse monoclonal antibody (MAD), 2E12, and is specific for an HIV-1 viral hantigen. It is used in the construction of a chimmeric MAD comprising heavy and light chains having murine V regions and human C regions. The chimmeric MADs are more effective than murine MAD 2E12 since they have an increased compactibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme reocgnition sites. The chimmeric MADs can be used as immuno- conjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also AAQ12057-63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - used to detect, kill and remove HIV
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Light (kappa) chain variable region of murine 2E12 immunoglobulin.
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Matches:
Conservative:
                                                                             Chimeric antibodies; immunoconjugates; HIV; AIDS
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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
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                                                                                                                                                                                                                                                                                                                                               Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                             1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrplleSerGlyValSerGly
                                                                                                                                        96 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC
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                                                      41 PheSerCysArgSerSerLysSerLeubeuTyrLysAspGlyLysThrTyrLeuSerTrp
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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in fa smaller doses than antibodies that antagonise cocaine by simply binding.

WPI; 1998-077166/07

Landry

N-PSDB; AAV09789

Disclosure, Fig 21, 147pp, English.

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275
prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2AlO antibody (AAMAS909) represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2AlO has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
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Mus sp

COLUMBIA NEW YORK

(UYCO ) UNIV

97WO-US010965.

25-JUN-1997;

overdose; addiction.

WO9749800-A1

ds snW

31-DEC-1997

(first entry)

16-JUN-1998

AAW39801;

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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
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                                                                                                                                                                                                                                                                                                                                              18; Page 73; 147pp; English
                                                                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                 97WO-US010965
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P-PSDB; AAV09802.
                                                                                   25-JUN-1997;
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                                                 31-DEC-1997.
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Sequence 113 AA;

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 2.25e-51 547.00 98.23% 92.04% 69.68% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: No.

US-09-674-716B-2 (1-437) x AAW39803 (1-113)

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276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335

AAW39801 standard; protein; 113 AA

RESULT 7 AAW39801 ID AAW3

215

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AW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAM39806 represents the heavy chain) was identified using TSAl, which is an immunogenic conjugate of an identified using TSAl, which is an immunogenic conjugate of 0.11. The antibodies reduce the concentration of occaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 TITCIGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GATATIGIGATAACCCAGGAIGAACICCICCAAICCIGICACTICIGGAGAAICAGITICC
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                                                                                               Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment, overdose, addiction.
                                                                       of catalytic antibody 3B9
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                                                                        Variable domain of the Kappa light chain
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                                                                      AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine, p53 protein, PAb-421; monoclonal antibody; mAb; IDI-1; anti-idiotypic antibody; DNA-binding domain; dermatological; immunosuppressive; anti-inflammatory; autoimmune response; SLB; systemic lupus erythematosus; diagnossis; treatment; autoantigen; light chain variable region; VL; complementarity determining region; CDR.
                            80
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SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle
                                                                                                81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro
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(7abel= CDR /note= "Complementarity determining region"
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                                                                                                                                              GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC
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                             Conservative:
Mismatches:
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AAW39801-05 represent the amino acid sequences of the variable domain of

Sequence 122 AA;

(UYCO ) UNIV COLUMBIA NEW YORK.

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TITCIGCAGAGACAATCICCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
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                                                                                                                                                                                                                                                                                                                                           GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
         prepared and used to immunise mice for production of hybridomas.

Catalytic antibodies were identified by their capacity to release 3H-
benzoic acid from 3H-phenyl occaine. The 6A12 antibody (AAW39807
represents the heavy chain) was identified using TSA1, which is an
immunogenic conjugate of a phosphate monoester transition state analogue.

Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the
concentration of cocaine in a subject, and are used particularly for the
treatment of an overdose. They are also used for treating addiction (by
reducing the in vivo concentration that can be achieved)
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catalytic antibodies which are able to degrade
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                                                                                                    New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                         The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzolc acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are use particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATATTGTGATAACCCCAGGATGAACTCTCCCAGTCCTGTCACTTCTGGAGAATCAGTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; huma monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICACGITCGGCTCGGGGACAAGITGGAAATAAACGT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                     Disclosure; Fig 19; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-674-716B-2 (1-437) x AAW39886
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530.00
96.46%
90.27%
67.52%
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                                                          WPI; 1998-077166/07.
N-PSDB; AAV09793.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                               Sequence 113 AA;
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This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human fragment of the light chain complementarity determining regions (see AAY32254 56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimarize or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II determining regions to render them capable of binding to the CD23 type II complexity and heavy chain complementarity. CC molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple arthritis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulleraitive collitis, crohn's disease, Sjogran's syndrome, allergies, allergies asthma, cutte asthmatic exacerbation, rhinitis, eczema, graft-collitis, crohn's disease, Sjogran's syndrome, allergies, allergies casthma, cutte asthmatic exacerbation, rhinitis, eczema, graft-constrins) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions constructs and various ligands and determining the binding agents
                urticaria; nephrotic syndrome; glomerulonephritis;
hillammacory bowel disease; ulcerative colitis; Crohn's disease;
Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis;
graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell receptor specific antibodies useful for treating e.g. arthritis,
   Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
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he= "framework r
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103. .113
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                                                                                                                        Homo sapiens.
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                                                                                                                                      Synthetic
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                                                                                   GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
                                                                                                                                                                                                                                                                                                                                                                                   81 SerArgValGluAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neurogordetcitve; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple solerosis; atherosenesis; atheroselerosis; asthema; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-mediated
                                                                                                                                                                                                                                        41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeulleTyrLeuMetSerThrArgAla
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                                                                                                        21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanized immunoglobulin for treating a CC-chemokine receptor 2-m disorder in a patient, comprises a binding specificity for CCR2, non-human antigen binding region and human immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse germline kappa light chain variable (VK) region, 167/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory glomerulopathy, vascular intervention;
neointimal hyperplasia, VK; kappa light chain variable region.
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Indels:
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                                               US-09-674-716B-2 (1-437) x AAY32262 (1-116)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE06969 standard; protein; 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Larosa GJ, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488888/53
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(CCR2),

516.00 92.98% 86.84%

Score: Percent Similarity: Best Local Similarity:

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comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting to treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2 mediated disorders such as inflammatory disorder, autoimmune of disorders such as inflammatory disorder, autoimmune disorders such as rheumatorid arthritis and multiple sclerosis.

CCR2-mediated disorders such as inflammatory disorder, autoimmune of atterosensis and atherosclerosis, and for inhibiting restences. They are useful in therapy or disappnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allegy, anaphylaxis, malignancy, chronic and acute confiammation, histamine and ISE-mediated allergic reaction, shock, stencesis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restences associated with vascular intervention, including angioplasty and/or stent placement in a mammal, and inhibiting neolitimal hyperplasia of a vessel in a mammal, and inhibiting neolitimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa in the chain variable (VK) region, 167/24
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### Sequence 100 AA;

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Matches:
Conservative:
Mismatches:
Indels: Gaps: .36e-47 509.00 100.008 99.008 64.84% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

## US-09-674-716B-2 (1-437) x AAE06969 (1-100)

335 395 215 TITCIGCAGAGACCAGGACAAICTCCTCAGCTCCTGAIGIAITITGAIGICCACCCGIGCA 275 40 9 80 20 AspileValileThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 276 81 96 156 216 61 336 ò g ò Db ò g ò g  $\delta$ g

ADE28461 standard; protein; 239 AA

#### ADE28461;

(first entry) 29-JAN-2004

Human anti-CD40 antibody 23-28-1 variable region light chain protein.

anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; variable region light chain; 23-28-1. RESULT 13
ADE28461
ID ADE28
XX
AC ADE28
DT 29-JA
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XW
AntiXW

### Homo sapiens

WO2003040170-A2

15-MAY-2003

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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CBO. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder souch as cancer, viral and bacerial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region light chain protein of the invention.
                                                                                                                                                                                                           New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feng X;
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Mismatches:
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Matches:
                                                                                                                               Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                              claim 1; SEQ ID NO 68; 177pp; English.
                                                                                                                               Corvalan J,
            08-NOV-2002; 2002WO-US036107.
                                               09-NOV-2001; 2001US-0348980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508.00
84.33%
71.64%
64.71%
                                                                             (PFIZ ) PFIZER PROD INC (ABGE-) ABGENIX INC.
                                                                                                                               Bedian V, Gladue RP,
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N-PSDB; ADE28460.
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# US-09-674-716B-2 (1-437) x ADE28461 (1-239)

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Ob	н	
λΌ	96	96 GATATTGTGATAACCCGAGGATGAACCTCTCCGTCACTTCTGGAGAATCAGTTTCC 155
Db	21	AspilevalMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
٥٨	156	ATCTCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215
Ob	41	IleSerCysArgSerSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60
δλ	216	TTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCACCCGTGCA 275
ΩÞ	61	TyrLeuGlnLysProGlyGlnSerProGlnLeuLeulleTyrLeuGlySerAsnArgAla 80
λŏ	276	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335
, <b>q</b> 0	81	SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100
λ̈́o	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTACTGTCAACAACTTGTAGAGTATCCA 395
Dp	101	SerargvalGlualaGluaspValGlyvalTyrTyrCysMetGlnValLeuGlnThrPro 120
δλ	396	TTCACGTTCGGCTCGGGACAAGTTGGAAATAAAACGTACG 437
Dp	121	PhethrpheGlyProGlyThrLysValAspileLysArgthr 134

RESULT

215

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TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335
                                                                        GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
                                                                                                                                                                                                                                                                                                                                                                                                     Human, parathyroid hormone related protein, PTHrp, monoclonal antibody, hypercalcaemia, rheumatoid arthritis, bone cancer, metastasis, pain, fracture, cachexia, tooth disease, periodontal disease, gingiva, sepsis, systemic inflammatory response syndrome; SIRS; hypophosphataemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human monoclonal antibody to parathyroid hormone related protein. - seful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
ATGAGGTTCTCTGTTCAGTTTCTGGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG
                      |||||||
|MetArg******AladinLeuLeuGlyLeuLeuMetPheTrpValSerGlySerSerGly
                                                                                                                                                                        41 IleSerCysArgSerSerGlnSerLeuLeuHisserAsnGlyAsnAsnTyrLeuAspTrp
                                                                                                                                                                                                                                                SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle
                                                                                                          21 AspileValMetThrGln***ProLeuSerLeuProValThrProGlyGluProAlaSer
                                                                                                                                                                                                                          216 ITTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA
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                                                                                                                                                        Humar, parathyroid hormone related protein, PTHrP, monoclonal antibody, hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis, pain; fracture; cachexia; tooth disease; periodontal disease, gingiva; sepsis; systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A human monoclonal antibody to parathyroid hormone related protein. - useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
                                                                                                                        Humar PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.
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          AAY82617 standard; protein; 239 AA
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N-PSDB; AAA13927.
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The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or its fragments, following the stimulation of PTHrP has the following

Claim 31; Page 45-46; 88pp; Japanese.

Gaps:

US-09-674-716B-2 (1-437) x AAY82617 (1-239)

Query Match:

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81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeubysIle 100
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                                                                                                                                                                                                                                                                                                                                                                   properties: (a) inhibits intracellular elevation of CAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastrasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphateaemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PTHYP monoclonal antibody clone protein sequence from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08672345C
Petent No. 5948658
CENERAL INFORTION:
CENERAL INFORTION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSES:
ADDRESSESSE:
COOPER and Dunham LLP
STREET: 1185 Avenue of the Americas
US-09-214-095D-119

US-08-672-345C-6

US-08-672-345C-6

US-09-214-095D-6

US-09-214-095D-104

US-08-438-129-104

US-08-438-129-10

US-08-438-129-10

US-08-479-614-2

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US-08-58-191-2

US-08-589-939-7

US-08-589-939-7

US-08-589-939-7

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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
IENGTH: 113 amino acids
TYPE: amino acid
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-MODEL=frame+ n2p.model -DEV=xlp
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-D=Issued Patents AA -QFWT=fastan -SUFFTX=ri -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCAHIGN=200 -THE SCORE=per -THE MAX=100 -THE MINE -ALIGN=15
-MODEL=LOCAL -OUTFMT=pto -NOFM=ext -HEAPS/IZE=500 -MINLEN=0 -NAXLEN=200000000
-USER=US09674716 @CGN 1 1 107 @runat 30092004 070259 25901 -NCPU=6 -ICPU=3
-NO MMAP -LARREQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THERADS 1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 98, Appli
Sequence 108, App
Sequence 5, Appli
Sequence 7, Appli
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Sequence 97, Appl
Sequence 5, Appli
Sequence 7, Appli
Sequence 100, App
                                                                                                                                     September 30, 2004, 08:41:28; Search time 10.688 Seconds (without alignments) 4221.672 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.

    protein search, using frame_plus_n2p model

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336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
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APPLICANT: Landry, Donald
ITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
ITILE DE PREPERBOY
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 113
TYPE: PRT
TYPE: PRT
ORGANISM: Murinae gen. sp.
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 8, Application US/09214095D
; Patent No. 6280987
                                                                                                                                           1.49e-59
555.00
97.35%
94.69%
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555.00
97.35%
94.69%
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                                                                           US-08-672-345C-98
                                                                                                                            Alignment Scores:
Pred. No.:
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Pred. No.:
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DB:
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| Sequence 98 Application US/08672345C
| Patent No. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. |
| TITLE OF INFORMATION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS: 108
| CORRESPONDENCE ADDRESS: 108
| CORRESPONDENCE ADDRESS: 108
| CONFIRM NOW YORK ATTENTY: New York COUNTRY: USA ZIF: New York COUNTRY: USA ZIF: New York COWPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATION DATA: COMPUTER: IBM PC COMPATIBLE OPERATION DATA: APPLICATION NUMBER: US/08/672,345C FILING DATE: 24-JUN-1996 CURRENT APPLICATION NUMBER: US/08/672,345C FILING DATE: 24-JUN-1996 CURRENT APPLICATION NUMBER: US/08/672,345C FILING DATE: 24-JUN-1996 CURRENT APPLICATION NUMBER: US/08/672,345C FILING DATE: 22-JUN-1996 CURRENT STEATHONE INFORMATION: REFERENCE/DOCKET NUMBER: 0575/51400 TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERIFICE: SECUENCE CHARA
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Matches:
Conservative:
Mismatches:
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                         , MOLECULE TYPE: protein US-08-672-345C-8
                                                                                                                                                      Percent Similarity:
Best Local Similarity: 9
Query Match:
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RESULT 6
US-08-672-345C-7
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IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40
                                                                                                          41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgAla
                                                                                     276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC
                                                                                                                                               336 AGTAGAGGTGAAGGCTGAGGATGTGGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA
                             216 TITCTGCAGAGACCAGGACAAICTCCTCAGCTCCTGATGTATTTGATGTCCACCGTGCA
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US-09-214-095D-108
US-09-214-095D-108
Sequence 108, Application US/09214095D
Sequence 108, Application US/09214095D
Sequence 108, Application US/09214095D
SEQUENCE INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FILING DATE: 1999-07-19
CURRENT FILING DATE: 1999-07-19
SOFTWARE: Patentin version 3.0
SECTION 108
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-08-672-345C-5
; Sequence 5, Application US/08672345C
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Best Local Similarity:
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ORGANISM: Murine
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MEDIUM TYPE: Floppy disk
COMPUTER: Elb PC compatible
COMPUTER: Elb PC compatible
COMPUTER: Elb PC compatible
COMPUTER: DEAD OF MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-9400
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                                                          ANTI-COCAINE CATALYTIC ANTIBODY
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Mismatches:
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Matches:
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                                                                                                         ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 5:
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98.23%
92.04%
69.68%
                                          Landry Donald,
                                                                                 108
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald
TITLE OF INVENTION: ANTI
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
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US-08-672-345C-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 TITCIGCAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
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Sequence 7, Application US/08672345C
Patent No. 5948650

Patent No. 5948650s

APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READALIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
APPLICATION UNMERR: US/08/672,345C
FILING DATE: 24-UUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-674-716B-2 (1-437) x US-08-672-345C-7 (1-113)
                                                                                                                              ADDRESSE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WALE. JOHN P. P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-39-0400
TELEPHONE: 212-39-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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98.23%
92.04%
69.68%
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STRANDEDNESS: si
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                      GENERAL INFORMATION:

APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-CCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper and Dunham Lip
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 1036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBMP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT INFORMATION
OPERATING SYSTEM: 1996
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: 0575/51400
TELEPRANE: JOAN P. REGISTRATION NUMBER: 0575/51400
TELEPRANE: 212-278-0400
TELEPRANE: 212-278-0400
TELEPRANE: 212-278-0400
TELEPRANE: 212-391-0525
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHRACTERISTICS:
LENGTH: Amino acids
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1017
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Conservative:
Mismatches:
Indels:
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Sequence 95, Application US/08672345C Patent No. 5948658 GENERAL INFORMATION:
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547.00
98.23%
92.04%
69.68%
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
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Best Local Similarity:
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1.43e-58
547.00
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US-09-214-095D-7
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Murinae gen. Sp.
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
LENGTH: 113
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DB:
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Sequence 97, Application US/08672345C

Patent No. 5948658
GENERAL INFORMATION:
APPLICANT:
INFORMATION:
APPLICANT:
APPLICANT:
INFORMATION:
ANTI-COCAINE CATALYTIC ANTIBODY
ITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES:
ADDRESSE:
COCATAL New York
STARET: New York
COUNTRY: New York
STATE: New York
COUNTRY: USA
ITER: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TEADABLE FORM:
COMPUTER TEADABLE
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: I LOPPY disk
MEDIUM TYPE: I LOPPY disk
COMPUTER: I BM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONEY AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-279-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: AMINO ACIDS.
TOPOLOGY: linear:
TOPOLOGY: linear:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 TICACGITCGGCTCGGGGACAAGTTGGAAATAAAACGT 434
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Matches:
Conservative:
Mismatches:
Indels:
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547.00
98.23%
92.04%
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Best Local Similarity:
Query Match:
DB:
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276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 TITCIGCAGAGACCAGGACAAICTCCTCAGCTCCTGATGTATTTGATGTCCCACCCGTGCA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 AGTAGAGTGAAGGCTGAGGATGTGGGGTGTATTACTGTCAACAACATGTAGAGTATCCA 395
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Factor No. 6280987
GENERAL INFORMATION:
FAPLICANTI LANGIV, Donald
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
LENGTH: 113
US-09-12,
US-09-13,
US-09-
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Mismatches:
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Matches:
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Db 61 S 00	Db 101 P  RESULT 12 US-09-214-095D- ; Sequence 112, ; Patent No. 62 ; GENERAL INFOR ; APPLICANT: ; TITLE OF INV	CURRENT APPL CURRENT APPL CURRENT FILI CURRENT FILI NUMBER OF SER SOFTWARE: SOFTWARE: LENGTH: 113 LENGTH: 113 TYPE: PRT ORGANISM: M	Alignment Score Pred. No.:	Percent Similar Best Local Simi Query Match: DB:	US-09-674-716B-	Db 1 Av 156 Av			Oy 276 Tr	81	2y 396 TT	RESULT 13 US-09-214-095D-1 ; Sequence 119, ; Patent No. 628	; APPLICANT: 1 ; TITLE OF INVI	CURRENT APPLI CURRENT FILIN
### S47.00 Matches: 104  ###################################	96 GAIATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCATTCTGGAGAATCATTTCC  1 ASPMETVAIMETTACINININININININININININININININININININ	Db   41 PheLeuGlnArgProGlyArgSerProGlnLeuLeulleTyrLeuMetSerThrArgAla 60     Qy   276 TCAGGAGTCTCAGGACTTTAGTGGAGTGGGTCAGCACAGATTTCACCCTGGAAATC 335	Qy 396 TTCACGTTCGGCTCGGCGACAAAGTTGGAAATAAAACGT 434 	RESULT 11 US-09-214-095D-100 ; Sequence 100, Application US/09214095D ; Patent No. 6280987.	; APPLICANT: Landry, Donald; ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY; FILE REFERENCE: 51400-A-PCT-US	; CURKENT FILICATION NUMBER: US/09/214,095D ; CURRENT FILING DATE: 199-07-19 ; NUMBER OF SEQ ID NOS: 121 ; SOFTWARE: PatentIn version 3.0	; SEQ ID NO 100 ; LENGTH: 113 ; TYPE: PR: ; ORGANISM: Murine	US-09-214-095D-100	ores: larity: imilarity:	Gaps: 9-214-095D-100 (1-113)	Oy 96 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155	Oy 156 AICTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215	Qy 216 TITCIGCAGAGACCAGGACAAICTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275	, Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGGGCTCAGGCACAGATTTCACCCTGGAAATC 335

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395
                                                                 ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215
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SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 80
                                                 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA
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112, Application US/09214095D

12, 6280987

12, 6280987

T: Landry, Donald

T: Landry, Donald

ANTI-COCAINE CATALYTIC ANTIBODY

APPLICATION NUMBER: US/09/214,095D

APPLICATION NUMBER: US/09/214,095D

FILING DATE: 1999-07-19

F. SEQ. ID NOS: 121

12, Patentin version 3.0
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129, Application US/09214095D
6280957
628087
120 Landry, Donald
110/ENYTION: ANTI-COCAINE CATALYTIC ANTIBODY
12BACE: 51400-A-PCT-US
12BICATION UNMER: US/09/214,095D
12LING DATE: 1999-07-19
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Conservative:
Mismatches:
Indels:
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69.68%
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; NUMBER OF SEQ ID NOS: 121 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 119 ; LENGTH: 280 ; TYPE: PRT ; ORGANISM: Murine US-09-214-095D-119	Alignment Scores:  Pred. No.: Score: Score: Score: Sect. Similarity: Best Local Similarity:	US-09-674-716B-2 (1-437) x US-09-214-095D-119 (1-280)  QY	Db   152 GlyGluSerValSerTleSerCysArgSerSerArgSerLeuleuTyrArgAspGlyLys 171	321 TTCACCTGGAAATCAGTAGAGTGAGGCTGAGGATGTGGTGTGTTATTACTGTCAACAA 321 TTCACCTGGAAATCAGTAGAGTGAGGCTGAGGATGTGGTGTGTTATTACTGTCAACAA 212 PheThileoldulleSerArgValLysAladluAspValGyValTyrTyrCysG1nHis 381 CTTGTAGAGTATCCATTCACGTTGGGCTGGGGACAAAGTTGGAAATAAAAGGT 434 [  ::	RESULT 14  US-08-672-345C-6  is Sequence 6, Application US/08672345C  sequence 6, Application US/08672345C  sequence 1 no. 5948658  GENERAL INFORMATION:  APPLICANT: Landry Donald, W.  TITLE OF INVENTION: ANTI-CCCAINE CATALYTIC ANTIBODY  NUMBER OF SEQUENCES: ADDRESSEE: Cooper and Dunham LLP  STREET: 1.185 Avenue of the Americas  CITY: New York  COMPUTRY: USA  ZIP: New York  COMPUTRY: LBM PC compatible  COMPUTRY: ASA  SPETION NUMBER: US/08/672,345C  CLASSIFICATION: 435  ATTORNEY/AGRIT INPORMATION:  REGISTRATION NUMBER: 28,678  TELLECOMMUNICATION INPORMATION:

us-09-674-716b-2.rai

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276 TCAGGAGICTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCACCCTGGAAATC 335
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
US-08-672-345C-96
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541.00
97.35%
91.15%
68.92%
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Score:
Score:
Score:
Special Similarity:
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Query Match:
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Sequence 108, Applia Sequence 5, Applia Sequence 110, Applia Sequence 112, Applia Sequence 119, Applia Sequence 32, Applia Seq
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47, Appl
32, Appl
56, Appli
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APPLICANN: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 05755/51400-B
CURRENT PILING DATE: 108/09/04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-112-8
PRIOR FILING DATE: 1997-06-25
PRIOR FILING DATE: 1997-06-25
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFFWARE: PATENTIN VERSION 3.1
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09940727B; Publication No. US20030077793A1; GENERAL INFORMATION:
      ; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8
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US-09-940-727B-8
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LENGTH: 113
        Command line parameters:

-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-Q=/Cgn2 1/USFPC spool p/USC9674716/runat 30092004 070302 26027/app_query.fasta_1.3164
-D=Published Applications AA -QFMT=fasta_ -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -GTART=1 -END=-1 -MATKIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPRMT=pc -NORM=ext -HEAPSIZE=S00 -MINLEN=0
-MAXIEN=2000000000 -USER=US09674716 @CGN 1 1 496 @runat 30092004 070302_26027
-NCPU-6 -ICON-100 - WARN -LIMEOUT=3 -NO MAYP -LARSEQUERY /NGG $\overline{SCORE} = 0 - MAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=3 - THREADS=1 -XGAPDP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                         September 30, 2004, 08:54:09; Search time 57.3185 Seconds (without alignments) 4906.833 Million cell updates/sec
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| cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptcdata/1/pubpaa/US06_NEW PUB.pep:*
| cgn2_6/ptcdata/1/pubpaa/US06_NEW PUB.pep:*
| cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptcdata/1/pubpaa/US08_NEW PUB.pep:*
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| cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Perfect score:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-940-727B-5
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Pred. No.:
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US-09-940-727B-108

Sequence 108, Application US/09940727B

Publication No. US20030077793A1

GENERAL INFORMATION:

APPLICANT: Landry, Donald W

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1999-106-25

PRIOR FILING DATE: 1997-06-25

NUMBER OF SEQ ID NOS: 121

SEQ ID NO 108

LENGTH: 113
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Best Local Similarity:
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CRGANISM: mouse
US-09-940-727B-108
Alignment Scores:
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.56 ATCTCCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215

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AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTTACTGTCAACAACTTGTAGAGTATCCA 395
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21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40
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Sequence 5, Application US/09940727B

Publication No. US20030077793A1

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400

CURRENT APPLICATION NUMBER: US/09/940,727B

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1997-16-25

PRIOR FILING DATE: 1996-06-25

NUMBER: OF SEQ ID NOS: 121

SEQ ID NO 5

LENGTH: 113

TANDE: DEATH OF THE NOWER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434
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Percent Similarity:
Best Local Similarity: 5
Query Match:
DB:
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LENGTH: 113
TYPE: PRT
ORGANISM: mouse
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US-09-940-727B-112
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; ORGANISM: mouse
US-09-940-727B-112
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0.57/51400-B;
CURRENT APPLICATION NUMBER: 09/214,095
CURRENT FILING DATE: 2002-09-04
CURRENT FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 7
434
                   101 PheThrPheGlySerGlyThrLysLeuGlulleLysArg 113
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Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
ITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILER REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
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Matches:
Conservative:
Mismatches:
Indels:
TTCACGTTCGGCGCCCAAAGTTGGAAATAAAACGT
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                                                                                     ; Sequence 7, Application US/09940727B; Publication No. US20030077793A1; GENERAL INFORMATION:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7
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US-09-940-727B-100
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US-09-940-727B-7
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APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE REPERENCE: 057551400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1996-12-28
PRIOR FILING DATE: 1997-06-25
PRIOR FILING DATE: 1997-06-25
NUMBER: OF SEQ ID NOS: 121
SEQ ID NO 112
SEQ ID NO 112
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Matches:
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PRECENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 112, Application US/09940727B; Publication No. US20030077793A1; GENERAL INFORMATION:
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Qy         201 ACATACTTGAATTGGTTTCTGGAGGACCAGGACAATCTCCTGAGCTCCTGATGTATTTG 260           Db         172 ThrTytLeuAsnTrpPheLeuGlnArgProGlyArgProProGlnLeuLeuIsTyrLeu 191           Qy         261 ATGTCGACCGTGCATCAGACGGTTTAGTGGCAGTGGGTCAGGACAGAT 320           Db         192 MetSerThrArgSerSerGlyValSerSapArgPheSerGlySerGlyPhrAsp 211           Qy         321 TTCACCCTGGAAATCAGAAGGTGAGGATGTGGGTGTGTATACTGTCAACAA 380           Db         212 PheThrLeuGluIleSerArgValLySalaGluAspValGlyValTyrTyrCysGlnHis 231           Qy         381 CTTGTAGAGTTCATTCACGTTCAGGGTCGGGACAAAATTATAAAACGT 434           Qy         381 CTTGTAGAGTTCATTCACGTTCAGGGTCGGGACAAAATTATAAAACGT 434           Db         222 PheThrLeuGluIleSerArgValLySalaGluAspValGAAATAAAAACGT 434           Db         222 DheThrLeuGluIleSerArgValLySalaGluAspValGAAATAAAAACGT 434	SULT 8 -02-940-727B-6 -02-940-727B-6 -03-940-727B-6 -03-940-727B-6 -03-940-727B-6 -03-940-727B-6 -03-940-727B-6 -03-940-737B-6 -03-940-737B-6 -03-940-737B-7793A03-03-03-03-03-03-03-03-03-03-03-03-03-	PRIOR APPLICATION NUMBER: 08/672,345	96	Qy         156 ATCTCTGCAGGTCTGTATAAGGATGGGAAGACATACTTGAATTGG         215
Score:   S47.00   Matches:   104   Percent Similarity:   98.23	Oy 216 TTTCTGCAGACACCACCCCCCCCCCCCCCCCCCCCCCCC	RESULT 7 US-09-940-727B-119 Sequence 119, Application US/09940727B Fublication No. US20030077793A1 GENERAL INFORMATION: APPLICANT: Landry, Donald W TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY FILE REFERENCE: 0575/51400-B CURRENT APPLICATION NUMBER: US/09/940,727B CURRENT FILING DATE: 2002-09-04 PRIOR FILING DATE: 1998-12-28 PRIOR FILING DATE: 1997-06-25 PRIOR FILING DATE: 1997-06-25 PRIOR FILING DATE: 1997-06-25 PRIOR FILING DATE: 1997-06-25 NUMBER OF SEQ ID NOS: 121 SOFTWARE: PATENTIN NUMBER: 08/672,345 NUMBER OF SEQ ID NOS: 121	; SEQ ID NO 119 ; LENGTH: 280 ; TYPE: PRT ; ORGANISM: mouse US-09-940-7278-119.	Alignment Scores:  4.88e-48  Pred. No.:  547.00  Matches:  105  Score:  547.00  Matches:  105  Score:  106  Best Local Similarity:  69.68  Mismatches:  108  Matches:  109  Conservative:  8  Mismatches:  100  Best Local Similarity:  100  Matches:  100  Gaps:  100  Matches:  100  Gaps:  100  Matches:  100  Gaps:  100  Matches:  100  Gaps:  100  Gaps:  100

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GGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
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Indels:
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PCT/US97/10965
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US-09-840-459-32
Sequence 32, Application US/09840459
Sequence 32, Application US/09840459
Patent No. US20020150576A1
Patent No. US20020150576A1
APPLICANT: Large Area Caregory J.
APPLICANT: Newman, Walter
APPLICANT: O'Berien, Siobhan H.
APPLICANT: O'Berien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
                                           Sequence 104, Application US/09940727B
; Sequence 104, Application US/09940727B
; Publication No. US20030077793A1
; Publication No. US20030077793A1
; REDERRAL INFORMATION: Danald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/5140: 050/614, 095
; CURRENT APPLICATION NUMBER: 05/09/214, 095
; PRIOR FILING DATE: 1998-12-28
; PRIOR FILING DATE: 1998-12-28
; PRIOR FILING DATE: 1998-16-25
; PRIOR FILING DATE: 1998-6-65
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: mouse
US-09-940-727B-104
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Pred. No.:
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APPLICANT: LADOSA, Gregory J.
APPLICANT: LADOSA, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Ones, S. Tarran
APPLICANT: Ones, S. Tarran
APPLICANT: O'Refe, Theresa
APPLICANT: NUMBER: US/10/766,773
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
NUMBER: O'REG ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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Matches:
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION WURBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
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509.00
100.00%
99.00%
64.84%
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Best Local Similarity:
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US-10-766-773-32
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LENGTH: 100
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81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrFro 100
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US-10-733-563-32

i Sequence 32, Application US/10733563

publication No. US20040151721A1

GENERAL INFORMATION:
I APPLICANT: O'Keefe, Theresa

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

CURRENT FILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: US 60/392,364

PRIOR PILING DATE: 2002-10-17

PRIOR APPLICATION NUMBER: US 60/392,364

PRIOR APPLICATION NUMBER: US 60/392,364

PRIOR APPLICATION NUMBER: US 60/350,166

PRIOR APPLICATION NUMBER: US 60/350,166

PRIOR PILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 122

SOFTWARE: FeatSEQ for Windows Version 4.0

TYPE: PRI

CENTRAL 100

TYPE: PRI

CORGANISM: Mus musculus

US-10-733-563-32
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; SEQ ID NO 32

: LENGTE: 100

: TYPE: PRT

: ORGANISM: Mus musculus

US-10-766-773-32
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-766-610-32
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                                      TTCACGTTCGGCTCGGGGACAAGTTGGAAATAAAACGTACG 437
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                                                                                                                        Sequence 40, Application US/10292088;
Publication No. US2030211100A1;
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GGADUE, RONALD P.
APPLICANT: CALDUE, RONALD P.
APPLICANT: GALOUE, ROALLAN, JOSE
APPLICANT: GTADUE, RONALD P.
APPLICANT: GALOUE, ROALLAN, JOSE
APPLICANT: FENGL XIAO-CHI
APPLICANT: FENGL XIAO-CHI
APPLICANT: FENGL XIAO-CHI
APPLICANT: FENGL XIAO-CHI
CURRENT FILING DATE: 2003-03-14
CURRENT FILING DATE: 2003-03-14
FRIOR FILING DATE: 2001-11-09
NUMBER: PATCHING DATE: 2001-11-09
NUMBER: PATCHING DATE: 2001-11-09
SEQ ID NO 40
LENGTH: 239
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-292-088-40
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                                                                                                                                                                                                                                                                                                                                                                                   96 GATATIGIGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                216 TITCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 TTCACGTTCGGCTCGGGGACAAGTTGGAAATAAACGTACG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ArgThrPheGlyGlnGlyThrLysLeuGluMetLysArgThr 134
                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                   US-09-674-716B-2 (1-437) x US-10-404-724-41 (1-239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: September 30, 2004, 09:48:30 e: 59.3185 secs
                                                                                                                                                    Indels:
                                                                                                 506.00
83.58%
73.88%
64.46%
TYPE: PRT
) ORGANISM: Homo sapiens
US-10-404-724-41
                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                       Alignment Scores:
                                                                                   . No. :
```

Haup sheet

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 30, 2004, 05:55:56; Search time 17.3559 Seconds (without alignments) 88.677 Million cell updates/sec Run on:

US-09-674-716B-3 81 1 RSSKSLLYKDGKTYLN 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Length	112	120	120	120	112	133	83	111	120	120	133	114	101	113	122	112	133	249	87	91	101	103	103	112	113	132	133	140
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Score	81	81	81	81	99	65	64	64	64	64	64	63	61	61	61	60	60	9	n O	50	5 0	59	29	5 O	S O	50	S)	59
Result No.	1 11 8	m	4	w	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

100.0%; Score 81; DB 1; Length 113;

Query Match

	light pteolyt	Ig kappa chain V r Ig kappa chain - h	kappa chain	Ig kappa chain V r Ig kappa chain V r	kappa	kappa chain			Ig kappa chain V r
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142 2 120 2	110 2			9 9 9					
9 72.8 8 71.6		57 70.4							
		34 35			39		7	4	45 5

## ALIGNMENTS

RESULT 1 K7M316
Ig kappa chain V region (M167) - mouse C:Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
R. Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978 A;Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prote
A;Reference number: A01908; MUID:79000273; PMID:99160 A:Accession: A01908
A, Molecule type: protein
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
hain disulfide bonds. In some cases, such as IgA and IgM. the subunits associate into lar
C. Control of the con
F;23-93/Disulfide bonds: #status predicted
Query Match Best Local Similarity 100.0%; Score 81; DB 1; Length 112; Best Local Similarity 100.0%; Pred. No. 3.1e-06; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RSSKSLLYKDGKTYLN 16
 Db 24 RSSKSLLYKDGKTYLN 39
RESULT
 C,Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
 R, Appella, E.
Mol. Immunol. 17, 711-718, 1980 A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylchol
A01910; MUID: 81052016; PMID: 6776396
 A; Accession: AUI910 A; Molecule type: protein
A) Residues: 1-113 AAPP. C. Comment. This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappanain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into landary in in
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: neterotetramer F;16-95/Domain: immunoglobulin homology <imm></imm>
F;23-93/Disulfide bonds: #status predicted

RESULT 3 KVMS67

16; Conservative

Best Local Similarity

Matches

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Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0273
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
A;Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n A;Reference number: PL0231; MJID:90111618; PMID:2104919
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                                                                                                                                                                                                                               C. Accession: B29775
R. Jouvin-Marche, E.; Rudikoff, S.
Immunoganetics 24, 191-201, 1986
A. Title: Evolution of a V-kapa gene family.
A. Reference number: A91751; MUD:87006895; PMID:3093373
A, Recession: B29775
A, Molecule type: DNA
A, Residues: 1-120 < Joun
A, Residues: 1-120 < Joun
A, Residues: 171
A, Note: this sequence was determined from the germline gene
C, Genetics:
A, Introns: 17/1
C, Superiamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F;11-120/Product: Ig kappa chain V region 24,1 #status predicted <MAI>F;36-115/Domain: immunoglobulin homology < LNM>
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C;Species: Homo sapiens (man)
C;Accession: S40324 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40324
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
                                                                                                                                                                 C;Species: Mus pahari
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
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F;16-25/Domain: immunoglobulin homology <IMM>
F;16-59/Domain: immunoglobulin homology <IMM>
F;16-59/Region: immunoglobulin homology <IMM>
F;16-54/Region: complementarity-determining 1
F;55-61/Region: complementarity-determining 2
F;55-29/Region: complementarity-determining 3
F;94-102/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.5%; Score 66; DB 2; Length 112; Best Local Similarity 75.0%; Pred. No. 0.00097; Matches 12; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 81; DB 2; Length 12 Best Local Similarity 100.0%; Pred. No. 3.3e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                        Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 RSSKSLLYKDGKTYLN 59
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A; Residues: 1-112 <SHL>
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
Hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asylva

C.Species: Mus pahari

R.Jouvin-Marche, E.; Rudikoff, S.

R.Jouvin-Marche, E.; Rudikoff, S.

R.Jouvin-Marche, E.; Rudikoff, S.

R.Jouvin-Marche, E.; Rudikoff, S.

A.Reference number: A91751; MUD:87006895; PMID:3093373

A.Reference number: A91751; MUD:87006895; PMID:3093373

A.Reference number: A91751; MUD:87006895; PMID:3093373

A.Residues: 1-120 <-300A

A.Residues: 1-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /-120 /
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Cell 25, 47-58, 1981
A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A;Reference number: A01909; MUID:82002223; PMID:6791832
A;Accession: A01909
                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor V region (VK167) - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000 C;Accession: A01909
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fil-20/Domain: signal sequence #status predicted <SIG>
Fil-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
Fi36-115/Domain: immunoglobulin homology <IMM>
Fi36-113/Disulfide bonds: #status predicted
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                                            0; Indels
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A;Residues: 1-120 <SEL>
A;Note: the sequence was determined from the germline gene
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 81; DB 1; I 100.0%; Pred. No. 3.3e-06; Live 0; Mismatches 0;
100.0%; Pred. No. 3.1e-06; tive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.0

16; Conservative

Local Similarity

Best Loca Matches

24 KSSQSLLHSDGKTYLN 39

셤

Best Loc Matches

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"Je kappa chain V region (A17) - human

"G'species: Homo sapiens (man)

G'species: Homo sapiens (man)

G'species: Homo sapiens (man)

G'species: Anone sapiens (man)

G'species: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000

G'species: Accession: $42268

A'Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regic

A'Reference number: A49043; MUID:92201291; PMID:1551402

A'Accession: $42268

A'Status: preliminary

A'Accession: S42268

A'Status: preliminary

A'Accession: S42268

A'Status: preliminary
                                                                                                                                                                                                                                     C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
C.Species: Obs. 1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Species: Obs. 1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Species: Obs. 1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Species: Obs. 1023-1029, 1992
A.Stautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zoc A; Rittle: The human immunoglobulin kappa locus. Characterization of the duplicated A regic A; Reference number: A49043; MUID:92201291; PMID:1551402
A; Recession: S42267
A; Residues: preliminary
A; Robicoule type: DNA
A; Residues: 1-120 clad>
A; Residues: 1-120 clad>
A; Residues: 1-120 clad>
A; Residues: EMBL:X63402
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K2HURP
K2HURP
K2HURP
K2HURP
K2HURP
K2HURP
K2HURP
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 30-dun-1987 #text_change 15-Aug-1997
C;Accession: A01890
R;Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nicleic Acids Res. 13, 6499-6513, 1985
A;Title: Human immunoglobulin kappa 1ight chain genes of subgroups II and III.
A;Reference number: A93588; MUID:86041852; PMID:2997711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>
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19.0%; Score 64; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 17/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 120; Match 79.0%; Score 64; DB 2; Length 120; Local Similarity 75.0%; Pred. No. 0.0022; les 12; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                           Ig kappa chain V region (A1) - human
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A;Cross-references: EMBL:X63403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 12;
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S20709
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20709
R;Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osh submitted to the EMBL Data Library, April 1992
A;Reference number: S20706
A;Reference number: S20706
A;Accession: S20709
A;Molecule type: DNA
A;Residues: 1-111 < RRE>
A;Accession: S20709
A;Molecule type: DNA
A;Residues: 1-111 < RRE>
A;Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656
C;Guperfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
S34055
Ig Akapta chain V region - human
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34095
R;Wagner. G.D; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34095
A;Accession: S34095
A;Accession: S34095
A;Accession: S44095
A;Residues: 1-83 *WAG>
A;Residues: 1-83 *WAG>
A;Residues: 1-83 *WAG>
A;Cross-references: EMBL:X67179
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;1-80/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: $40312; MUID:94080891; PMID:8258341
A; Accession: $40324
A; Status: preliminary; translation not shown
A; Status: preliminary; translation not shown
A; Residues: 1-133 «KLE»
A; Cross-references: EMBL:X72434
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
P; 33-112/Domain: immunoglobulin homology <IMM>
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79.0%; Score 64; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 0.0021;
Matches 12; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                      80.2%; Score 65; DB 2; Length 133 clarity 75.0%; Pred. No. 0.0017; Conservative 2; Mismatches 2; Indels
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Best Local Similarity 75.v.
Best Local 21 Conservative
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nes 12; Conserv
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A;Molecule type: DNA A;Residues: 1-133 «KLO» A;Note: the sequence was determined from the differentiated gene C;Genetics:

A;Gene: GDB:IGKV2 A;Cross-references: GDB:136265

A; Map position: 2p12-2p12

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A/Generic GDB:1GKV2
A/Conserreferences: GDB:136265
A/Cross-references: GDB:136265
A/Cross-references: GDB:136265
A/Cross-references: GDB:136265
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into landing disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into landic Sysperfamally: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:16-95/Domain: immunoglobulin pomology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: A01886

R;Riesen, W.F.; Jaton, J.C.

Biochemistry 15, 3829-3833, 1976

A;Title: Variable region sequence of the light chain from a Waldenstroem's IgM with speci A;Reference number: A01886; WUID:76253627; PMID:821524

A;Accession: A01886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 1-113 <RIE>
C,Comment: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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C,Date: 24-Apr-1964 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                               Gaps
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0
A; Experimental source: B cell, strain [NZB x NZW]F1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMA>
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                                                                                                                                                                                                 Length 101;
                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kappa chain V-II region (Fr) - human (tentative sequence)
                                                                                                                                                                                         Query Match 75.3%; Score 61; DB 2; Best Local Similarity 80.0%; Pred. No. 0.0059; Matches 12; Conservative 2; Mismatches 1
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Job time : 18.3559 secs
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Accession: 849572
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
S;Danitted to the EMBL Data Library, November 1994
A;Description: K+1+ dual receptor B cells are present in the human peripheral repertoire
A;Reference number: 849571
                                                                                                                                                                                                                                              Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ket hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into laisulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lockeywords: heterotetramer; immunoglobulin homology ckeywords: heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>F;1-43/Region: framework IF F;4-59/Region: complementarity-determining IF F;6-74/Region: complementarity-determining 2
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Query Match 79.0%; Score 64; DB 1; Length 133; Best Local Similarity 75.0%; Pred. No. 0.0025; Matches 12; Conservative 2; Mismatches 2; Indels

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F;114-122/Rēgion: complementarity-determining 3 F;123-133/Region: framework 4 F;43-113/Disulfide bonds: #status predicted

182-113/Region: framework 3

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RESULT 14
PH1057
Glassian V region (clone 178.145) - mouse (fragment)
CS pledies: Mus musculus (house mouse)
CS pledies: Musculus (house mouse)
CS pledies: Musculus (house mouse)
CS pledies: Musculus (hill, R.J.; Marion, T.N.
Musculus musculus pluga anti-DNA antibodies are the products of clonally selective FA placession: PH1057
A pluga acid sequence not shown

77.8%; Score 63; DB 2; Length 114; 75.0%; Pred. No. 0.0031; Live 2; Mismatches 2; Indels

Query Match
Best Local Similarity 75.03
"...hes 12; Conservative

A; Molecule type: mRNA A; Residues: 1-114 <GIA> Status: preliminary

ò В Q12007 saccharomyc O998d3 sordaria ma Q8x096 enurospora Q9p8f3 gibberella Q6693 yersinia pe Q8d0d4 yersinia pe Q6602 trypanosoma Q9cmu7 pasteurella Q67538 aquifex aeo Q8pef6 xanthomonas Q8pef9 xanthomonas Q9py44 sulfolobus Q77209 trypanosoma Q8177 centerococcu Q7vkh9 haemophilus Q81k97 cucumis mel Q9xdt5 clostridium Q8svzl mycoplasma Q8x105 thermotoga Q278l basmodium Q45820 clostridium Q458

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September 30, 2004, 05:55:56; Search time 52.339 Seconds (without alignments) 96.454 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
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1: sp_archea.*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
7: sp_mhc:*
7: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vortebrate:*
14: sp_unclassified:*
15: sp_vortebrate:*
16: sp_bacteriap:*
17: sp_roteriap:*
18: sp_vortebrate:*
19: sp_vortebrate:*
19: sp_vortebrate:*
10: sp_vortebrate:*
11: sp_vortebrate:*
12: sp_vortebrate:*
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14: sp_vortebrate:*
15: sp_vortebrate:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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81
1 RSSKSLLYKDGKTYLN 16
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result	,	Query	Query	9	£	רייים פר היייה מיייה
1001	יי מכינים יי מכינים	ייייייייייייייייייייייייייייייייייייייי	ייייייייייייייייייייייייייייייייייייייי	9 :		
,	64	79.0	86	4	Q7Z3Y5	Q7z3y5 homo sapien
7	61	75.3	239	4	Q8TCD0	Q8tcd0 homo sapien
m	59	72.8	148	11	Q8K122	Q8k122 mus musculu
4	57	70.4	114	4	Q9UL80	Q9ul80 homo sapien
Ŋ	50	61.7	239	4	QBNEKO	Q8nek0 homo sapien
9	20	61.7	758	10	Q9C9E8	Q9c9e8 arabidopsis
7	49	60.5	238	11	Q8VCI6	Q8vci6 mus musculu
60	48	59.3	104	11	Q9JL82	Q9j182 mus musculu
0	48	59.3	239	11	QSKOFS	Q8k0f8 mus musculu
10	48	59.3	239	11	Q8VC55	Q8vc55 mus musculu
11	48	59.3	1561	17	026451	O26451 methanobact
12	46	56.8	238	11	Q99M37	Q99m37 mus musculu
13	46	56.8		16	Q9L035	Q91035 streptomyce
14	46	56.8	573	N	P97179	P97179 streptomyce
15	46	56.8		7	086876	O86876 streptomyce
16	44	54.3	419	16	Q9CG26	Q9cg26 lactococcus

ALIGNMENTS	1 723YS, PRELIMINARY; PR1 723YS; 1-OCT-2003 (TYEMBLYEL: 25, CYCEAT	01-CCT-2003 (TrEMBLrel. 25, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last annotation update) Rearranged VRA17 V gene segment (Fragment). VRA17 V gene segment (Fragment). Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (1)1	SEQUENCE FROM N.A. TISSUE-Add&frain lymphoma; TISSUE-Add&frain lymphoma; Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R., Hansmann M.L., Brauninger A.; Hansmann M.L., Brauninger A.; "Analysis of a clonally related mantle cell and Hodgkin lymphoma indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg cell precursor in a germinal center."; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AJS64426; CAD92033.1; NON TER 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Match  19.0%; Score 64; DB 4; Length 86;  Best Local Similarity 75.0%; Pred. No. 0.0042;  Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;    RSSKSLLYKDGKTYLN 16
	3UL 23Y			Query Matches Matches Matches Oy  Oy  Db  RESULT 2  QBTCD0  ID Q8TCD0
	A H PO E	F F E B S S S S S S S S S S S S S S S S S S	SHRRRRRS	\$ 6 8 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

DDT BENEFIELD DE STANDER SON SERVICE SON S

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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BG030814; AH30814.1; -.
EMBL, BC33639; S23639.
PIR, S34091; S34091.
PIR, S40357; S40357.
InterPro; IPR0031010; Ig-11.
InterPro; IPR003597; Ig-d..
InterPro; IPR003597; Ig-d..
InterPro; IPR003597; Ig-d..
InterPro; IPR003597; Ig-d..
PIN PF0047; Ig-d..
InterPro; IPR003597; Ig-d..
InterPro; IPR003597; Ig-d..
                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
70.4%; Score 57; DB 4; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.085;
Matches 11; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 114
114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                         114 AA.
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                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSSKSLLYKDGKTYLN 16
                                                      PRELIMINARY;
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TISSUE=Prostate;
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NON TER
SEQUENCE
                                                      Q9UL80
Q9UL80;
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Q8NEK0
     RESULT 4
                                                                                 ACCOORDINATION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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                                                                                                                Eukaryota, Medazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-Salivary gland;
Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Bubmitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
R InterPro; IPR001359; Ig.
R InterPro; IPR00110; Ig-like.
R Fram; PR00047; Ig, 1.
R SMART; SM00409; IG; 1.
R SMART; SM00409; IG; 1.
R PROSITE; PS00835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.3%; Score 61; DB 4; Length 239; Best Local Similarity 68.8%; Pred. No. 0.041; Matches 11; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 148 AA; 16345 MW; 183920BBD9F3BS21 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 148 AA
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44 RSTQSLVYSDGNTYLN 59
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Q8K122 RESULT 3 Q8K122

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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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N (1)

C TISSUE=Colon;

Strausberg R.;

Strausberg R.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R SUBMITTED (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R PIR, A27887; A27887.

R PIR, B37248; B32248.

R PIR, B3787; B3787;

R PIR, B31485; B31485.

R PIR, B31486; B31485.

R PIR, B2530; F3233.

R PIR, B2530; F32530.

R PIR, B11034; PH1031.

R PIR, PH1034; PH1034.

R PIR, PH1034; PH1034.

R PIR, PH1034; PH1034.

R PIR, S16112; S16112.

R PIR, S16112; S16112.

R PIR, S60066; S60066.

R PROSTIE: P800290; IG MHC.

R PROST
                                                                                                 OI-WAR-2002 (TrEMBLrel. 20, Created)
OI-WAR-2002 (TrEMBLrel. 20, Last sequence update)
OI-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.2.,
Best Local 9, Conservative
                                                                                       PRELIMINARY;
                                                                                       Q8VCI6 PRELIMINARY;
Q8VCI6;
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                        RESULT 7
Q8VCI6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lariante 408:816-820(2000).

Mature 408:816-820(2000).

EMBL; AC016529; AAG52586.1; -.

PIR; C96749; C96749.

G0; G0:0003677; F:DNA binding; IEA.

G0; G0:0003677; F:DNA methyltransferase activity; IEA.

G0; G0:000310; F:N-methyltransferase activity; IEA.

G1; G0:000310; F:M-methyltransferase activity; IEA.

G1; G0:000310; F:M-methyltransferase activity; IEA.

G1; G0:00031; F:M-methyltransferase activity; IEA.

G1; G0:00031; F:M-methyltransferase activi
                                                                                                                                    Match (1.7%; Score 50; DB 4; Length 239; Local Similarity 62.5%; Pred. No. 2.8; es 10; Conservative 3; Mismatches 3; Indels
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00209; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 Aa; 26024 MW; F5E20AD3B0552COA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9C9E8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                 44 RSSOSLIHSDGYNYID 59
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194 SQKLIYKDGKFHLN 207
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Les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches
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                                                   60.5%; Score 49; DB 11; Length 238; 56.2%; Pred. No. 4.2; cive 5; Mismatches 2; Indels
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                    1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                               43 RSSQSLVHSNGNTYLH 58
                                                                                                                                                                                                                                                                         Q9JL82,
Q9JL82,
01-OCT-2000 (TEMBLRE1.15,
01-OCT-2000 (TEMBLRE1.15,
01-OCT-2003 (TEMBLRE1.25,
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1 RSSKSLLYKDGKTYLN 16
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44 KSSQSLFYTNGKMYLS 59
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                             Query Match
Best Local Similarity 56.2<sup>5</sup>
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 62.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                      MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (UN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC031499; AAH31498.1; -.

EMBL; BC031499; AAH31498.1; -.

RD; IKN2; 13-MAR-02.

GO; GJ:0008152; P:metabolism; IEA.

GO; GJ:0008152; P:metabolism; IEA.

InterPro; IPR002199; ADH-Short.

RICEPRO; IPR003599; Ig.

REART; SM00409; IG; 2.

REART; SM00409; IG; 2.

REART; SM00409; IG; IGV; I.

REART; SM00409; IGV; I.

RESITE; PS00090; IG IKK; 2.

RESOURCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;
Anti-myosin immunoglobulin light chain variable region
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104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                with cardiac myosin.;
Infect. Immun. 68:5803-5808(2000).
EMBL, AF206024, AAF69322.1;
PTR; S26334; S26334.
HSSP, PO1607, IREL.
INCEPPO, IPR007110; IG-like.
InterPro, IPR007596; IG-v.
SWART; SMO0406; IGv; 1.
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16 RSSQSLVHTNGNTYLH 31
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TISSUS=Breast tumor;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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Q8K0F8;
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STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
                                                       Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
59.3%; Score 48; DB 11; Length 239; 56.2%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Straubberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL's BCO1781, AA421781.1;
R PIR; A33933, A3933.
R PDB; 1KC5; 24-JUL-02.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000576; F:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR007110; Ig-1ike.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR00710; Ig-1ike.
R InterPro; IPR00710; Ig-1ike.
R InterPro; IPR003596; Ig-v.
P Fam; PF00047; Ig's.
R Pfam; PF00047; Ig's.
R PROSITE; SN00406; IG-XII.
R PROSITE; PS00290; IG-XIIC.
W Hypothetical protein.
W Hypothetical protein.
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                                                       Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Magnesium chelatase subunit.
                                                       3,
                                                                                                                                                                                                                                                                                                      239 AA.
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                                                    4; Mismatches
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SEQUENCE FROM N.A.
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Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadfora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics.";

"J. Bacteriol. 179:7135-7155(1997).

BEMBL: AE000820; AAB84857.1;

"J. Bacteriol. 179:7135-7155(1997).

RIR: C69145; C69145.

GO: GO:0003779; F:actin binding; IEA.

GO: GO:0003779; F:actin binding; IEA.

GO: GO:0003779; Robn/Mg_chitase.

InterPro; IPR001589; Actind actind.

InterPro; IPR001589; Actind actind.

R PROSITE; PS00019; ActinIn_1; 1.

R PROSITE; PS00019; ActiNIN_1; 1.

Complete proteome.

Complete proteome.

SW SEQUENCE 1561 AA; 170574 MW; 764561FA31D719CE CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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59.3%; Score 48; DB 17; Length 1561;

Best Local Similarity 64.3%; Pred. No. 47;

Matches 9; Conservative 2; Mismatches 3; Indels C
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Strauber RAW, N.T.

Strauber RAW, N.T.

Submitted (JAN 2001) to the EMBL/GenBank/DDBJ databases.

R PIR; A31248; A32248.

R PIR; B32248; B32248.

R PIR; B32248; B32248.

R PIR; B32248; B32248.

R PIR; B12248; B32248.

R PIR; B12530; F32530.

R PIR; PH1042; PH1042.

R PIR; PH1043; PH1043.

R PIR; PH1043; PH1044.

R PIR; S1450; S24501.

R PIR; S24501; S24501.

R PIR; S24503; S24503.

R PDB; ILO2; 31-JUL-02.

R PDB; ILO2; 31-JUL-02.

R PDB; ILO2; 31-JUL-02.
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Last annotation update)
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InterPro; IPR033006; Ig_MHC.
InterPro; IPR03596; Ig_V.
Pfam; PR00547; ig; 2.
SMART; SM00406; IGV; 1.
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Hypothetical protein.
Mus musculus (Mouse)
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of cradered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyes coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.B., James K.D.; Harris D.B., Quall N.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                         Gaps
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Nature 417:141-147(2002).

BEMEL; AL939130; AL98957; 1AQM.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0005975; P:catalytic activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                     Score 46; DB 11; Length 238;
Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Seeger K.J, Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
PROSITE; PS50835; IG_LIKE; 2...
PROSITE; PS0290; IG_MHC; 1..
Hypothetical protein...
SEQUENCE 238 Aa; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                    56.8%; Scor.
53.3%; Pred. No. 10,
... 5; Mismatches
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006444; CBD 4.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
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MEDLINE=97000351; PubMed=8843436;
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AMLB OR SCO7020 OR SCIH10.09.
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                                                                                                                                                               Query Match
Best Local Similarity 53.33
Matches 8; Conservative
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yin X.H., Gagnat J., Gerbaud C., Guerineau M., Virolle M.J., Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 28591, CAB06622.1; --
HSSP; P29957; LAQM.
                                                                                                                                                              Ouery Match

56.8%; Score 46; DB 16; Length 506;
Best Local Similarity 57.1%; Pred. No. 30;
Matches 8; Conservative 3; Mismatches 3; Indels
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Pfam; PF02806; alpha-amylase C; 1.
Pfam; PF00686; CBM 20; 1.
PRINTS, PR00110; ALPHAMYLASE.
PRODON; PD001568; CBD 4; 1.
SWART; SM00642; Aamy; 1.
COMPLETE PROCEOURY C; 1.
SEQUENCE 506 AA; 53868 MW; FCC92A3BED9D2DAE CRC64;
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SMART; SM00632; Aamy_C; 1.
SEQUENCE 573 AA; 61214 MW; B474019661C9D6A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            01-NAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; 70:2004556; F:alpha-amylase activity; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003975; F:catalytic activity; IEA.
GO; GO:0003975; F:catalytic activity; IEA.
InterPro; IPR006048; Alpha-amyl-cat.
InterPro; IPR006048; Alpha-amyl-cat.
InterPro; IPR006049; Alpha-amyl-cat.
InterPro; IPR002044; GD-4.
InterPro; IPR002044; Glyco-hydro_13.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF002806; alpha-amylase; 1.
Pfam; PF002806; alpha-amylase; 1.
Promp; PF00686; CBM_20; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SYNART; SN00642; Aamy: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase.
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P97179
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Gaps

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Created)
Last sequence update)
Last annotation update)

086876 PRELIMINARY; 086876 08.08 01-NOV-1998 (TERMELREL: 08, L5 01-NOY-1998 (TERMELREL: 08, L6 01-OCT-2003 (TERMELREL: 25, L6 Alpha-amylase.

SEPPER !

PRT;

RESULT 15 086876

306 RNGETLTYKDGATY 319

qq

1 RSSKSLLYKDGKTY 14

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0; Gaps
Streptomyces lividans.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1916;
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                                                                                                                                                                                                                            Isiegas C., Parro V., Mellado R.P.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD001568; Lbd., SMART; SM00642; Aamy, 1.
SMART; SM00632; Aamy C; 1.
SMART; SM00632; Aamy C; 1.
                                                                                                                                                                                                                                                                                                                                         GO, GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003975; P:catbohydrate metabolism; IEA.
InterPro; IPR006048; Alpha-amyl-cat.
InterPro; IPR006049; Alpha-amyl-cat.
InterPro; IPR006049; GIPA-amyl-cat.
InterPro; IPR002044; CBD-4.
InterPro; IPR006046; GIYCO-hydro_13.
Pfam; PF00128; alpha-amylase.1.
Pfam; PF00128; alpha-amylase.2; 1.
Pfam; PF001686; CBM_20; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMADT. SMO0606; CBD-4; 1.
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KV2A MOUSE
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                                                                                          September 30, 2004, 05:55:56; Search time 9.76271 Seconds (without alignments) 85.337 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SYM_UREPA
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KV2G_MOUSE
KV2D_HUMAN
KV2E_MOUSE
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
FRAMEWORK-3.
FRAMEWORK-4.
BY SIMILARITY.
   P18956
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-II region MOPC 167.
Mus musculus (Mouse)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
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                                                                  Y549 RICPR
YTXB BACSU
YDCM METS1
LPXA SALTI
LPXA SALTY
LPXA YERPE
ZN80 GORGO
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P100_LEIMA
TOP1_VACCV
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SMART; SM0406; 1GV; 1.
PROSITE; PS50835; 1G LIKE; 1.
Imwunoglobulin V region.
DOMAIN 24 39 CON
DOMAIN 40 54 FRJ
DOMAIN 62 93 FRJ
DOMAIN 62 93 FRJ
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(Human)
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                                                                                                       Gaps
15-JUL-1999 (Rel. 38, Last annotation update)
MS Rappa chain V-II region MOPC 511.
MS musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 81; DB 1; Length 11 100.0%; Pred. No. 4.3e-07; Live 0; Mismatches 0; Indels
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21-UTL-1996 (Rel. 01, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
18-ARAppa chain V-II region VRappal67 precursor.
Mus musculus (Mouse).
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HSSP; PB0362; 1WTL.
INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR007110; Ig-like.
Pfam; PP00047; ig; 1.
PROSITE; PS56035; IG LIKE; 1.
Immunoglobulin V region.
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                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     IG KAPPA CHAIN V-II REGION VKAPPA167.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-II REGION RPMI 6410.
PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A.
BELLINESER6041882, PubMed=2997711,
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.,
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6e-07;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          63BB571F0E4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81; DB 1;
Pred. No. 4.6e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
12-ULL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region RPMI 6410 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AA.
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                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-3.
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FIR, A01980; KJHURP.
HSSP, P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
Ffam; PF00047; ig/ 1.
FROMT; SMOR16; IGv. 1.
FROMT; SMOR16; IGv. 1.
FROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 13:6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
HSSP; P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
SRART; SW00406; IGv; 1.
IMMUNGglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                             13280 MW;
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Best Local Similarity 100.
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Chang U.-Y., Herbst H., Aebersold R., Braun D.G.;
A new isotype sequence (V kappa 27) of the variable region of kappa-
I ight chains from a mouse'hybridoma-derived anti-(streptococcal group
I polysaccharide) antibody containing an additional cysteine residue.
If Application of the dimethylaminoazobenzene isothiocyanate technique
for the isolation of peptides.";
Biochem. J. 21:173-180(1983).
C.-I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGANINGT THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
C. HISP: PROJES; INTL.
C. III-TOPYO: IPROJESS: Ig_V.
C. RISP: PROJESS: Ig_V.
C. RISP: PROJESS: Ig_V.
C. RISP: PROJESS: IG_LIKE: I.
C. RIMAT: SMO406: IG_LIKE: I.
C. RIMAT: SMO406: IG_LIKE: I.
C. RIMANDAJOULIN V region; Monoclonal antibody; Hybridoma.
C. RIMANDALIN V region; Monoclonal antibody RADINALING.
C. RIMANDALING.
C. RIMAND
21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17 kappa chain V-II region 7534.1.
Wus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutharia, Rodentia, Schurognathi, Muridae, Murinae,
MCBI_TaxID=10090;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12496 MW; 42C019D10ADA3C91 CRC64;
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555
62
103
113
113 AA;
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KV2G MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watriable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";

"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";

"In Signature of the light chain was isolated FROM a Waldenstrom's MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.

HASSP, POLGOT, IREI.

GO; GO; GO; GO; GO; GO; GO; FREI.

GO; GO; GO; GO; FREI.

GO; GO; GO; GO; FREI.

GO; GO; GO; GO; GO; FREI.

InterPro; IPRO07110; Ig-like.

InterPro; IPRO07110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
          COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                        Score 64; DB 1; Length 133;
Pred. No. 0.00047;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12660 MW; 0C0DA39E46DB96BE CRC64;
                                                                                                                                                  14707 MW; S13CCAF3673009EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update)
15-VUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-II region FR.
Homo sapiens (Human)
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                                                                                                     BY SIMILARITY
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BY SIMILARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00047; ig; i.
SMART; SM00406; IGV; 1.
PROSTIE; PS50815; IG LIKE; 1.
Immunoglobulin V region.
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RSSQSLVYSDGNTYLN 59
                                                                                                                                                                                                                                                                                                1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                  79.0%;
                                                                                                                                                                                                                         75.0%;
                                                                                                                                                                                                                                             12; Conservative
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nes 10; Conservative
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                                                                                                                                                                                                                         Local Similarity
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KV2B HUMAN
ID KV2B HUMAN
AC POIGIS;
                                                                              DOMAIN
DISULFID
NON TER
SEQUENCE
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     DOMAIN
DOMAIN
DOMAIN
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KV2F MOUSE
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MEDLINE=8117821; FubMed=6404298;
Novotny J., Margolies M.N.;
Novotny J., Margolies M.N.;
Mamino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Biochemistry 22:1153-1158(1983).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT BINDS DIGOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUZG MOUSE STANDARD; PRT; 113 AA.
P01631.
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1986 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1998 (Rel. 38, Last annotation update)
15-UUL-1998 (Rel. 38, Last annotation update)
15-UUL-1986 (Rel. 01, Created)
16-UUL-1986 (Rel. 01, Created)
16-UUL-1986 (Rel. 01, Created)
17-UUL-1986 (Rel. 01, Created)
18-UUL-1986 (Rel. 01, Creat
                                                                                                                  ·.
67.9%; Score 55; DB 1; Length 113; 73.3%; Pred. No. 0.015; 2; Indels iive 2; Mismatches 2; Indels
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HSSP; P80362; 1WTL.
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113 AA.

PRT;

STANDARD;

KV2F MOUSE P01630;

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Gaps

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MEDIJERS 8518968; PubMed 6441768;

A Rebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
A Abbersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
Thurine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6

origin: monoclonal antibodies 17829.1 and 22825.1 specific for the group A-streptococcal polysaccharide.";
L. Group A-streptococcal polysaccharide.";
L. Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
PIR, A01912; KVMS17.
REEL.
RICHEROUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY. PIR, A01912; KVMS17.
RICHERO: IPR003710; Ig-like.
RICHERO: IPR003710; Ig-like.
RICHERO: IPR003710; Ig-like.
REPAR, PF00477; Ig-like.
REPAR, REPAR, PF00477; Ig-like.
REPAR, PF00477; Ig-like.
REPAR, PF00477; Ig-like.
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23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-II region 17529.1.
Mus musculus (Mouse)
Musmalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musi
                        COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                 65.4%; Score 53; DB 1; Length 113; llarity 68.8%; Pred. No. 0.032; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Score 52; DB 1; Length 113; 73.3%; Pred. No. 0.048; 2; Indels iive 2; Mismatches 2; Indels
                                                                                                       113
12316 MW; 0C3C38F81F1843CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4E93797046F8DB33 CRC64;
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(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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          FRAMEWORK-3.
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Best Local Similarity 73...
Best Local 11, Conservative
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113 AA;
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Best Local Similarity
Matches 11; Conser
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21-JUL-1986
15-JUL-1999
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P03976;
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Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Glenner G.G.,
Glen
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MEDLINE=74148480; PubMed=4596149;
Mutnam F.W., Whitley B.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                          fmmunoglobulin V region; Monoclonal antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                   12273 MW; F9F39CE949A84C2A CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-II region TEW.
Homo sapiens (Human).
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                                                                                                                                FRAMEWORK-1
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InterPro; IPR003596; Ig_v. Pfam; PPR00047; ig; 1. SMART; SMOA06; IGv; 1. PROSITE; PSS0835; IG_LIKE; 1.
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Best Local Similarity 62.5%;
Matches 10; Conservative
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KV2D_HUMAN
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KAPPA CHAIN V-II REGION GM607
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTALIY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12664 MW; 92CS7DC719E558B1 CRC64;
HSSP, PO1889; K2HUGM.
HSSP, P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
INTERPRO; IPR007110; IG-like.
                                                                                                                                                PETERNOSSYS; IG_V.
PREM; PP00047; ig_y1.
SMART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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01-OCT-1996 (Rel. 34, Last seq
10-OCT-2003 (Rel. 42, Last ann
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STRAIN=S288C / YP1;
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P42222;
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ERR1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                            "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                       Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region GM607 precursor (Fragment).
Imo sapians (Human).
                                                                                                                                                                                                                                                                        Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, B91639; KZHUCM.
HSSP, P01607; IREI.
GG, GG:0005576; C:extracellular; NAS.
GG), GG:0005575; P:antigen binding; NAS.
GG, GG:0006955; P:immune response; NAS.
GG, GG:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ag; I.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
DISULFID
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MEDLINE=70063440; PubMed=4188189;
                                                                                                                                                                               MEDLINE=68242259; PubMed=5586923;
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            Ig kappa chain v-11
Homo sapiens (Human)
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                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                           Hilschmann N.;
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STRAINS-S286 / AB372;
STRAINS-S286 / AB372;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Connor R., Dedman K., Devlin K., Gentles S., Hamilin N., Hunt S.,
Connor R., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
NAIII.",
Nature 387:90-93(1997).
                                     01-0cr-1996 (Rel. 34, Last sequence update)
10-0cr-2003 (Rel. 42, Last annotation update)
Enclase related protein 1 (EC 4.2.1.11)
ERRI OR YMR323W OR YM9924.15.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
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EMBL; Z00009; -; NOT\_ANNOTATED\_CDS

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RESULT 15
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAINS-JAL-1 / DSW 2661 / ATCC 43067;
MEDLINE-96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.E., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Compilete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-!- FUNCTION: Putative deacetylase (By similarity).
-!- SIMILARITY: Belongs to the histone deacetylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
MAGNISIUM (BY SIMILARITY).
MAGNISIUM (BY SIMILARITY).
MAGNISIUM (BY SIMILARITY).
143D6EF66FB03D13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUJ-1998 (Rel. 36, Created)
15-JUJ-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 343 AA
                                                                                                                                                                                                                                                                                                                                       Germonline; 143981; -.
SGD; S005920; ERR1.
InterPro; IPR00941; Enclase.
Pfam; PF00113; enclase; 1.
Pfam; PF00113; enclase. N; 1.
PRINTS; PR00148; ENCLASE.
ProDom; PD000902; Enclase; 1.
TIGREAMS; TICR01060; enc); 1.
PROSITE; PS00164; ENCLASE; 1.
Lyase; Glycolysis; Magnesium.
ACT SITE 160
METÂL.
247 247 MAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 296
321 321 MAG
437 AA; 47312 MW;
                                                                                                                                                                                                           EMBL; Z54141; CAA90841.1; -. EMBL; U23472; AAC48992.1; -. PIR; S69881. S69881. HSSP; P00924; 4ENL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |: ||||| ||
248 SAPSVFYKDGKYDLN 262
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Best Local Similarity 60.0.
Best Local 9; Conservative
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296
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Q57955;
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SEQUENCE
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RA SULTON

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CC -1- SI

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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINSERIND 2210633 / Serotype 03:K6;
STRAINSERIND 2210643; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iljima Y., Najima M., Nakano M., Yamashita A., Kuboca Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
-!- SIMILARITY: Belongs to the L31P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                   51.9%; Score 42; DB 1; Length 343; 69.2%; Pred. No. 9; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 86;
Pred. No. 2.9;
                                                                           Interpro; IPR000286; His deacetylse.
Pfam; PF00850; Hist deacetyl; 1.
PRINTS; PR01270; HDASUPER.
HYDOCHELCAl protein; HYClase; Complete proteome.
SEQUENCE 343 AA; 38174 MW; 8848EDB757FDC233 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF_00502; -; 1.

InterPro; ITR002150, Ribosomal L31.

PERM; PF01197; Ribosomal L31; 1.

PRINTS; PR01249; RIBOSOMĀLL31.

RINGSTER, PS01143; RIBOSOMĀLL31, 1.

Ribosomal protein; Complete proteome.

SEQUENCE 86 AA; 9995 MW; 59010EF3786573BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
508 ribosomal protein L31 type B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
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EMBL, U67502; AAB98526.1; -. PIR; G64366; G64366.
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Best Local Similarity 69.2-
Best Local Similarity 69.2-
Declaration 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                     3 SKSLLYKDGKTYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                           73 SKSFNYYDGDTYL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPME2 OR VP2331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R31B VIBPA
Q87MCS;
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R31B_VIBPA
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=35000HP / AICC 700724;
MUNSON R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
Johnson R.S. Jr., Ray W.C., Mang J., Forst C., Hood L.;
Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the LilP family of ribosomal proteins.
Subfamily B.
                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 89;
Pred. No. 3.1;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00502; -; 1.
InterPro; IPR02150; Ribosomal_Li31.
Pf01197; Ribosomal_Li31; 1.
PROSITE; PS01143; RIBOSOMAL_Li31; 1.
RRIBOSOMAl_Drotein; Complete profecome.
SEQUENCE 89 AA; 10167 MW; 4BF9B2435E60530F CRC64;
   15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein L31 type B.
RPME2 OR HD1927.
 89 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017156; AAP96649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
'had 6; Conserva
                                                                                                                               Haemophilus ducreyi.
                                                                                                                                                                             NCBI_TaxID=730;
 R31B HAEDU
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Search completed: September 30, 2004, 06:01:14 Job time : 11.7627 secs

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Conservative

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September 30, 2004, 05:55:56; Search time 78.1017 Seconds (without alignments) 57.883 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              1586107 seqs, 282547505 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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81
1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                     Searched:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

A\_Geneseq\_29Jan04:\*
1: geneseq11980s:\*
2: geneseq11980s:\*
3: geneseq12000s:\*
4: geneseq12001s:\*
5: geneseq12001s:\*
7: geneseq12003as:\*
7: geneseq12003bs:\*
8: geneseq12003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	4	69	62 Humani	_	œ	Aaw39882 Light cha	4	2 Mouse	4	4 Light	Aaw39815 Light cha	m		22	1 Variab	Ŋ	9 Light	Aaw39897 Light cha		N	0440	Aae06992 Human kap	3905	5889 Human mA	Aay56670 Partial p	
SUMMARIES	ID	AAY32254	AAE06969	AAY32262	AAY32261	AAW39818	AAW39882	AAW39804	AAR12232	AAR12354	AAW39824	AAW39815	AAW39803	AAW39886	AAW39802	AAW39801	AAW39875	AAW39839	AAW39897	AAW39805	AAY70802	AAY70790	AAE06992	ABR55905	ABR55889	AAY56670	
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	Length	16.	100	116	145	16	113	113	131	132	16	16	113	113	113	113	16	16	113	114	20	122	112	91	91	93	
æ	ch	100.0	100.0	100.0	100.0	95.1	95.1	95.1	93.8	93.8	95.6	92.6	92.6	92.6	95.6	2	85.2	85.2	85.2	85.2	82.7	82.7	80.2	79.0	79.0	79.0	
	Score	81	81	81	81	77	77	77	76	76	75	75	75	75	75	75	69	69	69	69	67	67	65	64	64	64	
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. Aae06960 Mouse ger	Aae06961 Mouse ger	Aae35907 Human A17	Abo27142 Human ger	Abo27143 Human ger		Aaws3585 Light cha		Human	Abb99636 2A2 monoc	Adc61024 Human ant		Adel3192 HZVII lig	Adel3218 Humanised	Aar52057 Light cha		Aab12170 Mouse HBV	Aab12171 Humanised	Aab12173 Humanised	Aay42306 Human ant	•
AAE06960	AAE06961	AAE35907	ABO27142	AB027143	ADC61021	AAW53585	AAE07003	AAE06993	ABB99636	ADC61024	ADC61023	ADE13192	ADE13218	AAR52057	AAU76445	AAB12170	AAB12171	AAB12173	AAY42306	
4	4	ø	9	v	_	~	4	4	v	7	^	7	^	N	m	m	m	m	~	1
100	100	100	100	100	103	112	112	112	112	112	112	112	112	113	113	113	113	113	132	1
79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	o o	σ	79.0	79.0	79.0	79.0		0.64	
64	64	64	49	64	4.4	64	64	64	64	64	49	64	4	4	4.	4.	4.4	4	4.4	;
26	27	28	60		3.5	3.6	1 K	٠ 4	i in	9 6	) (r	- cc	9 6	, 4 , C	, 4	. 4	4 4	4 4	. 4	י ד

cD23; PCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroidiis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; Crohn's disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; sjograft-versus-host disease; COPD; bronchitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy. Light chain CDR L1 of mouse anti-CD23 MAb C11. Ą. AAY32254 standard; peptide; 16 (first entry) 15-FEB-2000 AAY32254; RESULT 1 AAY32254 

Mus musculus.

WO9958679-A1.

18-NOV-1999.

99WO-GB001434. 98GB-00009839. 09-MAY-1998; 07-MAY-1999;

(GLAX ) GLAXO GROUP LTD.

Shearin J; Ellis JH, Rapson NT, Crowe SJ, Bonnefoy JMP,

WPI; 2000-053101/04. N-PSDB; AAZ34739.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 1; Page 40; 81pp; English.

This sequence represents complementarity determinating region 1 (CDR LI) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (See also AAY32254). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

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render them capable of binding to the CD23 type II molecule expressed on hematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative collits, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma acute asthmatic exacerbation, rhinits, eczema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes are also useful for studying interactions between CD23 and various ligands and determining the binding agents ; Length 16; 0; Indels 100.0%; Score 81; DB 3; L ilarity 100.0%; Pred. No. 8.1e-07; Conservative 0; Mismatches 0; 16 1 RSSKSLLYKDGKTYLN Similarity Sequence 16 AA; Ma. Local Sim Query Match Matches 

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Gaps

1 RSSKSLLYKDGKTYLN 16

g

AAE06969 standard; protein; 100 AA.

AAE06969;

16-OCT-2001 (first entry)

Mouse germline kappa light chain variable (VK) region, 167/24.

Mouse, humanised antibody, CC-chemokine receptor 2, CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; Cyfostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; multiple sclerosis; atherogenesis; atherosclerosis; allograft rejection; fibrodic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region. 

Mus sp.

WO200157226-A1.

09-AUG-2001

02-FEB-2001; 2001WO-US003537

03-FEB-2000; 2000US-00497625

(MILL-) MILLENNIUM PHARM INC

Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin, WPI; 2001-488888/53.

O'keefe T;

O'brien S,

Jones ST,

Newman W,

Horvath C,

Larosa GJ,

Disclosure; Page 151; 183pp; English

103. .113 /note= "framework region 4"

99WO-GB001434

07-MAY-1999; 18-NOV-1999.

94. .102 /note= "CDR 3"

Region

The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating

ô CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, at disorders such as rheumatoid arthritis and multiple sclerosis, at atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or disquosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and Ig2- mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, aethma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting necoming marrowing of the lumen of a vessel in a mammal, and inhibiting medicinal hyperplasia of a wessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa urticaria, nephrotic syndrome; glomerulonephritis; disease; structure collits; Crohr's disease; Sjogren's syndrome; allergy, asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; Gaps CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region, CDR; autoimmune disease; inflammation; arthritis; lugus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; . 0 100.0%; Score 81; DB 4; Length 100; 100.0%; Pred. No. 6.3e-06; ive 0; Mismatches 0; Indels Humanised anti-CD23 MAb C11 light chain variable region. .54 ce= "framework region 2" /note= "framework region 1" <u>-</u> light chain variable (VK) region, 167/24 Location/Qualifiers AAY32262 standard; protein; 116 AA. ..93 ..e= "framework r /nocc 55. .61 -- "CDR 2" "CDR 1" 1 RSSKSLLYKDGKTYLN 16 24 RSSKSLLYKDGKTYLN 39 IS-FEB-2000 (first entry) Conservative .39 'note= /note= /note= Local Similarity les 16; Conserv Sequence 100 AA; Homo sapiens. Synthetic. AAY32262; Query Match therapy. Key Region Region Region Region Homo Matches RESULT 3 δ

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                                                                                                                                                                                                                                                                                                                          This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGKVII) and the light chain complementarity determining regions (see AAY32254-56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino caid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arbhritis, lupus erythematosus, Hashimoto's thyroiditis, multiple carbritis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomeralopphritis, inflammatory bowel disease, ulcreative colitis, colitis, colophis, inflammatory bowel disease, ulcreating colitis, colitis, colophismatic exacerbation, rhinitis, eczema, graft-oversus-host disease, COPD, insultis, borochitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions controls and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD23; FCERII; IgE receptor; monoclonal antibody; Cl1; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoco's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; slogren's syndrome; allergy; asthma; thinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                               Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                  Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                  Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32261 standard; protein; 145 AA
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                                                                                                                                                                                                                                                                                            Claim 9; Fig 3; 81pp; English.
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       98GB-00009839
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Best Local Similarity 100.
Matches 16; Conservative
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/note= "(
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/note= "
                                                                                                  Bonnefoy JMP, Crowe SJ,
                                                       (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                WPI; 2000-053101/04.
N-PSDB; AAZ34747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
          09-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy.
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AAY32261
ID AAY32261
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AC AAY
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This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies see attered antibodies, such as chimeric or humanised antibodies see ANY32262 and ANY32262 and ANY32263), which complise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining ceptons (see ANY3224-59) to render them capable of binding to the CD23 type II molecule expressed on haemacropoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple cof arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple cof arthritis, crohn's disease, glogren's syndrome, allergic asthma, collisis, crohn's disease, glogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic asthmatic asthma, acute asthmatic axacerbation, rhinitis, eczema, graft-collisis, crohn's disease, (COPD, insullitis, bronchitis (particularly chronic bernonchits) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions companies and various ligands and determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ellis JH, Rapson NT,
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125. .134
/note= "CDR L3"
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       GROUP LTD.
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                                                                                                      WO9958679-A1
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   Region
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97WO-US010965.

25-JUN-1997;

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AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treatment addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                    New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in fassmaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 81; 147pp; English
                                                                                                                                           (UYCO ) UNIV COLUMBIA NEW YORK
                                                                       96US-00672345.
                                                                                                                                                                                                                                                                                    WPI; 1998-077166/07.
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                                                                       25-JUN-1996;
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Matches
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NAME OF THE PROPERTY OF THE PR
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ö Gaps .; 0 95.1%; Score 77; DB 2; Length 16; 93.8%; Pred. No. 3.9e-06; ive 1; Mismatches 0; Indels Light chain of the catalytic antibody 2A10. AAW39882 standard, protein, 113 AA. 1 RSSKSLLYEDGKTYLN 1 RSSKSLLYKDGKTYLN 16-JUN-1998 (first entry) Local Similarity 93.8 les 15; Conservative

Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction

96US-00672345. 25-JUN-1997; 25-JUN-1996; 31-DEC-1997

(UYCO ) UNIV COLUMBIA NEW YORK

WPI; 1998-077166/07. N-PSDB; AAV09789. Landry DW;

AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2AlO antibody (AAW39809 benzoic acid from 3H-phenyl mas identified using TSAl, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2AlO has a per minute Koat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the

Claim 16; Page 73-74; 147pp; English.

New catalytic antibodies able to decompose cocaine, single-chain

ö The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomes. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The particularly for the treatment of an overdose. They are also used treating addiction (by reducing the in vivo concentration that can be analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding. New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding. Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine; immunogenic conjugate, reduction, cocaine; treatment, Gaps Variable domain of the Kappa light chain of catalytic antibody 2A10. ; 0 95.1%; Score 77; DB 2; Length 113; 93.8%; Pred. No. 3.5e-05; Live 1; Mismatches 0; Indels Disclosure; Fig 21; 147pp; English AAW39804 standard; protein; 113 AA. (UYCO ) UNIV COLUMBIA NEW YORK. 1 RSSKSLLYKDGKTYLN 16 24 RSSKSLLYEDGKTYLN 39 97WO-US010965 16-JUN-1998 (first entry) Conservative overdose; addiction. WPI; 1998-077166/07. Local Similarity Les 15; Conserv Sequence 113 AA; 25-JUN-1997; WO9749800-A1 25-JUN-1996; 31-DEC-1997. AAW39804; Query Match Mus sp. Landry Matches RESULT 7 AAW39804 8 g

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This is the light (kappa) - chain variable (V) region of a mouse monoclonal antibody (MAb), 2E12, and is specific for an HIV-1 viral haring wartigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 2E12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immuno- conjugates, in association with e.g. toxins for HIV reatment. They can also be used in diagnosis of HIV. See also AAQ12057-63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric mouse-human antibodies - used to detect, kill and remove HIV -1 antigen from sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable domain, lambda light chain, catalytic antibody; degradation; cocaine, cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                               Light (kappa) chain variable region of murine 2512 immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
                                                                                                                  Chimeric antibodies; immunoconjugates; HIV; AIDS
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93.8%; Pred. No. 6.1e-05;
ive 1; Mismatches 0;
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                                                  (first entry)
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                               (revised)
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N-PSDB; AAQ12056.
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                                                                                                                                                       fus musculus
                               25-MAR-2003
15-AUG-1991
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AAR12354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The mouse VL gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
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                                                                                     Length 113;
                                                                                                                        0; Indels
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                                                                                     95.1%; Score 77; DB 2; I 93.8%; Pred. No. 3.5e-05; iive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                    AAR12232 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Mouse MAb 2E12 L chain V region
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Best Local Similarity
For 15; Conservative
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(first entry)
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(GREC ) GREEN CROSS CORP.
(ZOMA-) ZOMA CORP.
                                                                                       Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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                                                       Sequence 113 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1989;
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19-AUG-1991
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AAR12354
ID AAR:
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WO9749800-A1

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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 83; 147pp; English
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nes 14; Conservative
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                                                                                                                                         25-JUN-1997;
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AAW39815-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 3B9, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-berzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified using TSAl, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in fassmaller doses than antibodies that antagonise cocaine by simply binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                         Claim 11; Page 80; 147pp; English
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Best Local Similarity 87.55
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P-PSDB; AAV09802.
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92.6%; Score 75; DB 2; Length 16; 87.5%; Pred. No. 8.5e-06; 1ive 2; Mismatches 0; Indels

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(UYCO ) UNIV COLUMBIA NEW YORK

WPI; 1998-077166/07

Landry DW;

96US-00672345

97WO-US010965

25-JUN-1997; 25-JUN-1996; Variable domain, lambda light chain, catalytic antibody; degradation, cocaine, cocaine transition state analogue, TSA; benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment, overdose, addiction.

Variable domain of the Kappa light chain of catalytic antibody 6A12.

(first entry)

16-JUN-1998

AAW39802;

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AAW39802 standard; protein; 113

RESULT 14

AAW39802

24 RSSRSLLYRDGKTYLN 39

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benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW19808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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                                                                                                                                                               Score 75; DB 2; Length 113
Pred. No. 7.6e-05;
2; Mismatches 0; Indels
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Best Local Similarity, 87.5%;
Matches 14; Conservative
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N-PSDB; AAV09793.
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(UYCO ) UNIV COLUMBIA NEW YORK

Landry DW;

96US-00672345.

25-JUN-1997; 25-JUN-1996;

WO9749800-A1.

Mus sp.

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87.5%; Pred. No. 7.6e-05;
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Local Similarity 87.5 es 14; Conservative

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92.6%; Score 75; DB 2; Length 113; 87.5%; Pred. No. 7.6e-05; ive 2; Mismatches 0; Indels

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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occasine. A series of cocaine transition state analogues (FSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806 represents the heavy chain) was identified using TSAl, which is an immunogenic conjugate of a prosphate monoseter transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                      Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overcose; addiction
Variable domain of the Kappa light chain of catalytic antibody 3B9.
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P-PSDB; AAV09791.
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                                                                                                                                           Mus sp.
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Gaps . 0 Query Match 92.6%; Score 75; DB 2; Length 113; Best Local Similarity 87.5%; Pred. No. 7.6e-05; Matches 14; Conservative 2; Mismatches 0; Indels ò

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1 RSSKSLLYKDGKTYLN 16

24 RSSRSLLYRDGKTYLN 39

Search completed: September 30, 2004, 06:06:09 Job time : 80.1017 secs

Sequence 112, App Sequence 419, App Sequence 79, App1 Sequence 79, App1 Sequence 55, App1 Sequence 55, App1 Sequence 55, App1 Sequence 24, App1 Sequence 23, App1 Sequence 24, App1 Sequence 22, App1 Sequence 22, App1 Sequence 23, App1 Sequence 24, App1 Sequence 26, App1 Sequence 26, App1 Sequence 56, 
```
APPLICANT: LaRGARIAN
APPLICANT: LaRGAR, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Walter
APPLICANT: Horwath, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Therea
APPLICANT: O'Refe, Therea
APPLICANT: O'Refe, Therea
ATITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
FRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR PELICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PASISEQ for Windows Version 3.0
HUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 81, DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0;
10 US-09-940-727B-112

10 US-09-940-727B-113

10 US-09-940-727B-13

10 US-09-940-727B-13

10 US-09-940-727B-16

10 US-09-940-727B-16

10 US-09-940-727B-16

10 US-09-940-727B-16

10 US-09-940-459-55

16 US-10-766-610-55

18 US-10-766-610-55

19 US-09-940-459-61

10 US-10-766-610-23

11 US-10-153-869-23

12 US-10-453-698-23

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15 US-10-153-382-88

16 US-10-308-817-22

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16 US-10-308-817-22

16 US-10-766-610-23

17 US-10-766-610-23

18 US-10-766-610-23

19 US-10-766-610-23

10 US-10-766-610-23

11 US-10-766-610-23

12 US-10-733-563-23

13 US-10-733-563-24

14 US-10-733-563-24

15 US-10-733-563-24

16 US-10-733-563-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application US/09840459 Patent No. US20020150576A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSSKSLLYKDGKTYLN 16
      CRGANISM: Mus musculus US-09-840-459-32
         US-09-840-459-32
         ८८७७७७७७७७७७७५४४४४४४४४४४४४४४४४
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Sequence 6, Appli
Sequence 7, Appli
Sequence 100, App
Sequence 104, App
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Sequence 32, Appl
Sequence 22, Appl
Sequence 25, Appl
Sequence 8, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 28, Appl
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                                                                                                                                                           September 30, 2004, 06:01:30; Search time 268.475 Seconds (without alignments) 19.178 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_DUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_DUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_DUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 RSSKSLLYKDGKTYLN 16
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seg length: 200000000
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Maximum DB
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Gaps

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Length 100;

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100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels (
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Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/10733563
Fublication No. US20040151721A1
Gequence 32, Application US/10733563
Fublication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: O'REFE THERES
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 10448-213001
CURRENT FILING DATE: 2003-12-0
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR PILING DATE: 2002-06-26
PRIOR PILING DATE: 2002-06-16
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 122
SEQ ID NO 32
LENTH: 100
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US-09-90-127B-22

Sequence 22, Application US/09940727B

Sequence 22, Application US/09940727B

Publication No. US2003007793A1

GENERAL INFORMATION:

APPLICANT: Landry, Donald W

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT FILING DATE: 1999-12-04

PRIOR FILING DATE: 1999-12-04

PRIOR FILING DATE: 1999-12-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOSTWARE: PATENTIN VERSION 3.1

SEQ ID NO 22

LENGRIH: 16
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ORGANISM: Mus musculus
US-10-733-563-32
; ORGANISM: Mus musculus US-10-766-610-32
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                           GENERAL INFORMATION:

GREERAL INFORMATION:

APPLICANT: LaRges, Gregory J.

APPLICANT: Newman, Walter

APPLICANT: Newman, Walter

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Refe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

CURRENT APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2004-01-27

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR FILING DATE: 1999-07-22

PRIOR FILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 106

SOTTWARE: FastSEQ for Windows Version 3.0

LENGTH: 100

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APPLICANT: LARGAGING:
APPLICANT: LARGAGING:
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siohan H.
APPLICANT: O'Brien, Siohan H.
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCEZ ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILE REFERENCE: 1855.105-029
CURRENT FILING DATE: 2004-01-27
FRICH APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-06-23
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
NUMBER: OF SEQ ID NOS: 107
SOFTWARE: FEASTSEQ for Windows Version 3.0
TYPE: PRT
                                                                                                                             Sequence 32, Application US/10766773 Publication No. US20040126851A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-10-766-610-32
Sequence 32. Application US/10766610
Publication No. US20040132980A1
GENERAL INFORMATION:
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  24 RSSKSLLYKDGKTYLN 39
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US-10-766-773-32
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Pred. No. 1.8e-05;
1; Mismatches 0; Indels
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Sequence 19, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR PILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-8
PRIOR FILING DATE: 1998-12-8
NUMBER OF SEQ ID NOS: 121
SOFUR APPLICATION NUMBER: 08/672,345
NUMBER OF SEQ ID NOS: 121
SOFURWARE: BATENIN VERSION 3.1
                               Sequence 108, Application US/09940727B

Publication No. US2003007793A1

GENERAL INFORMATION:

APPLICANT: Landry. Donald W

TITLE OF INVENTION: ANTI-COAINE CATALYTIC ANTIBODY

TITLE OF INVENTION: ANTI-COAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: 09/214,095

PRIOR APPLICATION NUMBER: 2002-09-04

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1997-06-25

NUMBER OF SEQ ID NOS: 121

SOSTUBARE: PARENTIN VERSION 3.1

SEQ ID NOS: 121

SEQ ID NOS: 121

SEQ ID NOS: 121
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Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
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Best Local Similarity 93.8%;
Matches 15; Conservative
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US-09-940-727B-108
RESULT 8
JS-09-940-727B-108
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US-09-940-727B-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 77; DB 10; Length 16;
Pred. No. 2e-06;
1; Mismatches 0; Indels
    Indels
                                                                                                                                                                                          Sequence 25, Application US/09940727B

publication No. US2003007793A1

GENERAL INPORMATION:

APPLICANT: Landry.

ATLE OF INVENTION:

CURRENT ELING DATE: US/09/940,77B

CURRENT FILING DATE: 1992-04

PRIOR APPLICATION NUMBER: US/09/940,77B

CURRENT FILING DATE: 1998-12-28

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SEQ ID NOS: 121

SEQ ID NO SEQ ID NOS: 121

SEQ ID NO SEQ ID NOS: 121

SEQ ID NO SEQ ID NOS: 121
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Sequence 8, Application US/09940727B;
Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B;
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR RILING DATE: 1998-12-28
PRIOR RILING DATE: 1997-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFFWARE: Patentin version 3.1
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    Mismatches
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Best Local Similarity 93.8%;
Matches 15; Conservative
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    15, Conservative
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                                                                                                                                                             RESULT 6
US-09-940-727B-25
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US-09-940-727B-8
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ORGANISM:
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PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFFWARE: Patentin version 3.1
SEQ ID NO 6
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Best Local Similarity 87.5<sup>†</sup>
Matches 14; Conservative
                                                                                                                        ; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-6
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; ORGANISM: mouse
US-09-940-727B-7
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.6%; Score 75; DB 10; Length 16; Best Local Similarity 87.5%; Pred. No. 4.3e-06; Matches 14; Conservative 2; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT LANGY, Donald W
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 08/72,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 5: SEQ ID NOS: 121
SEQ ID NO 5: DATERTION 3.1
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Publication No. US20030077793A1
GENERAL INPORMATION:
I APPLICANT: Landry, Donald W
ITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: 1998-12-28
PRIOR APPLICATION NUMBER: 1998-12-28
PRIOR APPLICATION NUMBER: 1997-06-25
                 CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER: PE PRIOR FILING DATE: 1996-06-25
SEQ ID NOS: 121
SEQ ID NO 28
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     FILE REFERENCE: 0575/51400-B
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: mouse
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US-09-940-727B-5
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    Length 113;
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; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICAMTICAMTICAMTICAMTION:
; FILE REFERENCE:
; FILE REFERENCE:
; CURRENT APPLICATION WINBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; CURRENT FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; ROOFWHARE: PRIORATION NUMBER: 08/672,345
; REOR FILING DATE: 1996-06-25
; NUMBER: OF SEQ ID NOS: 121
; SEQ ID NO 7.
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US-09-940-727B-100
Sequence 100, Application US/09940727B
Fublication No. US2003007793A1
GENERAL IMFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFRENCE: 05/5/51400-B
CURRENT FILING DATE: 2002-09-04
CURRENT FILING DATE: 1998-12-28
FRIOR FILING DATE: 1998-12-28
FRIOR FILING DATE: 1996-06-25
FRIOR FILING DATE: 1997-06-25
FRIOR FILING DATE: 1997-06-35
Query Match 92.6%; Score 75; DB 10; L
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0;
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Search completed: September 30, 2004, 06:54:51 Job time: 268.475 secs

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43, Appl 179, Appl 9, Appli 9, Appli 99, Appli 113, Appl 22, Appl 25, Appl 26, Appl 26, Appl 27, Appl 26, Appl 26, Appl 27, Appl 28, Appl 28, Appl 29, Appl 31, Appl

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US-09-214-095D-43
US-09-214-095D-79
US-09-214-095D-19
US-08-672-345C-9
US-08-672-345C-99
US-09-472-087-13
US-09-472-087-13
US-09-472-087-25
US-09-472-087-25
US-09-472-087-25
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
     RESULT 1
US-08-672-345C-22
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     RESULT
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                                                                                                                            September 30, 2004, 06:00:45; Search time 27.1186 Seconds (without alignments) 30.459 Million cell updates/sec
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1. /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*

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3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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5. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.6
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S-08-672-345C-25
S-09-214-095D-22
S-09-214-095D-22
S-08-672-345C-98
S-08-672-345C-98
S-09-214-095D-108
S-09-214-095D-19
S-09-214-095D-19
S-09-214-095D-28
S-09-214-095D-28
S-09-214-095D-28
S-09-214-095D-28
S-08-672-345C-5
S-08-672-345C-6
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S-09-214-095D-5
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S-09-214-095D-104
S-09-214-095D-112
S-09-214-095D-112
S-08-672-345C-43
S-08-672-345C-43
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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81
1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Query
Match Length DB
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Perfect score:
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0
Sequence 2.2 Application US/08672345C

Sequence 2.2 Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:

APPLICANT: Landry Donald, W.

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDERSS:

ADDERSSE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

COUNTRY: USA

ZIP: 10036

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM C Compatible

COMPUTER: IBM C COMPATION:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFATION NUMBER: 05/75/51400

TELEFAX: 212-78-0400

TELEFAX: 212-78-0400

TELEFAX: 212-39-0400

TELEFAX: 212-39-0400

TELEFAX: 212-39-0400

TELEFAX: 212-39-0400

TELEFAX: 121-39-0525

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

TEMPORTHY: 1 TELEFAX: 212-39-0400

TEMPORTHY: 1 TELEFAX: 212-39-0400

TEMPORTHY: 1 TELEFAX: 212-39-0400

TELEFAX: 212-39-0400

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TELEFAX: 212-39-0400
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95.1%; Score 77; DB 2;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches
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US-08-672-345C-25

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1 RSSKSLLYKDGKTYLN 16
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TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.00
                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Murinae gen. sp. US-09-214-095D-25
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MOLECULE TYPE: protein
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Sequence 25, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
ITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONEVAGENT INPOMMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMULICATION INPORMATION:

TELECOMMULICATION INPORMATION:

TELECOMMULICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 51400-A-PCT-US
CURRENT APPLICATION HUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-214-095D-22
; Sequence 22, Application US/09214095D
Patent No. 6280987
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOFOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                            ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 15; Conserv
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US-09-214-095D-25

Sequence 25 Application US/09214095D

Fatent No. 6280987

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 51400-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

UNMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO 25
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Patent No. 5948688
GENERAL INFORTION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURSIN APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C FILING DATE: 24-JUN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 REPRENCE/DOCKET NUMBER: 0575/51400 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1185 Avenue of the Americas CITY: New York STATE: New York STATE: New York CUNTRY: USA ZIP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS COMPUTER: DATE: DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.1
Best Local Similarity 93.8
Matches 15; Conservative
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1 RSSKSLLYKDGKTYLN 16

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18-08-0/4-/Top-2.obem.td
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Best Local Similarity 93.8%; Pred. No. 1.5e-05; Matches 15; Conservative 1; Mismatches 0; Indels

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Length 113;
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95.1%; Score 77; DB 3; Length 113
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                         RESULT 8
US-09-214-095D-108
US-09-214-095D-108
Sequence 108 Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OP INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE CO INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERBYCE: 51400-A-POT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT PELLING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 113
TYPE: PR
CREAKINGH: Murine
US-09-214-095D-108
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MEDIUM TYPER: Floppy disk COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: S4-TUN-1996

CURRENT APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-TUN-1996

CLASSIFICATION NUMBER: US/08/672,345C

TIANG TOWNEY, AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 0575/51400

TELEPHONE: 212-278-0400

TELEPHONE: 212-391-0525

INFORMATION FOR EQUID NO: 19:
SEQUENCE CHRACTERISTICS:
LENGTH: 16 amino acids

WUDE: Amino acids

COMPUTER: ACADA TELEPHONE: Amino acids

COMPUTER: AMINO acids

LENGTH: 16 amino acids
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                                                                                   24 RSSKSLLYEDGKTYLN 39
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                                                                                                                                                                               | Sequence 
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GENERAL INFORMATION:
APPLICANT: Landry, Donald; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY; TITLE REPRENCE: 51400-4P-FCT-US; CURRENT APPLICATION NUMBER: US/09/214,095D; CURRENT FILICE DATE: 1999-07-19; NUMBER OF SEQ ID NOS: 121; SOFTWARE: Patentin version 3.0; SEQ ID NO 8; LINGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk.

COMPUTER PER FOCKOMPATIONE

COMPUTER PER FOCKOMPATIONE

SUSTIME: PATCHIN RELEASE #1.0, Version #1.30

SUSTRANE PAPLICATION DATE:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: White, John P. REGISTRATION NUMBER: 0575/51400

TELEPARATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELEPARATION NUMBER: 212-278-0400

TELEPARATION FOR SEQ ID NO: 98:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

TYPE: Amino acid

TYPE: Amino acid
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Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 0
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24 RSSKSLLYEDGKTYLN 39
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ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-672-345C-98
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US-08-672-345C-98
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US-09-214-095D-8
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US-08-672-345C-19

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Gaps
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0
                                                                                                            Length 16;
                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.6%; Score 75; DB 3; Length 16; 87.5%; Pred. No. 4.2e-06; Live 2; Mismatches 0; Indels
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Fatent No. 5948658
GENERAL INPORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1188 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NURSE: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERRATION NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEFONE: 212-238-0400
TELEFONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                       Score 75; DB 3; I
Pred. No. 4.2e-06;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDYTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         92.6%;
                                                                                                                                                                                                             1 RSSRSLLYRDGKTYLN 16
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                                                                                                     Query Match
Best Local Similarity 87.55
Matches 14; Conservative
LENGTH: 16
TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5 Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                               US-09-214-095D-19
                                                                                                                                                                                                                                                                                          RESULT 12
US-09-214-095D-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-214-095D-28
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0
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                                 Query Match 92.6%; Score 75; DB 2; Length 16; Best Local Similarity 87.5%; Pred. No. 4.2e-06; Matches 14; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 92.6%; Score 75; DB 2; Length 16; 1 Similarity 87.5%; Pred. No. 4.2e-06; 14; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                   RESULT 10
US-08-672-345C-28
US-08-672-345C-28
Sequence 28, Application US/08672345C
Patent No. 5948658
RENBRAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INTERMION: ANNI-COCAINE CATALYTIC ANTIBODY
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
ITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
ITILE REFERENCE: S1400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTOMORY INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/51400
TELECOMMULICATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                    1 RSSKSLLYKDGKTYLN 16
                                                                                                                                             1 RSSRSLLYRDGKTYLN 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-672-345C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-214-095D-19
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Search completed: Septe Job time: 28.1186 secs
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                                                                                                                                                                              Length 113;
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Best Local Similarity 87.5%; Pred. No. 3.2e-05;
Matches 14; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 05/5/51400
TELEPRATION NUMBER: 05/5/51400
TELEPRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRANE: 212-239-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TELEGER: Amino acids
TELEGER: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08672345C
Patent No. 5948658
GENERAL INPORMATION:
APPLICANT: LINFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                            Score 75; DB 2
Pred. No. 3.2e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSSKSLLYKDGKTYLN 16
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                                                                                                                                                                                                                                                                                               24 RSSRSLLYRDGKTYLN 39
                                                                                                                                                                              Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                       1 RSSKSLLYKDGKTYLN 16
                     LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-672-345C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-672-345C-6
                                                                                                                                                                                                                                                                          ò
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NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS: 108

CORRESPONDENCE ADDRESS: 108

STREET: 1155 Avenue of the Americas

CITY: New York

COMPUTER READABLE FORM:

APPLICATION NUMBER:

APPLICATION NUMBER:

CLASSIFICATION:

COMPUTER READABLE FORM:

APPLICATION NUMBER:

APPLICATION NUMBER:

CLASSIFICATION:

COMPUTER READABLE ```

Blank Sheet

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 30, 2004, 05:55:56; Search time 7.59322 Seconds (without alignments) 88.677 Million cell updates/sec Run on:

US-09-674-716B-5 31 1 LMSTRAS 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description         | g kappa chain V | kappa  | g kappa chain V | g kappa | conserved hypothet | hypothetical prote | flagellar motor sw | probable beta-keto | beta-ket | minichromosome mai |        | ~      | v      | hypothetical prote | probable transcrip | NADH2 dehydrogenas | probable ponA' pro |        | collagen alpha 1(I | hypothetical prote | agglutinin isolect | agglutinin isolect | hypothetical prote | tein   | -   | ne receptor | nthae | type I | conserved hypothet |
|-----------|---------------------|-----------------|--------|-----------------|---------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|-----|-------------|-------|--------|--------------------|
| SUMMERTES | ΩI                  | 95              | KVMS16 | KVMS51          | KVMS67  | E69832             | S50468             | C81451             | 8601               | E91171   | T39991             | T16198 | 834027 | T39225 | E95905             | D96028             | QXFF2Y             | C70791             | S21626 | CGHU1S             | T51460             | 0962               | T05936             | T26647             | T39105 | 892 | 584         | 45    | B72660 | 98                 |
|           | DB                  |                 | н      | ч               | Н       | ~                  | ~                  | N                  | N                  | ~        | 7                  | ~      | Н      | ~      | 7                  | ~                  | Н                  | 7                  | 7      | н                  | (7                 | 7                  | ~                  | 7                  | 2      | N   | N           | N     | N      | C)                 |
|           | Length              | 74              | 112    | 113             | 120     | 104                | 234                | 342                | 409                | 409      | 760                | 842    | 845    | 1401   | 112                | 313                | 341                | 810                | 1453   | 1464               | 177                | 212                | 212                | 326                | 341    | 390 | 511         | 532   | 265    | 627                |
| ٠         | %<br>Query<br>Match | 100.0           |        | 100.0           |         | 87.1               |                    |                    | 87.1               | ^        | 87.1               | 7.     | 7,     | 7      | ٣.                 | ω.                 | ٣.                 | ٣.                 | 83.9   | έ.                 | ċ                  | ö                  | ö                  | ö                  | ö      | ö   | ö           | 。     | ö      |                    |
|           | Score               | 31              | 31     | 31              | 31      | 27                 | 27                 | 27                 | 27                 | 27       | 27                 | 27     | 27     | 27     | 26                 | 56                 | 26                 | 26                 | 26     | 56                 | 25                 | 25                 | 25                 | 25                 | 25     | 25  | 25          | 25    | 25     | 25                 |
|           | Result<br>No.       | T               | (1)    | m               | 4       | ហ                  | φ                  | 7                  | σ                  | σv       | 10                 | 11     | 12     | 13     | 14                 | 15                 | 16                 | 17                 | 18     | 19                 | 20                 | 21                 | 22                 | 23                 | 24     | 25  | 26          | 27    | 28     | 29                 |

| alcohol oxidase (E<br>probable membrane | probable ATP-depen | ritamycin polyketi | gene Mnc DQ-beta i<br>hypothetical prote | conserved hypothet | hypothetical prote | hypothetical prote | IB1P8-4 protein [i | hypothetical prote | cytolysin II opero | emopamil-binding p | periplasmic immuno | conserved hypothet | Cof family protein |
|-----------------------------------------|--------------------|--------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| OXHQAP<br>S56293                        | T38885             | T17464             | 136903<br>G90913                         | T44544             | T01726             | H96833             | G71422             | T10331             | A43860             | A56122             | AB3319             | G97904             | G95033             |
| H 0                                     | 7                  | 01 0               | 24 04                                    | ď                  | N                  | N                  | ~                  | 7                  | 4                  | 7                  | ~                  | 7                  | 7                  |
| 664                                     | 887                | 5069               | 82<br>144                                | 152                | 164                | 171                | 171                | 176                | 190                | 229                | 250                | 270                | 270                |
| 80.6                                    | 80.6               | 90.6               | 77.4                                     | 77.4               | 77.4               | 77.4               | 77.4               | 77.4               | 77.4               | 77.4               | 77.4               | 77.4               | 77.4               |
| 25                                      | 25                 | 25                 | 0 0<br>4 4                               | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 |
| 30                                      | 32                 | 33                 | ო ო<br>4 ი                               | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

| C;Species: Mus musculus (house mouse) C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996 C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996 C;Accession: G30538 B;Claflin, J.L.; Berry, J. J. Immunol. 141, 4012-4019, 1988 J;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A;Reference number: A30534; MUJD:89035545; PMID:3141511 A;Reference number: A30534; MUJD:89035545; PMID:3141511 A;Recession: G30538 A;Status: G10538 A;Status: mRNA A;Residues: 1-74 <cla> C;Superfemily: immunoglobulin V region; immunoglobulin homology C;Superfemily: immunoglobulin C;Keywords: heterotetramer; immunoglobulin Query Match Best Local Similarity 100.0%; Scree 31; DB 2; Length 74; Best Local Similarity 100.0%; Pred. No. 0.75; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C) /cla>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | nuse)  tision 10-Feb-1989 #text_change 16-Aug-1996  tholine-specific antibody response to Strepto  id sequence not shown; not compared with con  egion; immunoglobulin homology  oglobulin  Score 31; DB 2; bength 74;  pred. No. 0.75;  pred. No. 0.75;  i pred. No. 10.75;  o; Mismatches 0; Indels 0; Gaps  mouse  nuse;  vision 30-Nov-1980 #text_change 16-Aug-1996                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT 1<br>030538<br>To kanna chain V region (253.15E2) - mouse (fragment)                                                                          |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| CyAccession: G30514  AyTitle: Gametices of the phosphocholine-specific antibody response to Streptococcus pneum AyTitle: Gametices of the phosphocholine-specific antibody response to Streptococcus pneum AyAccession: G30538  AyAccession: G30 | Richaelin, U.1.; Beary, J.  7. Accession: Gallan, U.2.; Beary, J.  7. Immunol. 141, 4012-4019, 1988  7. Accession: Gallaner: Of the phosphocholine-specific antibody response to Streptococcus pneum A; Accession: Gallaner: Along A; Muld. 189035545; PMID: 3141511  7. Accession: Gallaner: Muld. A; Accession: Gallaner: MRD: A; Muld. A; | C;Species: Mus musculus (house mouse)<br>C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996                                 |
| A; Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A; Reference number: A30534; MUID:89035545; PMID:3141511 A; Accession: G30538 A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran A; Molecule type: mRNA A; Molecule type: mRNA C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin Query Match Best Local Similarity 100.0%; Score 31; DB 2; Length 74; Best Local Similarity 100.0%; Pred. No. 0.75; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 LMSTRAS 7  Cy 24 LMSTRAS 30                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | A; Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum A; Reference number: A30534; MUID:89035545; PMID:3141511 A; Accession: G30538 A; Accession: G30538 A; Accession: G30538 A; MoID:89035545; PMID:3141511 A; Molecule type: MRNA A; Residues: 1-74 < CLA> C, Molecule type: mRNA A; Residues: 1-74 < CLA> C, Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin Query Match Best Local Similarity 100.0%; Score 31; DB 2; Length 74; Best Local Similarity 100.0%; Pred: No. 0.75; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C, Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C, Mismatches 0; Mismatches 0; Caps 0; C, Mismatches 0; C, Mismatches 0; C, Caps 0; C, C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | C;Accession: G30538<br>R;Claffin, J.L.; Berry, J.<br>J. Tuminol 141, 4012-4019.1988                                                                  |
| A,Accession: G30538 A,Accession: G30538 A,Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran A,Bataucus: preliminary; nucleic acid sequence not shown; not compared with conceptual tayouter pressions: new mRNA A,Residues: 1-74 < CLA> C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Reywords: heterotetramer; immunoglobulin D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | A;Accession: G30538 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran A;Nolecule type: mRNA A;Residues: 1-74 <cla> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin Query Match Best Local Similarity 100.0%; Pred. No. 0.75; Best Local Similarity 100.0%; Pred. No. 0.75; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 0; Indels 0; Raps  Qy 1 LMSTRAS 7  Db 24 LMSTRAS 3  RESULT 2  KVM316 IG Rappa chain V region (M167) - mouse 0; Species: Mus musculus (house mouse) 0; Date: 30-Nov-1980 #text_change 16-Aug-1996</cla>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | A,Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum<br>A,Reference number: A30534; MUID:89035545; PMID:3141511 |
| <pre>aunoglobulin homology l; DB 2; Length 74; c. 0.75; cches 0; Indels 0; Gaps</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | <pre>aunoglobulin homology 1; DB 2; Length 74; 5. 0.75; ches 0; Indels 0; Gaps Nov-1980 #text_change 16-Aug-1996</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | A;Accession: G30538<br>A;Atatus: preliminary, nucleic acid sequence not shown; not compared with conceptual tran<br>A;Molecule type: mRNA            |
| <pre>puery Match 100.0%; Score 31; DB 2; Length 74; lest Local Similarity 100.0%; Pred. No. 0.75; latches 7; Conservative 0; Mismatches 0; Indels 0; Gaps                 24 LMSTRAS 30</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | <pre>puery Match</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | A;Residues: 1-74 <cla><br/>C;Superfamily: immunoglobulin V region; immunoglobulin homology<br/>C;Keywords: heterotetramer; immunoglobulin</cla>      |
| 1 LMSTRAS<br>       <br>24 LMSTRAS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Cy 1 LMSTRAS 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 100.0%; Score 31; DB 2; Length 74;<br>Similarity 100.0%; Pred. No. 0.75;<br>7; Conservative 0; Mismatches 0; Indels 0; Gaps                          |
| 24 LMSTRAS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | DD 24 LMSTRAS 30 RESULT 2 KVMS16 Ig kappa chain V region (M167) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-NOv-1980 #sequence revision 30-Nov-1980 #text_change 16-Aug-1996                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RESULT 2<br>KVMS16<br>Ig kappa chain V region (M167) - mouse<br>C;Species: Mus musculus (house mouse)<br>C;Date: 30-Nov-1980 #sequence revision 30-Nov-1980 #text_change 16-Aug-1996                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 24 LMSTRAS                                                                                                                                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Cypate: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996                                                                          |

C,Accession: A01908
R,Rudikoff, S.; Porter, M.
B,Rudikoff, S.; Porter, M.
C,Accession: A01908
A,Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma proté
A,Reference number: A01908; MUD:79000273; PMID:99160
A,Rofession: A01908
A,Rofecule rype: protein
A,Residues: 1-112 - RUD>
C,Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. 7
C,Complex: An immunoglobulin heteroteramer subunit consists of two identical light (kapp hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into land; deperfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer
F,16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted

Gaps 0; Query Match 100.0%; Score 31; DB 1; Length 112; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 7; Conservative 0; Mismatches 0; Indels

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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: E6882; C40614
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G.; Azevedo, V.; Berterc
C; Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Choj
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 330, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krooph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parko, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanor,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Todato, V.; Uchiyama,
A;Tille: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A6950; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Popham, D.L.; Setlow, P. 1993
V. Bacteriol. 175, 4870-4876, 1993
A.Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpF gene,
A.Reference number: A40614; MUID:93328693; PMID:8335642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: S50468
R;Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda A;Accession: S50468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: GB: 299109, GB: AL009126, NID: 92633260, PIDN: CAB12849.1, PID: e1183011, A, Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: BMBL:U18778; NID:g603592; PID:g603602; GSPDB:GN00005; MIPS:YER010c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)
C,Species: Saccharomyces cerevisiae
C,Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 12;
0; Mismatches 1; Indels
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100.0%; Pred. No. 26;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.18;
85.78;
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Best Local Similarity 100.0
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-67 <POP>
A,Cross-references: GB:L10630
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A; Residues: 1-234 <DIE>
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A;Cross-references: S
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Afforced type: protein Afforced by Residues: 1-13 APP>
Afforced type: Comment. This APP>
Cycomment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
Cycomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la Cysuperfamily: immunoglobulin V region; immunoglobulin homology
Cykeywords: heterotetramer
F;16-95/Domain: immunoglobulin homology < IMM>
F;16-95/Domain: immunoglobulin pomology < IMM>
F;23-93/Disulfide bonds: #status predicted
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Call 25, 47-58, 1981

A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A;Reference number: A01909; MUID:82002223; PMID:6791832

A;Residues: 1000

A;Molecule type: DNA

C;Gomptex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

C;Gomptex: An immunoglobulin V region; immunoglobulin homology

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

E;1-20/Domain: signal sequence #status predicted <AMT>

E;2-1-120/Product: 19 kappa, chain V region (WK167) #status predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Immurol. 17, 711-718, 1980
A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylchd
A;Reference number: A01910; MUID:81052016; PMID:6776396
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                                                                                                                                                                                                                               Ig kappa chain V region (M511) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C;Accession: A01910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor V region (VK167) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C;Accession: A01909
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;1-20/Domain: signal sequence #status predicted <SIG>
;21-120/Product: Ig kappa chain V region (VK167) #status predicted <WAT>
;36-115/Domain: immunoqiobuin homology <IMM>
;43-113/Disulfide bonds: #status predicted
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BE6983
conserved hypothetical protein yhgB - Bacillus subtilis
N;Alternate names: hypothetical protein Y (pbpF 5' region)
C;Species: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Query Match
Best Local Similarity 100.0
Matches 7; Conservative

A; Accession: A01910

55 LMSTRAS 61

1 LMSTRAS 7

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RESULT 7

7; Conservative

Query Match Best Local Similarity Matches 7; Conserv

LMSTRAS 81

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Gaps

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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross references: EMBL:AL031158; PIDN:CAA20099.1; GSPDB:GN00067; SPDB:SPBC25D12.03c
A;Experimental source: strain 972h-; cosmid c25D12
R;Liang, D.T.; Forsburg, S.L.
Submitted to the EMBL Data Library, June 1998
A;Description: Fission yeast mcm7+ is an essential gene required for normal DNA replicati
A;Reference number: Z22955
A,Residues: 1-409 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37764.1; PID:g13363815; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC84341
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prote
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacession: T16198
R;Leimbach, D.
R;Leimbach, D.
R;Leimbach, D.
R;Description: The sequence of C. elegans cosmid F28B4.
A;Reference number: 218475
A;Reference number: T16198
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87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels
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C;Superfamily: replication licensing factor MCM7; MCM homology
F;170-662/Domain: MCM homology <MCM>
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A;Molecule type: DNA
A;Residues: 1-842 <LEI>
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87.1%; Score 27; DB 2;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches
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A;Experimental source: strain Sp.011
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A, Map position: 2
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77 MSTRAS 82
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A, Residues: 17-409 <STO>
A, Cross-references: GB:AE005174; NID:g12518154; PIDN:AAG58601.1; GSFDB:GN00145; UMGF:Z48
A, Experimental source: strain 0157:H7, substrain EDL933
C,Genetics:
A, Genetics:
C, Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
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Fig. Purkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller. L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
A.jtiller Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A.jtelerence number: A85480; MUID:21074935; PMID:11206551
                                                                  flagellar motor switch protein Cj0319 [imported] - Campylobacter jejuni (strain NCTC 114
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100.0%; Pred. No. 38;
ative 0; Mismatches
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Best Local Similarity 100...
Lag 6; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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A;Molecule type: DNA
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Query Match 87.1%; Score 27; DB 2; Length 842; Best Local Similarity 100.0%; Pred. No. 94; Matches 6; Conservative 0; Mismatches 0; Indels

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A/Status: preliminary
A/Status: preliminary
A/Molecule type: DNA
A/Exosa-references: GB:AL591985; PIDN:CAC48909.1; PID:q15140382; GSPDB:GN00167
A/Experimental source: strain 1021, megaplasmid pSymB
A/Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
D.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Rahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
A/Authors: Rahn, D.; Andenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A/Reference number: A66039; MUID:21368244; PMID:11474104
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-1401 <CHU>
A,Cross-references: EMBL:Z98763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9G1.02
A,Experimental source: strain 972h-; cosmid c9G1
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                                                                                                                                                    T39225
MAP kinase kinase kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: ()3-Dec-1999 #sequence_revision ()3-Dec-1999 #text_change 31-Jan-2000
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R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21837
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85.7%; Pred. No. 1.6e+02;
ive 0; Mismatches 1; Indels
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           300 MSTRAS 305
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Best Local Similarity
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A;Accession: S34027
A;Accession: S34027
A;Accession: S34027
A;Accession: S34027
A;Residues: 1-845 cJAC>
A;Cross-references: EMBL:Z21487; NID:g311665; PIDN:CAA79689.1; PID:g311678
B;Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S46054
A;Accession: S46074
A;Accession: S46074
A;Accession: S46074
A;Accession: S46074
A;Residues: 1-845 cBUS>
A;Residues: EMBL:Z36071; NID:g536576; PIDN:CAA85166.1; PID:g536577; GSPDB:GN000
B;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
Yeast 9, 797-806, 1993
A;Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
A;Reference number: S34925; MUID:93377417; PMID:8368014
A;Cross-references: EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4 C;Genetics: A;Gene: CESP:F28B4.2 A;Gene: CESP:F28B4.2 A;Introns: 1373; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2 C;Superfamily: CDC25-type gnanine nucleotide exchange activator homology F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)
NA-Alexanate names: cell division control protein CDC47; protein YBR1441; protein YBR202w
C;Species: Saccharomyces cerevisiae
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: S34027; S46074; S34925; S56049
R;Jacquet, M.
submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 2R
C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637
component of replication licensing factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribalton, S. submitted to the EMBL Data Library, September 1994
A;Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation A;Reference number: S56049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: S56049
A,Molecule type: DNA
A,Residues: 1-551,'G',533-555,'TLN',559-573,'Y',575-845 <DAL>
A,Residues: 1-551,'G',533-555,'TLN',559-573,'Y',575-845 <DAL>
A,Residues: 1-551,'G',533-555,'TLN',559-573,'Y',575-845 <DAL>
A,Cross-references: ENBL:U14730; NID:g608169; PIDN:AAA86309.1; PID:g608169
C,Comment: The complex of six MCM proteins is one of several proteins that must be phosphorylated and dissociate from the chromatin.
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                                                                                                                                                                                                                                                                                                                                  Gaps
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Gaps
Ouery Match

87.1%; Score 27; DB 1; Length 845;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels
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Gene: SGD:CDC47; MIPS:YBR202w Cross-references: SGD:S0000406; MIPS:YBR202w

A;Accession: S:4925 A;Molecule type: DNA A;Residues: 407-620 <BU2> A;Cross-references: EMBL:221487

probable transcription activator of the pca operon, LysR family protein [imported] - Sink

us-09-674-716b-5.open.rpr

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Cyaccesion: D96028

R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1.683-kb psymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431

A/Accession: D96028

A/Accession: D9
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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Pred. No. 63;
0; Mismatches 1; Indels
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Similarity 85.7%;
6; Conservative (
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Matches 6; Conserv
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A;Gene: pcaQ; SMb20580
A;Genome: plasmid
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Search completed: September 30, 2004, 06:00:33 Job time : 9.59322 secs

199 LMPTRAS 205

1 LMSTRAS 7

ò Dp Dank Sheet

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21-JUL-1986 (Rel. 01, Last sequence update)
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                                                                                          September 30, 2004, 05:55:56; Search time 4.27119 Seconds (without alignments) 85.337 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                         141681
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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KV2E MOUSE
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KV2E WOUSE
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YERG YEAST
WCM7 SCHPO
CC47 YEAST
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AG11 HUMAN
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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31
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| P07196 homo sapien P02547 sus scrofa P4724 paramecium P13941 rattus norv P05694 saccharomyc Q980269 saccharomyc O16102 drosophila. P5546 rhizobium s P38164 saccharomyc P32597 saccharomyc Q9us25 schizosach | 15         | 112 AA.<br>update)<br>on update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Craniata; Vertebrata; Euteleostomi;<br>Sciurognathi; Muridae; Mutinae; Mus.      | orylcholine bind<br>A MYELOMA PROTEI                                                                                                                        | CE OF THE V REGION OF THE HEAVY                                                      |                                                                              | PRAMEMORK-1. FRAMEWORK-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4. BY SIMILARITY. ASBEDFD6404B9726 CRC64; | DB 1, Length 112;<br>0.39;<br>hes 0; Indels 0; Gaps 0; |                                    | 113 AA.                                                                  |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|------------------------------------|--------------------------------------------------------------------------|
| NFL_HUMAN<br>NFL_PIG<br>PARF_PARTE<br>AGA3_RAT<br>METE YEAST<br>FTSK_BRAJA<br>AGATL_YEAST<br>CHD3_DROME<br>Y4GI_RHISN<br>Y4GI_RHISN<br>YHRI YEAST<br>YTH YEAST                                               | ALIGNMENTS | PRT; 1<br>id)<br>equence up<br>nnotation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | - : :                                                                            | 9160;<br>on from M167,<br>1978).<br>AIN WAS ISOLA                                                                                                           | AIN WAS ISOUR<br>E. THE SEQUE!<br>TERMINED.                                          | , i                                                                          | FRAMEWORK-1. COMPLEMENTARI FRAMEWORK-2. COMPLEMENTARI FRAMEWORK-3. COMPLEMENTARI FRAMEWORK-4. BY SIMILARITY MW; ASBEDFD6404                              | %; Score 31; D<br>%; Pred. No. 0.<br>0; Mismatches     |                                    | RD; PRT; 113 AP<br>Created)                                              |
| 77.4 543 1 1 2 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4                                                                                                                                                         |            | 1 MOUSE STANDARD;  - KV2A MOUSE STANDARD; - 101626; - 1011-1986 (Rel. 01, Created) - 1-011-1999 (Rel. 01, Last seq - 15-011-1999 (Rel. 01, Last seq - 15-011-1999 (Rel. 01, Last seq - 15-011-1999 (Rel. 01, Last and 15-011) - 101-1999 (Rel. 01, Last and 15-011) | (Mouse).<br>etazoa; Chorda<br>theria; Rodent<br>0090;                            | MEDLINE=79000273; PubMed=99160; Rudikoff S., Potter M.; Rudia Chain variable region from M167, a phosph myeloma protein."; Blochemietry 17.7703-2707(1978). | OSPHORYLCHOLIN<br>S ALSO BEEN DE<br>KVMS16.<br>; 1WTL.                               | R003596; Ig_v.<br>7; ig; 1.<br>06; IGv; 1.<br>0835; IG_LIKE;<br>in V region. | DOMAIN 1 23 FF DOMAIN 24 39 CC DOMAIN 24 39 CC DOMAIN 40 54 FF DOMAIN 62 93 FF DOMAIN 94 102 CC DOMAIN 103 112 FF DISULFID 2 39 FF NON TER 112 112 NW;   | n<br>Similarity 100.0%,<br>7; Conservative             | LMSTRAS 7<br>       <br>LMSTRAS 61 | STANDA!                                                                  |
| 44444444444444444444444444444444444444                                                                                                                                                                       |            | LT 1  MOUSE  XV2A MOUSE P01626; 21-UUI-1986 21-UUI-1996 15-UUI-1999 Iq kappa cha                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Mus musculus<br>Eukaryota; M<br>Mammalia; Eu<br>NCBI_TaxID=1<br>[1]<br>SEQUENCE. | MEDLINE=7900<br>Rudikoff S.,<br>"Kappa Chain<br>myeloma.prot<br>Biochemistry                                                                                | -!- MISCELLA<br>BINDS PH<br>CHAIN HA<br>PIR; A01908;<br>HSSP; P80362<br>InterPro; IP | InterPro; IP<br>Pfam; PF0004<br>SMART; SM004<br>PROSITE; PS5<br>Immunoglobul | DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN TER SEQUENCE 1                                                                            | Query Match<br>Best Local Simi<br>Matches 7;           | 1 LMS<br>                          | KRESULT 2<br>KV2C_MOUSE<br>ID KV2C_MOUSE<br>AC PO1628;<br>DT 21-UUL-1986 |
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SEQUENCE

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Kunst F. Jogasawara N., Mosser I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Caldwell B., Capuano V., Carter N.M.,
Broullet S. Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Pujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
A. Guiseppi G., Guy B.J., Haga K., Haiech J., Grandi G.,
A. Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A. Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Lardinols S., Lauber J., Lazarevic V.,
Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
A. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A. Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noback M.A., Holsappel S., Kewiet R., Terpstra P., Wambutt R., Wedler H., Venema G., Bron S.; Trin 172 kb prkA-addAB region from 83 degrees to 97 degrees of the Bacillus subtilis chromosome contains several dysfunctional genes, the glyB marker, many genes encoding transporter proteins, and the ubiquitous hit gene."
                                                                                                                                                                                                                                                                   IG KAPPA CHAIN V-II REGION VKAPPA167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Score 31; DB 1; Length 120; Pred. No. 0.42; 0; Mismatches 0; Indels
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COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yhgB.
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PIR, A01909, KVMS67.
HSSP, P80362; NWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596, Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGY; 1.
SMART; SM00406; IGY; 1.
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98240224; PubMed=9579061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13280 MW;
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100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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59
74
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STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
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                                                                                                                                                                                                                                                                      Appella E.;
"Amino acid sequence of the light chain variable region of M511, a
phosphorylcholine-binding murine myeloma protein.";
Mol. Immunol. 17:711-778(1980).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDILIPSE 8200223; PubMed=6791832; MEDILIPSE 220223; PubMed=6791832; Selaing E., Storb U.; munoglobulin light-chain variable-region "Somatic mutation of immunoglobulin light-chain variable-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
BY SIMILARITY.
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      15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region MOPC 511.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                        MEDLINE=81052016; PubMed=6776396;
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InterPro, IPR007110, Ig-like.
InterPro, IPR003596; Ig_v.
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Best Local Similarity luv...
7; Conservative
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113 AA;
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Nature 387:78-81(1997)

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SERANTS-2288C / AB972;
MEDLINE-97313264; PubMed=9169868;
MEDLINE-97313264; PubMed=9169868;
Dietrich F.S., Malligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
Cherry J.M., Chung E., Duncan M., Guzaman E., Hartzell G.,
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekuguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B., Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tognoni A., Wannier P., Vassarotti A., Viari A., Wambut R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikwa H.P., Zumstein E., Yoshikawa H., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus subtilis",
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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"Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbp? gene, which codes for a putative class A high-molecular-weight penicillin-binding protein.";
J. Bacteriol. 175:4870-4876(1993).
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01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical 25.6 kDa protein in NTF2-SRP1 intergenic region.
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85.7%; Pred. No. 4.1;
ive 0; Mismatches 1; Indels
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SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FD968 CRC64;
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DT 01-FEB-1995
DT 10-OCT-2003
DE HYPOTHETICAL
GN SACCHATOMYCE
OC SACC
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MEDINE-2148401; PubMed=11859360;

MEDINE-2148401; PubMed=11859360;

MOOD V. Gwilliam R., Rajlandram M.A., Lyne M., Lyne R., Stewart A.,

Mood V., Gwilliam R., Rajlandram M.A., Eaker S., Basham D., Bowman S.,

A Goulos K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Gone R., Hamlin N., Harris D., Hidalgo J., Hodgeon G.,

A Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A Holroyd S., Hornsby T., Howarth S., Muchen E., Jagels K.,

A Money P., Moule S., Mungall K., Murphy L., Niblet D., Odell C.,

A Money P., Moule S., Mungall K., Murphy L., Niblet D., Odell C.,

A Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

A Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

A Skelton J., Volckaert G., Rerk R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,

Borzym K., Langer I., Beck A., Lehrach H., Machler H.,

Borzym K., Langer I., Beck A., Lehrach H., Purnelle B.,

Borzym K., Langer I., Beck A., Lehrach H., Purnelle B.,

A Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
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ID MCM7 COT 2001 (Rel. 40, Created)

ID 16-OCT-2001 (Rel. 40, Last sequence update)

ID 16-OCT-2001 (Rel. 42, Last annotation update)

ID T 16-OCT-2001 (Rel. 42, Last annotation update)

ID MCM7 OR SPECSD12.03C

Schizosaccharcmyces pombe (Fission yeast).

OC Schizosaccharcmyceales; Schizosaccharcmycetaces;

OC Schizosaccharcmyces.

OC Schizosach
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Characteration of Schizosaccharomyces pombe mcm?(+) and cdc23(+)
(MCML0) and interactions with replication checkpoints.";
Genetics 159:471-486(2001).
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PIR; S50468; S50468.
Germonline; 128.0000812; YER010C.
InterPro; IPR005493; Methyltransf_6.
Byfam; PF03737; Methyltransf_6; 1.
Hypothetical protein:
SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;
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Eukaryota, Pungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NOBI_TaxID=4932;
                                                                                                   Dalton S.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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nes 6; Conservative
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SMART; SM00350; MCM; 1.
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Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Faulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2011 (Rel. 40, Last annotation update)
DNA replication licensing factor CDC47 (Cell division control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A globular complex formation by Ndal and the other five members of
the MCW protein family in fission yeast.";
Genes Cells 2:467-479(1997)
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Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                               STRAIN=972;
MEDLINE=98031880; PubMed=9366552;
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                                                                                                                                                                            SEQUENCE OF 367-466 FROM N.A.
                                                                                                                                     Nature 415:871-880(2002).
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Matches 6; Conservative
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760 AA;
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GO; GO:0005334; C:cytoplasm; IDA.

GO; GO:0005534; C:nucleus; IDA.

GO; GO:0005524; C:nucleus; IDA.

GO; GO:0005524; E:ATP binding; IDA.

GO; GO:0005267; P:Pre-replicative complex; IDA.

GO; GO:0005267; P:Pre-replicative complex formation and maint. . .; IPI.

InterPro; IPR003593; AAA, ATPase.

InterPro; IPR00493; MCM.

InterPro; IPR00493; MCM.

PETM; PRO0493; MCMFAMILY.

PRINTS; PR01663; MCMFAMILY.

PRINTS; PR01663; MCMFAMILY.

PRINTS; PR01663; MCMFAMILY.

PRINTS; PR01663; MCMFAMILY.
MEDLINE-5286;
MEDLINE-9337417; PubMed=8368014;
MEDLINE-93377417; PubMed=8368014;
MEDLINE-93377417; PubMed=8368014;
"A 12.8 kb segment, on the right arm of chromosome II from Saccharomyces cerevisiae including part of the DUR1,2 gene, contains flave putative new genes.";
Yeast 9.797-806(1993).
--- SUBCELIGIAR LOCATION: Nuclear (By similarity).
--- SIMILARITY: Belongs to the MCM family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00847; MCM 1; 1.
PROSITE; PS50051; MCM 2; 1.
Transcription regulation; DNA-binding; Nuclear protein;
DNA replication; Cell cycle; ATP-binding.
DOMAIN 410 617
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558 TLN -> NPG (IN REF. 2).
574 Y -> I (IN REF. 2).
94942 MW, ADA66C719D96DB4A CRC64;
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ATP (POTENTIAL).
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O14299; P87062; Q92384;
16-OCT-2001 (Rel. 40, Created)
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STEALN-972;

KELLINE=21848401; PubMed=11859360;

KEDLINE=21848401; PubMed=11859360;

KELLINE=21848401; PubMed=11859360;

KENDLINE=21848401; PubMed=11859360;

KENDLINE=21848401; PubMed=11859360;

KENDLINE=21848401; PubMed=11859360;

KENDLINE=21848401; PubMed=11859360;

KENDLINE=21848401; PubMed=11859360;

KENDLINE=21848401; PubMed=11859360;

KENDLINE S., Brown D., Baker S., Basham D., Bowman S.,

KENDLINE S., Goble A., Hamlin N., Harris D., Hidalgo U., Hodgson G.,

KENDLINE S., Goble A., Hamlin N., Harris D., Hidalgo U., Hodgson G.,

KENDLINE S., Goble A., Hamlin N., Harris D., Hidalgo U., Hodgson G.,

KENDLINE S., Goble A., Hamlin N., Harris D., Hidalgo U., Hodgson G.,

KENDLINE S., Woule S., Mungall K., Murphy L., Nibblett D., Odell C.,

KENDLINE K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,

KENDLINE S., Saunders R., Saquares S., Stevens K.,

KENDLINE S., Stevens K.,

KENDLINE S., Marls N., Walsh S.V., Warren T., Whitehead S.,

KENDLINE S., Langer I., Beck A., Lehrach H., Morbutt R., Hilbert H.,

KENDLINE S., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

KENDLINE S., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

KENDLINE S., Moreno S., Gloux S., Lelaure V., Mottier S.,

KENDLINE S., Moreno S., Hamler D., Sanchez M., Garzon A., Thode G.,

KANDLI D., Lowe T., Moreno S., Amertrond S., Forbsurg S.L.,

KANDLI D., Lowe T., Moreno S., Amertrond S., Kensterning S.L.,

KANDLI D., Lowe T., Moreno S., Amertrond S., Kensterning S.L.,

KANDLI D., Lowe T., Moreno S., Bulsen I., Potashkin J.,

KH. "The genome sequence of Schizosaccharomyces pombe.";

KH. "The genome sequence of Schizosaccharomyces pombe."; MEDLINES 9731762; PubMed=9188094; Mussell P.; Shiozaki M.; Bussell P.; Shiozaki M.; Shiozaki M.; Sussell P.; Shiozaki M.; 16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
MAP kinase kinase kinase wise 4 (EC 2.7.1.-) (MAP kinase kinase kinase wak!)
WIS4 OR WAK! OR WIK! OR SPAC9G1.02.
Schizosaccharomyces pombe (Fisation yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales; NCBI\_TAXID=4896; "The Mcs4 response regulator coordinately controls the stress-activated Wak1-Wis1-Styl MAP kinase pathway and fission yeast cell STRAIN=972; MEDLINE=97282620; PubMed=9136929; Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K., Millar J.B.A.; Genes Dev. 11:1008-1022(1997). SEQUENCE OF 96-1401 FROM N.A. SEQUENCE OF 457-543 FROM N.A. Nature 415:871-880(2002). cycle." 

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STRAIN=JCM 10545 / 7;

STRAIN=JCM 10545 / 7;

MEDLINE=21456156; PubMed=11572479;

MEDLINE=21456156; PubMed=11572479;

MEDLINE=21456156; PubMed=11572479;

Medrarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anslai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
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Sulfolobus.
(NOB_TaxID=111955;
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85.7%; Pred. No. 72;
ive 0; Mismatches 1; Indels
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Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
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RESA SULTO

ID RASSA SULTO

COTSER;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

CN 28-FEB-2003 (Rel. 41, Last sequence update)

CN 28-FEB-2003 (Rel. 41, Last sequence in update)

CN 28-FEB-2003 (Rel. 41, Last sequence of an aerobic thermoac;

RA Aoshizawa T., Rahada S., Yanaqii M., Nishimura M., RA Aoshizawa T., Kakuchi H.;

RA Oshizawa T., Rada S., Yanaqii M., Nishimura M., RA Oshizawa T., Rada S., Yanaqii M., Nishimura M., RA Oshizawa T., Rada S., Yanaqii M., Nishimura M., RA Oshizawa T., Rada S., Yanaqii M., Nishimura M., RA Oshizawa T., Rada S., Yanaqii M., Nishimura M., RA Oshizawa Sequence of an aerobic thermoac;

RT "Complete genome sequence of an aerobic thermoac;

RT "Complete genome sequence of an aerobic thermoac;

RT Crenarchaeon, Sulfolobus tokodaii strain?";
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Best Local Similarity
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81 LMSTRTS 87
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                          RESULT 11
NU2M_DROYA
   SO RE RESERVED
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                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Drosophila melanogaster mitochondrial DNA, a novel organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 304:234-241(1983).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 -!- SIMILARITY: Belongs to the S3AE family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=96423163; PubMed=8825764;
Lewis D.L., Farr C.L., Kaguni L.S.;
"Drosophila melanogaster mitcochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons.";
Insect Mol. Biol. 4:263-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                        Score 26; DB 1; Length 193;
Pred. No. 15;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                        _proteome.
V; 78A94B87B961D751 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3)
                                                                                                                                                                                                                              Pfam; PF01015; Ribosomal S3Ae; 1.
ProDcm; PD003035; Ribosomal S3AE; 1.
PROSTE; PS01191; RIBOSOWAL_S3AE; PALSE NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 193 AA; 22180 MW; 78A94B87B961D'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 AA
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InterPro; IPR001593; Ribosomal_S3AE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
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MEDLINE=83245048; PubMed=6408489;
                                                                                                                                                                            EMBL; AP000982; BAB65443.1; -.
                                                                                                                                                                                                                                                                                                                                        h 83.9%;
Similarity 71.4%;
5; Conservative
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EMBL; J01404; AAB59238.1; -.
PIR; A00419; QXFF2M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                142 ILSTRAS 148
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                1 LMSTRAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic code."
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NU2M DROME
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Clary D.O., Wolstenholme D.R.;
Genes for cytochrome c oxidase subunit I, URF2, and three tRNAs in
Drosophila mitochondrial DNA.";
Nucleic Acids Res. 11:6859-6872(1983).
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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SEQUENCE FROM N.A.

MEDIJINE=86089137; Pubmed=3001325;

Clary D.O., Wolstenholme D.R.;

The mitochondrisal DNA molecular of Drosophila yakuba: nucleotide
sequence, gene organization, and genetic code.";

J. Mol. Evol. 22:252-271(1985).
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0
                                                                                                                                                                                           Transmembrane.
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                                                                                                                                                                                                                                                                                                 1; Length 341;
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Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-83090428; PubMed-6294611;
Clary D.O., Goddard J.M., Martin S.C., Fauron C.M.-R.,
Wolstenholme D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Drosophila mitochondrial DNA: a novel gene order."; Nucleic Acids Res. 10:6619-6637(1982).
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1-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3)
                                                                                                                                                                                           2B8E9528C28007D8
                                                                                                                                                                                                                                                                                          Score 26; DB
Pred. No. 28;
0; Mismatches
FlyBase; FBgn0013680; mt:ND2.
InterPro; IPR003917; NaDHub_oxred2.
InterPro; IPR001750; Oxidored_q1.
Pfam, PF00361; oxidored_q1; I.
PRINTS; PR01436; NADHDHGNASE2.
Oxidoreductase; NAD; Ubiquinone; Mitc SEQUENCE 341 AA; 39773 MW; 288895
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MEDLINE=88011348; PubMed=3116271;
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                                                                                                                                                                                                                                                                                              83.9%;
85.7%;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=83141374; PubMed=6298597; MEDLINE=83141374; PubMed=6298597; Monson J.M., Friedman J., McCarthy B.J.; Mosquence analysis of a mouse pro alpha 1 (I) procollagen gene: evidence for a mouse B element within the gene."; Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE-83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse pro alpha 1(I) procollagen gen
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                               EMBL; X03240; CAA26985.1; -.
EMBL; X03240; CAA26942.1; -.
EMBL; X05215; CAA29342.1; -.
ELRIS, ESSARE, CAFEZ,
FLYBase; FBGN001712, NADFULD oxxed2.
InterPro; IPR0015917; NADFULD oxxed2.
Pfam; PF00361; oxidored_q1; 1.
PRINTS; PR01436; NADFUHGNASE2.
ERQUENCE 341 AA; 39495 MW; E6117DE50BE9D4AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE OF 518-1128 FROM N.A.
MEDLINE=86137403, PubMed=3841523,
French B.T., Lee W.-H., Maul G.;
"Nucleotide sequence of a cDNA clone for mouse pro alpha 1(1)
                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 1; Length 341;
Pred. No. 28;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA11_MOUSE STANDARD; PRT; 1453 AA. 191087, Q66635; Cant. 11, Created) 01-UJL-1989 (Rel. 11, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Collagen alpha 1(1) chain precursor.
     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matrîx Biol. 14:593-595 (1995).
                                                                                                                                                                                                                                                                                                                                                                      83.9%;
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 85.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 39:311-312(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMSTRAS
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CA11 MOUSE
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Matches
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                                                                                                -!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.-!- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R PIR, SG7243; 231626.

R MGD; MGI:88467; Colla1.

R InterPro; IPR0008161; Clalagen.

R InterPro; IPR0008161; Fib collagen.

R InterPro; IPR001007; VWF_C.

R InterPro; IPR001107; VWF_C.

R InterPro; IPR001107; VWF_C.

R Pfam; PF011391; Collagen; 18.

R Probom; PD000007; Clg_helix; 1.

R Probom; PD000007; Fib collagen_C; 1.

R SMART; SM00038; COLFI; 1.

R SMART; SM000314; VWFC; 1.

R PROSITE; PS01208; VWFC; 1.

R PROSITE; PS01208; VWFC_2; 1.

R Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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TRIPLE-HELICAL REGION.
NONHELICAL REGION.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains. TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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COLLAGEN ALPHA 1(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
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1453 AA; 137944 MW; 3B802E535DF81808 CRC64;
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K03034; AAA37332.1; JOINED.
K03034; AAA37332.1; JOINED.
K03035; AAA37332.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA37332.1; -.
AAA37332.1; JOINED
AAA37332.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U08020; AAA88912.1; -.
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CAA29927.1;
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                                                                                   hydroxyapatite.
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168
1182
1354
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EMBL; M17491; F
EMBL; X06753; C
EMBL; K03036; I
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SIGNAL
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CA11_CANFA
ID _CA11_CANFA
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CARBOHYD
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                                                                                                                                                                                                              EMBL, AF153062; AAD34619.1; -...

InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
InterPro; IPR001601; Collagen.
R InterPro; IPR001007; VWF C.
R InterPro; IPR001007; VWF C.
R Pfam; PF01410; Collagen; 18.
R Probom; PD000007; Clg helix; 2.
R Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00314; VWC; 1.
R SMART; SM00214; VWC; 1.
R PROSITE; PS01208; VWC 1.
R PROSITE; PS01208; VWC 1.
R PROSITE; PS01208; VWC 2.
R EXTRACELULAR matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLOCNAC...) (POTENTIAL).
G -> A (in Ol; severe).
MW; 58E3674D2B570697 CRC64;
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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COLLAGEN ALPHA 1(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
WWFC.
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1 22 BY SIMILARITY.
                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(1) chain precursor.
                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT OI ALA-208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 VWFC domain.
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Similarity 85.7%;
6; Conservative
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11188
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                                                                                                            Canis familiaris (Dog)
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1189 121
741 74
1089 109
1361 136
208 20
1460 AA;
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Best Local Similarity
Matches 6; Conserv
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SIGNAL
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VARIANT
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Click E.M., Bornstein P.; In and characterization of the cyanogen bromide peptides from "Isolation and characterization of the cyanogen bromide peptides from the alpha 1 and alpha 2 chains of human skin collagen."; Biochemistry 9:4699-4706(1970).
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MEDLINE=88097389; PubMed=1480516;
Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
"Regulatory elements in the first intron contribute to
transcriptional control of the human alpha 1(1) collagen gene.";
[8]
Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
"A comparative study of glycopeptides derived from selected
exterbarder collagens. A possible role of the carbohydrate in fibril
formation.";
J. Biol. Chem. 245:5042-5048(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-181 FROM N.A.

SEQUENCE OF 1-181 FROM N.A.

Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,

Myers J., Williams C., Ramirez F.;

Myers J., Williams C., Ramirez F.;

conservation of a pattern of introns and exons.";

Nature 310:337-340(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-88124208; PubMed-3340531;
Maekelae J.K., Raassina M., Virta A., Vuorio E.;
"Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE OF 425-1464 FROM N.A.
MEDLINE=84080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-472 FROM N.A.
MEDLINES89025644; PubMed-3178743;
MEDLINES89025644; PubMed-3178743;
Jachisch G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jachisch R., Prockup D.J.,
Structure of a full-length cDNA clone for the prepro alpha 1(I)
"Structure of a full-length cDNA clone for the prepro alpha 1(I)
inchem. J. 253:919-922 (1988).
CA11 HUMAN STANDARD; PRT; 1464 AA. P02452; Q14037; Q15176; 21-UUL-1986 (Rel. 01, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Collagen alpha 1(1) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 16:349-349(1988).
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MEDLINE=71001508; PubMed=4319110;
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MEDILINE-9755959, PubMed-9101290,
MEDILINE-9755959, PubMed-9101290,
"Mutations in fibrillar collagens (types I, II, III, and XI), fibrilassociated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseases of bone, cartilage, and blood vessels."; Hum. Mutat. 9:300-315(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT OI-II CXS-926.

MEDLINE=88033031; PubMed=3667599;
Vogel B.E., Minor R.R., Freund M., Prockop D.J.,

A point mutation in a type I procollagen gene converts glycine 748
of the alpha I chain to cysteine and destabilizes the triple helix in
a lethal variant of osteogenesis imperfecta.";

J. Biol. Chem. 262:14737-14744(1987).
                                                                                                                                                                                                                                                                                                                                                                                                             Kuivaniemi H., Tromp G., Prockop D.J.; "Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G., "Lethal perinatal osteogenesis imperfecta due to the substitution of arginine for glycine at residue 391 of the alpha 1(1) chain of type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT OI-II ARG-842.
MEDINE=88989828; PubMed=3403550;
MEDINE=88989828; PubMed=3. Dahl H.H., Chan D., Cole W.G.;
Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;
"Substitution of arginine for glycine 664 in the collagen alpha 1(I)
chain in lethal perinatal osteogenesis imperfecta. Demonstration of
the peptide defect by in vitro expression of the mutant cDNA.";
J. Biol. Chem. 263:11627-11630(1988).
                                                                                                                                                                SEQUENCE OF 1-44 FROM N.A.
MEDLINE-88033098; PubMed=2822714;
Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;
"Lethal osteogenesis imperfecta resulting from a single nucleotide
change in one human pro alpha 1(1) collagen allele.";
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MEDLINE=86287390; PubMed=3016737;
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MEDLINE-87222295; PubMed=3108247;
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MEDLINE=97169389; PubMed=9016532;
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MEDLINE-89255493; PubMed-2470760;
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J. Clin. Invest. 83:574-584(1989).
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MEDLINE=90064507; PubMed=2585496;

MEDLINE=90064507; PubMed=2585496;

Wigher C.S.; full c.S.; f
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Agglutinin isolectin 1 precursor (WGA1) (Isolectin A).
Triticum aestivum (Mheat)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae; Pooideae,
NCBI_TaxID=4565;
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BEDINES-91370843; PubMed=2491677;
Smith J.J., saikhel N.V.;
"Nucleotide sequences of cDNA clones encoding wheat germ agglutinin
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MEDLINE=91039324; PubMed=2231724;
MEDLINE=510.5.1.
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"2.2-A resolution structure analysis of two refined
N-acetylneuraminyl-lactose-wheat germ agglutinin isolectin
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PIR, S09623; 809623.
PDB; 7WGA; 15-0CT-90.
PDB; 1WGC; 15-0CT-90.
PDB; 2CWG; 31-JAN-94.
InterPro; 19701002; Chitin binding_1.
PFG, SPRO0102; Chitin bind 1; 4.
PRINTS; PRO0451; CHITINBINDMG.
PRODOM; PRO06609; Chitin binding_1; 4.
PROSITE; PSS0041; CHITINBIND_12; 4.
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PROSITE; PSS0041; CHITINBIND_12; 4.
PROSITE; PSG0026; CHITINDIN_11; 4.
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Plant Mol. Biol. 13:601-603(1989)
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J. Mol. Biol. 215:635-651(1990).
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| Q862r9 bos taurus Q95c8 bos taurus Q95c19 rhizobum m Q60785 mus musculu Q92c19 rhizobum m Q60785 mus musculu Q92c16 chrysomya c Q9mg16 cochliomyia Q9mg17 drosophila Q9mg17 drosophila Q9mg17 drosophila Q9mg16 drosophila Q9mg16 drosophila Q9mg21 drosophila Q9mg21 drosophila Q9mg21 drosophila Q9mg21 drosophila Q9md21 drosophila Q9md22 drosophila Q9md21 drosophila Q9md21 drosophila Q9md21 drosophila Q9md21 drosophila Q9md20 drosophila Q8md20 mrosophila Q8md20 mrosophila Q8md20 mrosophila Q8md20 mrosophila Q8md30 mrosophila Q8md30 mrosophila Q8md30 mrosophila Q8md30 mrosophila Q8md31 homo sapien Q8md31 homo sapien | date) update)  Planctomycetales;  ". Lombardot T., mann K., Rabus R., ctomycete Pirellula sp. 2003).  812 CRC64; 6; Length 847; 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| 17 26 83.9 212 6 Q862R9 18 26 83.9 284 4 Q16050 26 83.9 287 6 Q57DB 21 26 83.9 313 16 Q95TLB 22 26 83.9 338 8 Q9BZJG 23 26 83.9 340 8 Q9KRP1 25 26 83.9 341 8 Q9KRP1 26 83.9 341 8 Q9KRP1 27 26 83.9 341 8 Q9KRP2 28 26 83.9 341 8 Q9KRP2 29 26 83.9 341 8 Q9KRP2 31 26 83.9 341 8 Q9KRP2 32 26 83.9 341 8 Q9KRP2 34 26 83.9 341 8 Q9KRP2 35 26 83.9 341 8 Q9KRP2 36 83.9 341 8 Q9KRP2 37 26 83.9 341 8 Q9KRP2 38 26 83.9 341 8 Q9KRP2 39 26 83.9 341 8 Q9KRP2 39 26 83.9 341 8 Q9KRP2 30 26 83.9 341 1 Q9FLF 30 26 83.9 420 16 Q7VJTB 31 26 83.9 420 16 Q7VJTB 32 26 83.9 1453 11 Q9FLF 34 26 83.9 1453 11 Q9FLF 35 26 83.9 1453 11 Q9FLF 36 83.9 1453 11 Q9FLF 37 26 83.9 1453 11 Q9FLF 38 26 83.9 1453 11 Q9FLF 39 26 83.9 1463 4 Q8K473 45 25 83.9 1463 4 Q8K473                                                                                                                                 | ALIGNMENTS  TUMTS  TUMTS  TOWTS  TOWTS  TOCT-2003 (TERBLEE]. 25, Created)  TOCT-2003 (TERBLEE]. 25, Last sequence up condopirellula baltica.  Anodopirellula baltica.  Acteria; Planctomycetes; Planctomycetacia; Last annotation composite and process.  ACTERIAL;  TAXID-11;  TOWENCE FROM N.A.  SELINB-22735913; PubMed-12835416;  COCKENET F.O., Kube M., Bauer M., Teeling H cockner F.O., Rube M., Bauer M., Teeling H cockner F.O., Rube M., Bauer M., Teeling H cockner F.O., Rube M., Bauer M., Teeling H complete genome sequence of the marine plan rain 1."  TOWENCE 947 AA, 89847 MW, 437EF2BEEDDB2  MARCH  MARCH  10cal Similarity 85.7%; Pred. NO. 1.40+168  TOWENCE 847 AA, 8957*; Pred. NO. 1.40+168  TOWENCE SIMILARIAL SCORESSE SERVENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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409 AA.

Length 342;

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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
putative betarketoacyl-ACP synthase (Putative 3-oxoacyl-(acyl-carrier-
84866 OR ECS4341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                         87.1%; Score 27; DB 16; Length 34
100.0%; Pred. No. 1e+02;
.ive 0; Mismatches 0; Indels
                                                                ED4D214417C1524C CRC64;
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PRINTS, PRO0954; FLGMOTORFLIG.
TIGRFAMS, TIGR00207; flig; 1.
Complete proteome.
SEQUENCE 342 AA; 38429 MW;
                                                                                           PRELIMINARY;
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SEQUENCE TROM N.A.
SEQUENCE 1168,
MEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandram M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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FLIG OR CJ0319.
Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
                                                                                                                                            Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA; 13061 MW; D77E2F6F42DEF735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-077-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                GO; GO:0009288; C:flagellum (sensu Bacteria); IEA. GO; GO:0003774; F:motor activity; IEA. GO; GO:0006395; P:chemotexis; IEA. GO; GO:000139; P:chemotexis; IEA. InterPro; IPR000090; Flg_Motor_Flig. Fig. PF01706; Flig-C; 1.
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EMBL; AE015688; AAN55499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reveals hypervariable sequences.";
Nature 403:665-668(2000).
BMBL, AL139074; CAB72786.1; -.
HSSP, CBH451, CB1451.
HSSP, COWAGA: 10C7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                Adhesion-related protein.
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                                                                                                                                                                                                              NCBI_TaxID=70863;
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STRAIN-COIS7.H7 / RIMD 0509952;

STRAIN-COIS7.H7 / RIMD 0509952;

STRAIN-COIS7.H7 / RIMD 0509952;

Hayashi T., Makino K., Ohnshoi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnshoi M., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli Complete genome comparison with a laboratory strain K-12.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., May B., Kirkpatifick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatifick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 AA; 44148 MW; A4DABOAFA11ED883 CRC64;
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EMBL, AE005571; AAG58601.1; -.

EMBL, AE005571; AAG58601.1; -.

REMEL, EP00631; F:Catalytic activity, IEA.

REMEL, PF00109; Ketoacyl-synth.

REMEL, PF00109; Ketoacyl-synth.

REMEL, REMEL, AE00601; EKETOACYL_SYNTHASE; 1.

REMEL, PROSITE; PS00601; EKETOACYL_SYNTHASE; 1.
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Local Similarity 100.
Les 6; Conservative
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                                2 MSTRAS 7
                                                                1 MSTRAS 6
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=06:H1 / CFT073 / ATCC 700928;

X MEDLINE=2288234; PubMed=12471157;

A Malch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S., Schwartz D.C., Perna N.T.,

Maylew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

A Maylew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

RY Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

RY Excensive mosaic structure revealed by the complete genome sequence RT of uropathogenic Escherichia coll.";

RI Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

BR GO; GO:00008334; F:catalytic activity; IEA.

BR GO; GO:0000833; P:fatty acid blosynthesis; IEA.

BR InterPro: IPR000794; Ketoacyl-synth.

BR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Planctomycetaceae, Pirellula.
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                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL: BX294144; CAD74747.1; -.
Complete proteome
SEQUENCE 505 AA; 55994 MW; 22B90195A3B1D941 CR
                                                  409 AA
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                                                                                                                                                        Putative beta-ketoacyl-ACP synthase
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Best Local Similarity 100...
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es 6; Conservative
                                                PRELIMINARY;
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                                                                                                                                                                                                   Escherichia coli 06
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SEQUENCE
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                                                                     Q8FJ15;
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Q7UQF6;
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                                                Q8FJ15
RESULT 5
Q8FJ15
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01-NOV-1996 (TrEMBLrel. 01, 01, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity luv..
Best Local 6; Conservative
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STRAIN=Bristol N2;
Leimbach D.;
                                                                                                                                                                                                                                                                                                                                                                                           48 LMSTRA 53
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STRAIN=CS7BL/6J; TISSUE=Brain;
MEDLINE=223546J;
The FANTOM CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation of 60,770 full-length cDRAs.";
Nature 420:563-573(2002).
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-IOWA;
Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
Vogel C., Teichmann S.A., Ivens A., Dear P.H.;

"Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum.";

Genome Res. 0.0-0(2003).

EMBL; BX538350; CAD9861B.1; -.

Hypothetical protein.

SRQUENCE 579 AA; 67569 WW; 3F153FD2678AEC75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                        Length 544;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 25, Last annotation update)
RAP guanine nucleotide exchange factor homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

87.1%; Score 27; DB 5; Length 579;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                   Query Match

87.1%; Score 27; DB 11; Length 54
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Cryptosporidium parvum.
Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF0018; RaSGEFN; 1.
SWART; SM00100; cNMP; 1.
SWART; SM00229; RasGEFN; 1.
PROSITE; PS50042; CNMP BINDING 3; 2.
PROSITE; PS50122; RASGEF WIER; 1.
PROSITE; S50121; RASGEF WIER; 1.
                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
56K.15.
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Q8BLC8
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ACCOUNT REPRESENTATION OF THE PROPERTY OF THE

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P. SEQUENCE FROM N.A.

STRINBERISCO NO.?

A Waterston R.;

Waterston R.;

"Direct Submission.";

"Direct Submission.";

"Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

R PIR; 716198; 716198; 716198.

R PIR; 716198; 716198; 716198.

R WormDep; F28B4.2; CE28222.

R GO; GO:0007218; P:granyl-nucleotide exchange factor activity; IEA.

R GO; GO:0007218; P:granyl-nucleotide signaling pathway; IEA.

R GO; GO:000726; P:small GTPase mediated signal transduction; IEA.

R GO; GO:000726; RasGEFN.

R InterPro; IPR0018937; RasGEF.

R InterPro; IPR0018937; RasGEF.

R InterPro; IPR001959; RA_Gomain.
R EMBL; AK045540; BAC32411.1; -.
R GD; MGI:1924777; C030018K18R1K.
R GO; GO:0005085; F:granyl-muclectide exchange factor activity; IEA.
GO; GO:0007264; F:sgranyl-muclectide exchange factor activity; IEA.
GO; GO:0007264; F:sgranyl-muclectide signal transduction; IEA.
InterPro; IPR001478; PDZ.
R InterPro; IPR001478; RasGEFN.
InterPro; IPR000593; Ras GEF.
R Pfam; PF00027; CNMP binding; 1.
R Pfam; PF00027; CNMP binding; 1.
R Pfam; PF00018; PDZ; 1.
R SMART; SM00100; CNMP; 1.
R SMART; SM00229; RasGEFN; 1.
R PROSITE; PS50042; CNMP BINDING 3; 2.
R PROSITE; PS50104; PDZ; 1.
R RNGITE; PS50104; PDZ; 1.
R PROSITE; PS50104; PDZ; 1.
R PROSITE; PS50104; PDZ; 1.
R PROSITE; PS50105;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 657;
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0
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MEDLINE=99069613; PubMed=9851916;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A INOUYE S., Jain R., Ueki T., Nariya H., Xu C., Hsu M.,

A Munoz-Dorado J., Farez-Vidal E., Inouye M.;

Their Coractence Analysis of 13 Eukaryotic-like Protein Ser/Thr Kinases of

Their Coexistence with Protein His Kinases.";

Their Coexistence with Protein His Kinases.";

RMBL, ARIS961; AAD42856.1; Coexistence of EMBL/GenBank/DDBJ databases.

EMBL, ARIS961; AAD42856.1; DBA.

GO; GO:0004627; F:ATP binding; IEA.

GO; GO:0004627; F:Protein Rinase activity; IEA.

GO; GO:0004627; F:Protein amino acid phosphorylation; IEA.

BR GO; GO:000468; P:Protein amino acid phosphorylation; IEA.

GO; GO:0016740; F:ransferase activity; IEA.

GO; GO:0016740; F:ransferase activity; IEA.

BR GO; GO:00165140; F:RT-like.

BR Fian; Profool 19 Prote kinase; 1.

BR Fian; Profool 19 Prote kinase; 1.

BR Profon; DBO00001; Prote kinase; 1.

BR PROSITE; PSO0107; PROTEIN KINASE ATP; 1.

BR PROSITE; PSO0117; PROTEIN KINASE DOM; 1.

KW ATP-binding; Kinase; Transferase.

SEQUENCE 1049 AA; 114313 MW; 7752862DAA25338C CRC64;
                          Myxococcus xanthus.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
NCBI_TaxID=34;
  Serine/threonine kinase PKN8
                                                                                                                                                             SEQUENCE FROM N.A.
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Q8LJJ7;
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Miyagi Y., Yamashita T., Okuda K., Mishina M., Kawamoto S.;
"Delphilin: A novel PDZ-containing protein associates with the GluR-
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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85.7%; Pred. No. 3.1e+02;
ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                            87.1%; Score 27; DB 5; Length 860; 100.0%; Pred. No. 2.6e+02; vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delta? subunit.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-! SINILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL, AF099933; AAG31020.1; -. HSSP; P29476; 10AV.
                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 860 AA; 96122 MW; 16088524FBC65CAS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TYEMBLrel. 16, Created)
01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-CGT-2003 (TYEMBLrel. 25, Last annotation update)
Glubr-delta2 philic-protein.
GRIDZIP OR DELPHILIN.
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Last sequence update)
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GO; GO:0019717; C:synaptosome; IDA.
GO; GO:0005515; F:prorein binding; IPI.
InterPro; IPR003104; FH2.
InterPro; IPR001478; PDZ.
                                                                                                                                   PROSITE; PS50200; RA; 1.
PROSITE; PS00720; RASGEF; 1.
PROSITE; PS50009; RASGEF_CAT; 1.
PROSITE; PS50212; RASGEF_NTER; 1.
Pfam; PF00788; RA; 1.
Pfam; PF00617; RasGEF; 1.
Pfam; PF00618; RasGEFN; 1.
SMART; SM00314; RA; 1.
SMART; SM00147; RasGEF; 1.
SMART; SM00229; RasGEFN; 1.
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01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
01-OCT-2003 (TrEMBLrel, 25,
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
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Pfam; PF00595; PDZ; 1.
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SMART; SM00228; PDZ; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  668 MSTRAS 673
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                                                                                                                                                                                                                                                                                                                                                                                     2 MSTRAS 7
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                                                                                                                                                                                                                                                                                                 Query Match
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COPESJ5
AC COPESJ5
DT 01-MAR.
DT 01-MAR.
DT 01-OCT.
DE GIURALYOR
OC BURATYOR
OC MAMMENTYOR
OC MAMMENTY
OC STRAIN=
RA MIYABI
RA GOLGO
C - 1- CAMPENTY
OC GOL
OC G
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Q9XBP6
ID Q9XBP
AC Q9XBP
DT 01-NO
DT 01-OC
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Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza; O
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EMBL, AP003227; BAC06232.1; -.
Gramene; OBLJJ7; -.
Gramene; OBLJJ7; -.
GO; GO:000785; C:chromatin; IEA.
GO; GO:0008026; F:ATP binding; IEA.
GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0016787; F:chromatin binding; IEA.
GO; GO:0006333; P:chromatin assembly/disassembly; IEA.
GO; GO:0006333; P:regulation of transcription, DNA-dependent; IEA.
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STRAINECY. Nipponbare;
Saski T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
87.1%; Score 27; DB 2; Length 1049;
85.7%; Pred. No. 3.2e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative chromodomain-helicase-DNA-binding protein.
P0016C10.33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1141 AA.
                                                                                        Local Similarity 85.7
nes 6, Conservative
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GO; GO:0003682; F:chro
GO; GO:0016787; F:hydr
GO; GO:0006333; P:chro
GO; GO:0006355; P:regu
InterPro; IPR000953; C
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MEDLINE=21396508; PubMed=11481431;
MEDLINE=21396508; PubMed=11481431;
MEDLINE=21396508; PubMed=11481431;
MEDLINE=21396508; PubMed=11481431;
Median S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb psymm megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.SA. 98:9889-9894(2001).

FIREL, AL603643; CAC48909.1; -.
PIRE, E55905; E55905.

GO, GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid; Hypothetical protein; Complete proteome.

SEQUENCE 112 AA; 11488 MW; 95FD54B0FC5CA90E CRC64;
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                 Query Match 87.1%; Score 27; DB 10; Length 1141; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein RB0509.
Rhizobium mellioti (Sinorhizobium mellioti).
Rhamid psymB (megaplasmid 2).
Bacteria: Proteobacteria: Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBL TaxID=382;
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IPR001410; DEAD.
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Q92W36
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Search completed: September 30, 2004, 05:59:28 Job time: 29.065 secs

1 LMSTRAS 7 : | | | | | | | 5 IMSTRSS 11

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GenCore version 5.1.6'
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                              Run on:
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September 30, 2004, 05:55:56; Search time 34.1695 Seconds (without alignments) 57.883 Million cell updates/sec US-09-674-716B-5 31 1 LMSTRAS 7 Title: Perfect score: Sequence:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|                          |       | æ     |        |     | SUMMERIES |                    |
|--------------------------|-------|-------|--------|-----|-----------|--------------------|
| Result<br>No.            | Score | تر زہ | Length | DB  | ΩI        | Description        |
| )<br>  ++ <br> <br> <br> | 31    | 100.0 | 7      | N   | AAW39825  | Aaw39825 Light cha |
| 71                       | 31    | 100.0 | 7      | N   | AAW39822  | Aaw39822 Light cha |
| М                        |       | 100.0 | 7      | 0   | AAW39819  | 9 Light            |
| 4                        | 31    | 100.0 | 7      | m   | AAY32255  | Aay32255 Light cha |
| Ŋ                        |       | 100.0 | 100    | 4   | AAE06969  | σ.                 |
| φ                        | 31    | 100.0 | 113    | α   | AAW39803  | Varia              |
| 7                        | 31    | 100.0 | 113    | (1  | AAW39886  | Aaw39886 Light cha |
| œ                        | .31   | 100.0 | 113    | N   | AAW39802  | Aaw39802 Variable  |
| o                        |       | 100.0 | 113    | ~   | AAW39882  | Aaw39882 Light cha |
| 10                       | 31    | 100.0 | 113    | (1  | AAW39804  | Aaw39804 Variable  |
| 11                       | 31    | 100.0 | 116    | ო   | AAY32262  | Aay32262 Humanised |
| 12                       | 31    | 100.0 | 145    | m   | AAY32261  | Mouse              |
| 13                       | 28    | 90.3  | 7      | 7   | AAW39816  | Aaw39816 Light cha |
| 14                       | 28    |       | 113    | 7   | AAW39801  | Aaw39801 Variable  |
| 15                       | 28    | 90.3  | 274    | N   | AAW39899  | Aaw39899 Single ch |
| 16                       | 28    | 90.3  | 979    | 7   | ADB64292  | Adb64292 Human pro |
| 17                       | 27    | 87.1  | 7      | N   | AAW39876  | Aaw39876 Light cha |
| 18                       | 27    | 87.1  | 68     | 4   | AAU64213  |                    |
| 19                       | 27    | 87.1  | 9      | 9   | ABM60732  | Abm60732 Propionib |
| 20                       | 27    | 7     | 119    | 9   | ABU00425  | Abu00425 Human nov |
| 21                       | 27    | 87.1  | 123    | 4   | AAU54742  | 42                 |
| 22                       | 27    | 87.1  | 123    | v   | ABM51261  | Abm51261 Propionib |
| 23                       | 27    | 87.1  | 131    | N   | AAR12232  | 32                 |
| 24                       | 27    | 87.1  | 'n     | (7) | AAR12354  | Aar12354 Light (ka |
| 25                       | 27    | 87.1  | 140    | 41  | AAM95756  | Aam95756 Human rep |
|                          |       |       |        |     |           |                    |

| Abg77402 Selected | Abj11304 Yeast sel | Ç,       | Abb52717 Escherich | Abp73372 Candida a |          | æ        | 7        |          | Abb33078 Peptide # |          | Abb27906 Human pep | Abb18546 Protein # | Aam66263 Human bon | Human    | Abg47927 Human liv | Aam01871 Peptide # | Abg35910 Human pep | Adb64310 Human pro | Abg10627 Novel hum |
|-------------------|--------------------|----------|--------------------|--------------------|----------|----------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ABG77402          | ABJ11304           | ABU26357 | ABB52717           |                    | ABR53640 | AAU39838 | ABM36357 | AAM14133 | ABB33078           | AAM26539 | ABB27906           | ABB18546           | AAM66263           | AAM53875 | ABG47927           | AAM01871           | ABG35910           | ADB64310           | ABG10627           |
| 218 5             | 218 5              |          | 409 4              |                    | _        | 77 4     | 77 6     | 115 4    | 115 4              | 115 4    | 115 4              | 115 4              | 115 4              | 115 4    | 115 4              | ·                  | 115 5              |                    | 134 4              |
| 87.1              | 87.1               | 87.1     | 7.1                | 7.1                | 7.1      | 83.9     | 83.9     | 83.9     | m                  | 83.9     | 83.9               | 83.9               | 83.9               | 83.9     | m                  | m                  |                    | 83.9               | 83.9               |
| 27                | 27                 | 27       | 27                 | 27                 | 27       |          | 26       | 56       | 26                 | 26       | 26                 | 26                 | 26                 | 26       | 56                 | 26                 | 26                 | 26                 | 56                 |
| 26                | 27                 | 28       | 53                 | 30                 | 31       | 32       | 33       | 34       | 35                 | 36       | 3:7                | 38                 | 33                 | 40       | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

Light chain CDR2 of catalytic antibody 12H1 AAW39825 standard; peptide; 7 AA. (first entry) 16-JUN-1998 AAW39825; 

Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.

WO9749800-A1. 31-DEC-1997. Mus sp.

97WO-US010965. 96US-00672345. 25-JUN-1997; 25-JUN-1996;

Landry DW;

(UYCO ) UNIV COLUMBIA NEW YORK

WPI; 1998-077166/07.

New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.

Claim 17; Page 83; 147pp; English.

AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transitions state analogues (TSAs) were prepared and used to immunise mince for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of O.16. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)

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Query Match

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Best Loc Matches

8

RESULT 2 AAW39822

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AAW39918-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                                                                                                                                   Light chain CDR2 of catalytic antibody 6A12.
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                    standard; peptide; 7 AA
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Matches 7; Conservative
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                    AAW39819
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  4AW39819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                       Gaps
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                                         100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06;
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                                                                                Indels
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                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                           AAW39822 standard; peptide; 7 AA
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overdose; addiction
                                                           Local Similarity
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Sequence 7 AA;
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Length 7; 0; Indels us-09-674-716b-5.open.rag

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This sequence represents complementarity determinating region 2 (CDR L2) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody Cl1 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain CDRs (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 commation for treatment of arthibitis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriaatis, uriticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, soppered syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, thinitis, eczema, graft vereuss-host disease, (CDP), insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various
inflammation, arthritis; lupus erythematosus; multiple sclerosis; tashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulomephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 40; 81pp; English
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                                                                                                                                                                       Mus musculus.
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Crowe SJ, Ellis JH, Rapson NT, Shearin J;

GROUP LID

99WO-GB001434. 98GB-00009839.

ö Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; Gaps ; 0 Mouse germline kappa light chain variable (VK) region, 167/24. 100.0%; Score 31; DB 3; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels AAE06969 standard; protein; 100 AA. (first entry) Query Match Best Local Similarity 100... 1 LMSTRAS 7 16-OCT-2001 AAE06969; 

Variable domain; lambda light chain; catalytic antibody; degradation;

Variable domain of the Kappa light chain of catalytic antibody 12H1.

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The patent discloses a humanised antibody or its antigen-binding CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting reference of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting always contraction of a cell expressing CCR2. They are useful for inhibiting always disorder, autoimmune CC are useful for inhibiting newtone in the proteins of the catherogenesis and atherosclerosis, and for inhibiting restenosis.

CCR2.mediated disorders such as inflammatory disorder, autoimmune at therogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in thermatory or diagnosis, and in the manufacture of a creating allergy, anaphylaxis, melignancy chronic and acute continuation, histamine and IgB- mediated allergic reaction, shock, inflammation, histamine and IgB- mediated allergic reaction, shock, stenosis, allografat rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal, thumanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting continual hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa
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multiple sclerosis, atherogenesis, atherosclerosis, restenosis, asthma; anaphylaxis, malignancy, inflammation; stenosis; allograft rejection; librotic disease, angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized immunoglobulin for treating a CC-chemokine receptor 2-media disorder in a patient, comprises a binding specificity for CCR2, and non-human antigen binding region and human immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                 O'brien S,
                                                                                                                                                                                                                                                                                                                                                                                                 Newman W, Jones ST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 151; 183pp; English
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                                                                                                                                                                                                                                                                  02-FEB-2001; 2001WO-US003537.
                                                                                                                                                                                                                                                                                                                03-FEB-2000; 2000US-00497625.
                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
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Best Local Similarity
7; Conserve
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cocaine;

96US-00672345,

25-JUN-1996;

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The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The matibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                  New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                               Disclosure; Fig 19; 147pp; English
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                                       (UYCO ) UNIV COLUMBIA NEW YORK.
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Best Local Similarity
7; Conserva
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                                                                             Landry DW;
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                                                                                                                                                                                                                                                                                                                                                                                       New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Kappa light chain of catalytic antibodies which are able to degrade occasine. As series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas (Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAM39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used partitularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW39801-05 represent the amino acid sequences of the variable domain of
e; cocaine transition state analogue; TSA; benzoic acid; cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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Pred. No. 12;
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                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
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Matches 7; Conservative
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                                   overdose; addiction
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                                                                             Gaps
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100.0%; Score 31; DB 2; Length 113; 100.0%; Pred. No. 12;
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RESULT 7 AAW39886

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0; Mismatches

Query Match
Best Local Similarity 100.
Matches 7; Conservative

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100.0%; Score 31; DB 2; Length 113; 100.0%; Pred. No. 12;

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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAS) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The AAL2 antibody (AAW39807 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody (AL2 has a per minute Koat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                           100.0%; Score 31; DB 2; Length 113; 100.0%; Pred. No. 12; 0; Indels ive 0; Mismatches 0; Indels
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Matches 7; Conservative
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Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

overdose; addiction

WO9749800-A1.

Mus sp.

31-DEC-1997.

25-JUN-1997;

COLUMBIA NEW YORK. 96US-00672345. 97WO-US010965.

(UYCO ) UNIV 25-JUN-1996;

Landry DW;

Variable domain of the Kappa light chain of catalytic antibody 2A10.

(first entry)

16-JUN-1998

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Gaps . 0

AAW39804;

AAW39804 standard; protein; 113 AA

AAW39804

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                                                                                                                                                                                                                                                                                                                                                                                                                            New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 73-74; 147pp; English.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-077166/07.
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RESULT 11 AAY32262

The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalyfic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for the treating addiction (by reducing the in vivo concentration that can be

Sequence 113 AA;

achieved

WO9958679-A1.

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CD23; PCERII; IgE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; signature collitis; eczema; insultis; graft.versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
                                                                                                                                                                                                                                                                                         Humanised anti-CD23 MAb C11 light chain variable region.
standard; protein; 116 AA
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                           15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy.
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/note= "CDR 3" 103. 113 /note= "framework region 4" "framework region 1" "framework region 2" <del>-</del> Location/Qualifiers 1. .23 /note= "framework re .. .93 .te= "framework r "CDR 1" "CDR 2" 39 . 54 .61 'note= 'note= note= 'note= sapiens Synthetic Key Region Region Region Region Region Region Ношо

99WO-GB001434. 98GB-00009839 07-MAY-1999; 09-MAY-1998; 18-NCV-1999

Location/Qualifiers

Mus musculus

.70 --- "CDR L1"

Region Region Region

/note= "( 83. .92

/note= "CDR L2" 125. .134 /note= "CDR L3"

WO9958679-A1

99WO-GB001434. 98GB-00009839

07-MAY-1999; 09-MAY-1998;

18-NOV-1999

(GLAX ) GLAXO GROUP LTD.

Shearin J; Rapson NT, Ellis JH, Crowe SJ, Bonnefoy JMP,

WPI; 2000-053101/04. N-PSDB; AAZ34747.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 9; Fig 3; 81pp; English.

This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGKVII) and the light chain complementarity determining regions (see AAY22254-56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprises sufficient of the amino clid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple arthritis, lupus erythematosus, dermatitis, psoriasis, utcitaria, nephrotic solutome, glomerulonebritis, inflammatory bowel disease, ulcerative collitis, Crohn's disease, Sjogran's syndrome, allergies, allergic asthma, intrinsic asthma, grute asthmatic exacerbation, rhinitis, eczema, graft-

This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAY32263 and AAY32263), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 8; Fig 2; 81pp; English.

Shearin J;

Ellis JH, Rapson NT,

Crowe SJ,

Bonnefoy JMP,

WPI; 2000-053101/04.

N-PSDB; AAZ34746

(GLAX ) GLAXO GROUP LTD

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versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell mailgrancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                          CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
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                                                                                         Query Match 100.0%; Score 31; DB 3; Length 116; Best Local Similarity 100.0%; Pred. No. 13; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Mouse anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                                                                                        AAY32261 standard; protein; 145 AA.
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                                                                 Sequence 116 AA;
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90.3%; Score 28; DB 2; Length 7; 85.7%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels

Query Match
Best Local Similarity 85.7
Matches 6; Conservative

Sequence 7 AA;

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1 LMSTRAS 7 |||||:| LMSTRSS

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type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermaitis, psoriasis, uritoaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogren's syndrome, allergies, allergies, allergies intrinsic asthma, acute asthmatic exacebation, rhinitis, eczema, graftversus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes) and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW39815-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 3B9, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified using TSAI, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treatment of an overdose. They are also used achieved)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain CDR2 of catalytic antibody 3B9.
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overdose; addiction.
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                                                                                                                                                                                                                                                       Sequence 145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a postpate monoseter transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overciose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
                                                                                                                                             Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                Variable domain of the Kappa light chain of catalytic antibody 3B9.
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Pred. No. 65;
1; Mismatches 0; Indels
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                AAW39801 standard; protein; 113 AA.
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                                                                                                                                                                                                                                                                                                                                        97WO-US010965.
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85.7%;
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P-PSDB; AAV09791.
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AAW39899 standard; protein; 274 AA.

RESULT 15 AAW39899 ID AAW3

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The present sequence represents the single chain Fv region of the monoclonal catalytic antibody 3B9, which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAS) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                   'note= "complementarity determining region 1 of the heavy
                                                                                                                                                                                                                                                                                                 /note= "complementarity determining region 3 of the heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "complementarity determining region 3 of the light
                                                                                      Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                Single chain Fv region of the catalytic antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain"
259. 263
/note= "Flag epitope sequence"
                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                120. .134
/note= "linker"
159. .174
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Sequence 274 AA;

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Gaps
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Score 28; DB 2; Length 274;
Pred. No. 1.7e+02;
1; Mismatches 0; Indels
  Query Match 90.3%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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186 LMSTRSS 192
                                                         1 LMSTRAS 7
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Search completed: September 30, 2004, 06:06:12 Job time : 37.1695 secs

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SEQ ID NO 23
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Sequence 26, Appl
Sequence 22, Appl
Sequence 32, Appl
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Sequence 32, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 104, Appli
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Sequence 12, Appli
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19.178 Million cell updates/sec
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(GGNIZ_6/PLOCATEAL/I/pubpaa/USO7 PUBCOWB.pep:*

(GGNIZ_6/PLOCATEAL/I/pubpaa/USO7 NEW PUB.pep:*

(GGNIZ_6/PLOCATEAL/I/pubpaa/USO6 PUBCOWB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-840-459-32

6 US-10-766-773-32

6 US-10-766-773-32

6 US-10-766-773-32

6 US-10-756-610-32

6 US-10-756-610-32

10S-09-940-727B-7

1 US-09-940-727B-104

US-09-940-727B-104

US-09-940-727B-104

US-09-940-727B-108

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US-09-940-727B-112
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                                                                                                                                                                                                                                        September 30, 2004, 06:01:30
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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App 2 8 90.3 113 10 US-09-9940-727B-100 Sequence 10.) App 2 8 90.3 276 12 US-10-425-114-49630 Sequence 49630, 28 90.3 276 12 US-10-329-119 Sequence 2914, 4 1 1 0 US-09-940-727B-109 Sequence 2914, 4 1 1 0 US-09-940-727B-80 Sequence 2914, 4 1 1 1 0 US-09-940-727B-80 Sequence 2914, 4 1 1 1 1 0 US-09-940-727B-80 Sequence 2914, 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 28 90.3 113 10 US-09-940-727B-100 Sequence 5. App 2 90.3 276 12 US-10-425-114-49630 Sequence 100. App 2 8 90.3 276 12 US-10-425-114-49630 Sequence 100. App 2 8 90.3 276 12 US-10-425-114-49630 Sequence 100. App 2 8 90.3 276 12 US-10-369-940-277B-109 Sequence 291. App 2 8 90.3 40.7 15 US-10-369-949-291 Sequence 291. App 2 8 7.1 10 US-09-940-777B-80 Sequence 291. App 2 8 7.1 10 US-09-940-777B-80 Sequence 2446, App 2 1 1 140 10 US-09-764-891-4414 Sequence 1986. App 2 1 1 140 10 US-09-764-891-4414 Sequence 4414, App 2 1 1 140 10 US-09-764-891-4414 Sequence 2256. App 2 1 1 141 16 US-10-32-256. Sequence 2256. 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App 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 28 90.3 113 10 US-99-940-127B-15 Sequence 5, App 29 90.3 113 10 US-09-940-127B-15 Sequence 10.0, App 29 90.3 276 10 US-09-940-127B-100 Sequence 10.0, App 28 90.3 276 10 US-10-425-114-49630 Sequence 10.0, App 28 90.3 276 10 US-09-940-127B-119 Sequence 291, App 28 90.3 979 15 US-10-104-047-2446 Sequence 291, App 27 87.1 140 10 US-09-940-127B-80 Sequence 291, App 27 87.1 140 10 US-09-940-127B-80 Sequence 291, App 27 87.1 140 10 US-09-940-127B-80 Sequence 291, App 27 87.1 140 10 US-09-940-128-128-18627 Sequence 291, App 14 US-10-169-493-1985 Sequence 291, App 14 US-10-169-493-1885 Sequence 291, App 14 US-10-169-493-1885 Sequence 291, App 14 US-10-189-493-1887 Sequence 291, App 15 US-09-940-198-18 Sequence 201, App 17 US-10-189-493-1987 Sequence 210683, App 220 15 US-10-139-794-201 Sequence 2107, App 28 83.9 133 15 US-10-139-794-81 Sequence 211, App 28 83.9 248 15 US-10-139-794-81 Sequence 211, App 28 83.9 248 15 US-10-139-794-81 Sequence 211, App 28 83.9 248 16 US-10-139-794-81 Sequence 211, App 28 83.9 248 16 US-10-139-794-81 Sequence 211, App 28 83.9 344 16 US-10-139-794-81 Sequence 211, App 28 83.9 344 16 US-10-139-794-81 Sequence 215, App 28 83.9 344 16 US-10-139-794-81 Sequence 216, App 28 83.9 344 16 US-10-139-794-81 Sequenc | 28 90.3 113 10 US-09-940-727B-100 Sequence 10.) App 2 90.3 276 12 US-10-425-114-49630 Sequence 10.0, App 2 8 90.3 276 12 US-10-425-114-49630 Sequence 49630, 28 90.3 276 12 US-10-329-109 Sequence 2914 App 2 8 90.3 40.7 10 US-09-940-727B-109 Sequence 2914 App 2 8 90.3 40.7 10 US-09-940-727B-80 Sequence 2914 App 2 8 90.3 979 15 US-10-104-047-2446 Sequence 2914 App 2 8 91.1 140 US-10-229-19862 Sequence 2914 App 2 8 91.1 140 US-10-329-19862 Sequence 2914 App 2 8 91.1 40 US-10-38-978-483 Sequence 4414 App 2 12 US-10-38-978-483 Sequence 4414 App 2 12 US-10-38-978-483 Sequence 22564, 27 87.1 845 15 US-10-38-978-835 Sequence 22564, 27 87.1 140 US-10-38-978-431 Sequence 22564, 27 87.1 140 US-10-38-978-431 Sequence 106973 Sequence 2264, 28 83.9 133 15 US-10-447-2464 Sequence 2264, 28 83.9 226 15 US-10-36-423-177 Sequence 244, 27 8 91.1 140 US-10-36-423-177 Sequence 246, 27 8 91.1 140 US-10-36-423-177 Sequence 246, 28 91.1 140 US-10-36-423-177 Sequence 246, 28 91.1 140 US-10-36-423-177 Sequence 24, 24 9 9 226 US-10-39-943-217 Sequence 24, 24 9 0 US-08-08-124 Sequence 24, 24 9 0 US-08-98-26-36-36-36-36-36-36-36-36-36-36-36-36-36 | 28 90.3 113 10 US-09-940-727B-100 Sequence 10.) App 2 90.3 113 10 US-09-940-727B-100 Sequence 10.0 App 2 90.3 276 12 US-10-425-114-49630 Sequence 10.0 App 2 90.3 276 12 US-10-425-114-49630 Sequence 10.0 App 2 90.3 276 12 US-10-369-940-272B-119 Sequence 291, App 2 90.3 40.7 10 US-09-940-727B-10 Sequence 291, App 2 90.3 979 15 US-10-104-047-2446 Sequence 291, App 2 90.3 979 15 US-10-104-047-2446 Sequence 291, App 2 90.3 979 15 US-10-104-047-2446 Sequence 10.0 App 2 90.3 979 15 US-10-104-104-104 Sequence 291, App 2 90.3 979 15 US-10-369-9493-2256 Sequence 2556, App 2 90.3 979 15 US-10-369-9493-2256 Sequence 2556, App 2 90.3 970 15 US-10-369-493-2256 Sequence 2556, App 2 90.3 970 15 US-10-369-493-2256 Sequence 2556, App 2 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 | 28 90.3 113 10 US-09-940-127B-15 Sequence 5. App<br>28 90.3 276 10 US-10-425-114-49630 Sequence 10.0, App<br>28 90.3 276 10 US-10-425-114-49630 Sequence 10.0, App<br>28 90.3 276 10 US-09-940-127B-119 Sequence 211, App<br>28 90.3 407 15 US-10-104-047-244 Sequence 211, App<br>29 90.3 979 15 US-10-104-047-244 Sequence 211, App<br>20 90.3 979 15 US-10-104-047-244 Sequence 211, App<br>20 87.1 140 10 US-09-940-127B-80 Sequence 214, App<br>21 87.1 140 10 US-09-044-414 Sequence 1414, App<br>22 87.1 140 10 US-09-044-139-19627 Sequence 1414, App<br>23 87.1 140 10 US-10-32-3254 Sequence 1414, App<br>24 87.1 141 15 US-10-32-385-7209 Sequence 217, App<br>25 83.9 133 15 9 US-10-369-433-1487 Sequence 217, App<br>26 83.9 220 15 US-10-139-944-81 Sequence 217, App<br>26 83.9 220 15 US-10-139-944-81 Sequence 110408<br>26 83.9 244 15 US-10-139-944-81 Sequence 1514, App<br>26 83.9 347 16 US-10-139-194-81 Sequence 1514, App<br>27 87.1 140 US-10-139-948-81 Sequence 1514, App<br>28 83.9 347 16 US-10-139-948-81 Sequence 1514, App<br>29 25 83.9 347 16 US-10-139-194-81 Sequence 1514, App<br>20 14 US-10-1468-031-1844 Sequence 1514, App<br>20 15 US-10-139-948-81 Sequence 246, App<br>21 83.9 344 14 US-10-106-688-636, Sequence 1514, App<br>22 83.9 441 14 US-10-106-688-636, Sequence 1514, App<br>24 83.9 441 14 US-10-106-688-636, Sequence 247, App<br>25 83.9 441 14 US-10-106-688-636, Sequence 110409<br>26 83.9 611 12 US-10-424-599-204138 Sequence 241, App | 28 90.3 113 10 US-99940-727B-100 Sequence 10.) App 2 8 90.3 276 12 US-10-425-114-49630 Sequence 10.0, App 2 8 90.3 276 12 US-10-425-114-49630 Sequence 49630, 28 90.3 276 12 US-10-329-190 Sequence 29146, 28 90.3 40.7 10 US-09-940-727B-109 Sequence 29146, 28 90.3 40.7 15 US-10-104-047-2446 Sequence 29146, 29 80.3 979 15 US-10-104-047-2446 Sequence 29146, 29 87.1 10 US-09-940-27B-80 Sequence 29146, 29 87.1 140 10 US-09-764-991-9827 Sequence 4414, 29 87.1 140 10 US-09-764-991-9827 Sequence 4414, 29 87.1 140 10 US-10-38-975-835 Sequence 4414, 29 87.1 140 10 US-10-38-975-835 Sequence 22564, 29 87.1 140 15 US-10-36-493-1087 Sequence 22564, 29 87.1 140 15 US-10-36-493-107 Sequence 106973 Sequence 2464, 29 87.1 140 15 US-10-36-493-177 Sequence 106973 Sequence 2464, 29 87.1 140 15 US-10-36-493-177 Sequence 2464, 20 87.1 140 15 US-10-36-493-177 Sequence 2464, 20 87.1 140 15 US-10-39-94-8 Sequence 2464, 20 87.1 140 15 US-10-39-94-8 Sequence 27.1 Apr 26 87.1 140 US-10-38-97-94-8 Sequence 24, Apr 26 83.9 364 16 US-10-47-563-1364 Sequence 24, Apr 26 83.9 44.1 14 US-10-38-97-94-8 Sequence 24, Apr 26 83.9 44.1 14 US-10-47-563-1364 Sequence 24, Apr 26 83.9 44.1 14 US-10-44-593-204138 Sequence 60058, Apr 26 83.9 44.1 14 US-10-44-59 | 28 90.3 113 10 US-09-940-727B-100 Sequence 10.) App 2 8 90.3 113 10 US-09-940-727B-100 Sequence 49630, 28 90.3 276 12 US-10-425-114-49630 Sequence 49630, 28 90.3 276 12 US-10-329-140 Sequence 2915, 49 12 US-10-369-493-291 Sequence 2917, 49 15 US-10-369-493-291 Sequence 2917, 49 17 10 US-09-764-891-4414 Sequence 2917, 40 10 US-09-764-891-4414 Sequence 4414, 40 10 US-09-764-891-4414 Sequence 4414, 40 10 US-09-764-891-4414 Sequence 2554, 40 10 US-09-764-891-4914 Sequence 2554, 40 10 US-09-764-991-4914 Sequence 2554, 40 10 US-09-493-2177 Sequence 106873 Sequence 2564, 40 10 US-09-493-2177 Sequence 2564, 40 10 US-09-493-2177 Sequence 2564, 40 10 US-09-493-2177 Sequence 24, 40 10 US-09-493-2174 Sequence 24, 40 10 US-09-493-2110409 Sequence 26, 40 10 US-09-493-2110409 Sequence 26, 40 10 US-09-493-2110409 Sequence 28, 40 10 US |

## AL IGNMENTS

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; Sequence 23, Application US/09940727B
; Publication No. USZ0030077733A1
; GRERAL INFORMATION:
    APPLICANT: Landry, Donald W
    TITLE OF INFORMATION:
    CURRENT LEADER, DOTO-B
    CURRENT APPLICATION NUMBER: US/09/940,727B
    CURRENT APPLICATION NUMBER: US/09/04
; PRIOR PLILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: O9/214,095
; PRIOR PLILING DATE: 1996-06-25
; PRIOR PLILING DATE: 09/672,345
; PRIOR PRIOR PLILING DATE: 09/672,345
; PRIOR PLILING
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Best Local Similarity 100.0%; Score 31; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels
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APPLICANT: LARORAGIO.

APPLICANT: LARORAGIO.

APPLICANT: Newmann. Christopher

APPLICANT: Newmann. Walter

APPLICANT: O'Erien, Siobhan H.

APPLICANT: O'Erien, Siobhan H.

APPLICANT: O'Reien, Siobhan H.

APPLICANT: O'Reien, Siobhan H.

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: HUMANIZED & O'SE THEREFOR

TITLE OF INVENTION: HUMANIZED & O'SE THEREFOR

TITLE OF INVENTION: HUMBER: US/10/766,773

CURRENT FILING DATE: 2004-01-27

FRIOR FILING DATE: 1999-07-23

PRIOR PILING DATE: 1998-07-23

PRIOR FILING DATE: 1998-07-23

FRIOR FILING DATE: 1098-07-23

ITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1852.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US/09/840,459
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR PILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FSLSEQ for Windows Version 3.0
SEQ ID NO 3.2
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/10766773 Publication No. US20040126851A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100..
Fines 7; Conservative
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ORGANISM: Mus musculus
US-09-840-459-32
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US-10-766-610-32
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Sequence 29, Application US/09940727B

Publication No US20030077793A1

GENERAL INPORMATION:

APPLICANT: Landry, Donald W

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: 09/214,095

PRIOR FILING DATE: 1998-1-2

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR FILING DATE: 1998-1-25

PRIOR FILING DATE: 1998-1-25

PRIOR FILING DATE: 1998-06-25

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.1

LENGTH: 7
         APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 057551400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 07/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR APPLICATION NUMBER: 1997-06-25
PRIOR APPLICATION NUMBER: 09/672,345
PRIOR APPLICATION NUMBER: 09/6-06
SOFTWARE: PatentIn Version 3.1
SSQ ID NO 26
SSQ ID NO 26
SSQ ID NO 26
SEMBLE 27
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Sequence 3.2, Application US/09840459
Patent No. US20020150576A1
APPLICANT: LAROSA, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Reide, S. Tarran
APPLICANT: O'Reide, S. Torran
APPLICANT: O'Reide, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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; ORGANISM: mouse
US-09-940-727B-29
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US-09-840-459-32
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Query Match 100.0%; Score 31; DB 10; Length 113; Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches 0; Indels (
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Sequence 6, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICAMT: Landry, Donald W
ITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 1996-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR PILING DATE: 1996-12-28
PRIOR FILING DATE: 1996-12-8
PRIOR FILING DATE: 1996-06-25
NUMBER: OS FOLD NOS: 121
SOFTWARE: PATENTH VERENCE NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1996-06-25
NUMBER: OS FOLD NOS: 121
SOFTWARE: PATENTH VERENCE NOS: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09940727B; Bublication No. US20030077793A1; Publication No. US20030077793A1; Publication No. US20030077793A1; APPLICANT: Landry, Donald W TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY; TLE REFERENCE: 0575/54400-B; CURRENT APPLICATION NUMBER: US/09/940,727B; CURRENT FILING DATE: 1998-12-28; PRIOR APPLICATION NUMBER: 09/214,095; PRIOR FILING DATE: 1998-12-28; PRIOR APPLICATION NUMBER: PCT/US97/10965; PRIOR APPLICATION NUMBER: 08/672,345; PRIOR PLING DATE: 1996-06-25; PRIOR PLING DATE: 1996-06-25; NUMBER OF SEQ ID NOS: 121; SEQ ID NO 7; LENGTH: 113
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Matches 7; Conservative
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; ORGANISM: mouse
US-09-940-727B-6
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                                           APPLICANT: HOTVALL, CHITCOLLY, APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/10/766,610
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: OS/40,459
PRIOR APPLICATION NUMBER: OS/40,459
PRIOR PLING DATE: 2001-02-03
PRIOR PLING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FREESEQ for Windows Version 3.0
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i Sequence 32, Application US/10733563

i Publication No. US20040151721A1

i GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
APPLICANT: Ponath, Paul
ITILE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
ITILE OF INVENTION: HERABLE OF USE THEREOF
FILE REFRENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-10-17
SPRIOR FILING DATE: 2003-10-19
SPRIOR PRIOR PR
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100.0%; Pred. No.
LaRosa, Gregory J.
Horvath, Christopher
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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; ORGANISM: Mus musculus
US-10-733-563-32
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03-09-940-727B-8

Sequence 8, Application US/09940727B

Publication No. US20030077793A1

GENERAL INFORMATION:

APPLICANT: LANGEY, Donald W

IITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
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Sequence 191879, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: AFOST Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREMENTS: 38-21 (5223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191879
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PUBLICACTION NO. US20030077793A1

GENERAL INFORMATION:
APPLICANT: Landry, Donald W

TITLE OF INTERNION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR APPLICATION NUMBER: 08/672,345

PRIOR APPLICATION NUMBER: 08/672,345

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PATCHIN VERSION 3.1
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ORGANISM: Glycine max
ERATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_15287C.1.pep
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
LENGTH: 113
TYPE: PRI
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Best Local Similarity luv...
7; Conservative
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Best Local Similarity luv...
7; Conservative
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US-09-940-727B-112
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i Sequence 104, Application US/09940727B

j Publication No. US20030077793A1

i GENERAL INFORMATION:

APPLICANT: Landry, Donald W

TILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

TILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

TILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

TILE OF INVENTION: 1998-12-03

PRIOR REPRESENCE: 2502-09-04

PRIOR APPLICATION NUMBER: 09/04-05

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1998-06-25

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOCTWARE: PatentIN version 3.1

SEQ ID NO 100

LENGRES CATALORS

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             FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION WURBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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Sequence 108, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
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Matches 7; Conservative
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Best Local Similarity
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                                                 Ouery Match 93.5%; Score 29; DB 12; Length 63; Best Local Similarity 85.7%; Pred. No. 19; Matches 6; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/0994072B
Sequence 20, Application US/0994072B
Publication No. US2003007793A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
CURRENT PELICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 1994-12-28
PRIOR FILING DATE: 1997-10965
PRIOR FILING DATE: 1997-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
SPRIOR FILING DATE: 1996-06-25
SPRIOR FILING DATE: 1996-06-25
SOFTWARE: PALENTION NUMBER: 06/72,345
PRIOR FILING DATE: 1996-06-25
SOFTWARE: PALENTION NUMBER: 06/72,345
PRIOR FILING DATE: 1996-06-25
SOFTWARE: PALENTIN VOISION 3.1
SEQ ID NO 20
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Best Local Similarity 85.7
Matches 6; Conservative
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24 IMSTRAS 30
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US-10-424-599-191879
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US-09-940-727B-20
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Search completed: September 30, 2004, 06:54:51 Job time : 117.458 secs

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Title:

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RESULT 1

US-08-487-550-8

I SAPPLICATION US/08487550

FATEUR NO. 6113898

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,

TITLE OF INVENTION: INTONOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEBE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street.

CITY: Alexandria

STATE: VA

COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: Elb PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: DEAD FOR SOTTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: US/08/487,550
FILING DATE: US/08/487,550
FILING DATE: NJWBER: US/08/487,550
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REPERENCE/POCKET NUMBER: 31,030
REPERENCE/POCKET NUMBER: 012712-131
TELECHONE: 703.836-6620
US-09-920-171-18

US-09-026-949-71

US-09-026-96-71

US-09-121-952A-71

US-09-121-952A-71

US-09-121-952A-71

US-09-121-952A-71

US-09-121-952A-71

US-09-121-952B-14

US-09-109-207C-14

US-09-206-114-16

US-09-206-114-16

US-09-206-114-16

US-09-206-114-16

US-09-206-114-16

US-09-206-114-16

US-09-206-114-17

US-09-206-114-17

US-09-206-114-17

US-09-206-114-17

US-09-406-124-81

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     Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-G=/cgn2_1/USFPC spool_PUSU964716/runat_30092004_070259_25901/app_query.fasta_1.3164
-DB=ISSUEd_PATED_FUSU964716/runat_30092004_070259_25901/app_query.fasta_1.3164
-DB=ISSUEd_PATED_FUSU964716/runat_30092004
-DB=ISSUEd_PATED_FUSU964716/runat_30092004
-LIST=45 -DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -AALIGN=15
-MODE=LOAD_-OTFMT=pto -NOEME=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716_GCRN 1_1107_@runat_30092004_070259_25901 -NOPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NG_SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7
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Sequence 8, Appli
Sequence 8, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 2, Appli
                                                                                                        (without alignments)
4221.672 Million cell updates/sec
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11. /Ggn2_6/ptodate/2/iaa/5A_COMB.pep:*
12. /Ggn2_6/ptodate/2/iaa/5B_COMB.pep:*
33. /Ggn2_6/ptodata/2/iaa/6A_COMB.pep:*
43. /Ggn2_6/ptodata/2/iaa/6B_COMB.pep:*
45. /Ggn2_6/ptodata/2/iaa/PCTUG_COMB.pep:*
6. /Ggn2_6/ptodata/2/iaa/PCTUG_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   - protein search, using frame_plus_n2p model
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US-09-56-090-8
US-08-466-1518-8
US-08-466-1518-8
US-09-802-096-8
US-09-802-096-8
US-09-202-55-2
US-09-054-255-2
US-09-282-605-18
US-09-283-605-18
US-09-283-846-2
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Matches:
Conservative:
Mismatches:
Indels:
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89.76%
LENGTH: 478 amino acids
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TOPOLOGY: linear
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Sequence 8, Application US/09526098;
Sequence 8, Application US/09526098;
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R. APPLICANT: ANGENCE AND TITLE OF INVENTION: "MONNEY WONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF;
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STREET: VA
COUMTRY: USA
STREET: VA
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300 GluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP DC COMPACIBLE
OPERATING SYSTEM: PC-COMPACIBLE
OPERATING SYSTEM: PC-COMPACIBLE
CONFWARE: Patentin Release #1.0, Version #1.30
SOFFWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE: 07-UWA-1995
ATONNEY/AGBRI INFORMATION:
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET UNMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET UNMBER: 012712-131
TELECOMMULCATION:
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1156 AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1215
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280 AspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHis
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Fatent No. 6037453
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITTY: South San Francisco
STATE: California
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94400.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/NS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/466163
APPLICATION NUMBER: 06/401-1995
-- TWO DATE: 06/401-1995
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US-08-466-151-8
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Matches:
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Mismatches:
Indels:
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2161.50
91.29%
89.76%
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-8
                                                                                TYPE: amino acid
TOPOLOGY: linear
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218 ASplyslysValGluProLysSerCysAsplysThrHisThrCysProProCysProAla
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SCANISM: Artificial sequence
PEATURE:
OTHER INFORMATION: humanized maell, version 1 heavy chain
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APPLICANT: Draction, Paula M.; APPLICANT: Draction, Paula M.; APPLICANT: Dresta, Leonard G.; TITLE OF INVENTION: Immunoglobulin Variants FILE REFRENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B; CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/185,899; PRIOR APPLICATION NUMBER: US 08/185,899; PRIOR FILING DATE: 1994-01-26; PRIOR APPLICATION NUMBER: US 07/879,495; PRIOR APPLICATION NUMBER: US 07/879,495; PRIOR APPLICATION NUMBER: US 07/844,768; PRIOR APPLICATION NUMBER: US 07/744,768; PRIOR FILING DATE: 1992-06-07; PRIOR APPLICATION NUMBER: US 07/744,768; PRIOR FILING DATE: 1991-08-14
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Conservative:
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FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
PAPELICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 99,044
REFERRENCE/DOCKET NUMBER: 99,18P2C1D1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SSOURNE GARACTERISTICS:
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92.76%
89.91%
89.46%
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TYPE: Amino Acid
TOPOLOGY: Linear
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Best Local Similarity:
Query Match:
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Pred. No.:
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Conservative:
Mismatches:
Indels:
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2151.50
92.76%
89.91%
89.46%
                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                    Alignment Scores:
Pred. No.:
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Patent No. 668593

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION:

FILLS REFERENCE: P07182510S

CURRENT APPLICATION NUMBER: US/09/802,096

CURRENT PILING DATE: 2001-0.8

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR PILING DATE: 1995-03-15

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-14

PRIOR FILING DATE: 1992-06-14

PRIOR FILING DATE: 1992-06-17

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| 1 GluvalGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 1 ICCCGGCAGCAGCAGCATCACTTTCAGTGGCTACTGGATCCCGGGTCCCAG 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ### ThrPheTyrLeuGlnWetAenSerLeuArgalaGluAspThrAlaValTyrTyrCysAla                                                                                                                                                                                                                                                                                              | 158 GlübrövalThrValSerTrpäsnSerGlyAläLeuThrSerGlyValHisThrPheBro 177  505 GCTGTCCTACAGGACTCTACTCCCTCAGGAGGGGGGGACCGTGCCCTCCAGG 564  178 AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSer 197  565 AGCTTGGGCACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAGGT 624  198 SerLeuGlyThrGlnThrTyrIleCysAanValAsnHisLySProSerAsnThrLysVal 217  525 GACAAGAAAGTGGAGCCCAAATCTTGTGACAAAACTCACAGTGCCCACGTGCCCAGGA 684  118 ASDLysLySValGluProLySSerCySASpLySThrHisThrCySProAla 237  685 CCTGAACTGGGGGGAGCGCAAATCTTCTCTTCTCTTCCCCCCAAAACCCAGGAACCCTC 744  118 ASDLysLySValGluProLySSerCySASpLySThrHisThrCySProProCySProAla 237  685 CCTGAACTGGGGGGACCGTGAGTCTTCCTCTTCCCCCAAAACCCAGGAACCCTC 744  119 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

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Sequence 2, Application US/09282505A
Patent No. 6194531
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: POLYPEPTIGE Variants
FILE REPERRICE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A

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CURRENT FILING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 45.1

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial Sequence
FEATURE:
COATR INFORMATION: Sequence is completely synthesized

Patent No. 6194551
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Patent No. 6242195
GENERAL INPORMATION:
FAPELICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFRENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
SEQ ID NO 2:
IENGTH: 451
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CRGANIGM: Artificial Sequence
FEATURE:
CTHER INFORMATION: E27 anti-1gE
US-09-054-255-2
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CTCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCTCATGATC 750                                                | 751 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 810                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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| Qy         1111 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACTACAAGACC 1170           Db         378 ProSerAspII=AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397           Qy         1171 ACGCCTCCCGTGGTGGACTCCGACGCTCTCTTCCTCTACAGCACCTCACGTGGAC 1230           Db         398 ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysSerUrkvalAsp 417           Qy         1231 AAGAGCAGGAGCAGGAGCTCTTCTCATGCTCGTGATGAGCTTCTGAC 1290           Qy         1231 AAGAGCAGGAAGCAGGAACCTCTTCTCATGCTCTGGAGCTTCTGGAC 1290           A18 LysSerAsgTrpGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnAshTs 437 | Oy 1291 AACCACTACACGCAGAAGAGCCTCTCCCGGGTPAA 1332<br> | RESULT 10<br>US-09-296-005-18<br>; Sequence 18, Application US/09296005<br>; Patent No. 6290957 | ; GENERAL INFORMATION:<br>; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe<br>; TITLE CF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides<br>; FILE PERERENTE. P1132017 | CURRENT APPLICATION NUMBER: US/09/296,005 CURRENT FILING DATE: 1999-04-21 ERRIER APPLICATION NUMBER: US 08/887,352 | MINNER OF SEQ ID NOS: 26   SEQ ID NOS: 26   SEQ ID NO 18   LENGTH: 451   TOTAL 451   TOT | ORGANISM: Artificial Sequence FEATURE: NAMEKEY: Artificial             | ; DOCALION: 1-451<br>; OTHER INFORMATION: Heavy chain sequence derived from MAE11<br>US-09-296-005-18 | Alignment Scores:  Alignment Scores:  Pred. No.:  2150.50  Matches:  Percent Similarity:  Best Local Similarity:  Best Match:  Alignment Similarity:  Best Match:  Alignment Similarity:  Best Match:  Alignment Similarity:  Alignme | OP-674-716B-18 (1-1335) x US-09-296-005-18 (1-451) | Oy 1 GAGGIGCAGCTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60 | Oy 61 TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAG 117 | Oy 118 GCTCCAGGGAAGGGCTCGAGTGGGTTGCTGAAATTAGAATTGAAATCTGATAATTATGCA 177 | AAAATCT<br>    :::<br>rLysAsn                     | Oy 238 AGACTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACA 297  Db 78 ThrPhefyrLeuGlinGetAssSerLeuArgalaGlinAspTrrCycala 97 | 298GAUTTCATAGACTGGGGCCAGGAACACTAGTC                                                     |

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AGGCCTCCCGTGCTCGACGCTCCTTCTTCTTCTTACAGCAAGCTCACCGTGGAC 1230
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                                                            AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG
                                                                                                                                                                                                                 GAGCAGTACAACAGCACGTACCGTGTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG
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CTCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAAACCCCAAGGACACCCTCATGATC
                                                                                                   TCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
                                                                                                                1291 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1332
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APPLICANT: BEORD Extraduese Idusogie et al.
TITLE OF INVENTION: POLYPEPTIGE Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION WUMBER: U3/09/680,145
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 09/282,505
PRIOR APPLICATION NUMBER: 09/282,505
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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US-09-680-145-2
; Sequence 2, Application US/09680145
; Patent No. 6538124
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NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INFORMATION: Sequence is
Patent No. 6538124
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ORGANISM: Artificial Sequence
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Pred. No.:
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                                                                                                                                                                 FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INPORMATION: Sequence is completely synthesized
Patent No. 6528624
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408
12
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Matches:
Conservative:
Mismatches:
Indels:
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                   APPLICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILLE REFERENCE: P1266R2
CURRENT APPLICATION NUMBER: US/09/282,846
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                    Gaps:
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2150.50
92.51%
89.87%
89.42%
                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
          GENERAL INFORMATION:
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; Patent No. 65:
US-09-282~846-2
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| Score   Similarity   92.51 | ArgdlySerHisTyrPhedlyHisTyrPhisPheAlavalTrpdlyGlnGlyThrLeuval ArgdlySerHisTyrPheGlyHisTyrPhisPheAlavalTrpdlyGlnGlyThrLeuval ArgdTySerHisTyrPheGlyHisTyrPhisPheAlavalTrpdlyGlnGlyThrLeuval ArgdTySerHisTyrPheGlyHisTyrPhisPheAlavalTrpdlyGlnGlyThrLeuval ThrValSerSerAlaSerThrLySGlyProSerValPheProLeuAlaProSerSerLyS AGCCTCTGGGGGCCCAGCGGCCCTGGCTGCTGCTGCAGGACTGCTTCCCGGACCG SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro GTGACGTGTCGTGGAACTCAGGCGCCTGGCTGGTAGGACTGCTTCCCGGACTG SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro GTGACGTGTCGTGGAACTCAGGCGCCTGACCAGGACTGCACCTTCCCGGACTGT ValThrValSerTrpAsnSerGlyAlaLeuGhrSerGlyValHisThrPheProGluVal Lin [ |

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TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT
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                                                                                                                                                                                                                                                                   APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CRESPONDENCES: ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: California
CCUNTRY: USA
                                                                                                             452
4407
114
33
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: OF COMPASIBLE WINDER: 
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                 1231 AAGAGCAGGTGGCAGCAGGGGAACGTCT
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Patent No. 6025158
GENERAL INFORMATION:
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2148.00
92.73%
89.65%
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SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
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Best Local Similarity:
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Pred. No.:
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                                  ACACATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCT 237
                                                                                                               238 AGACTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACA 297
                                                            238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetlle
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AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu---
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